Four Column Layout : : CHEAT SHEET

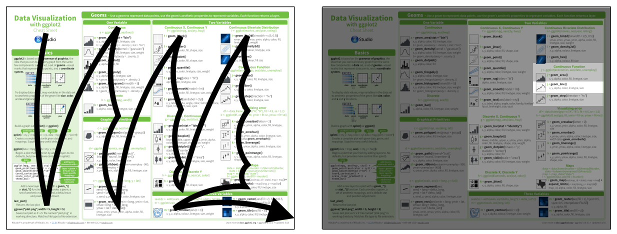
Basics

Thank you for making a new cheatsheet for R! These cheatsheets have an important job:

Cheatsheets make it easy for R users to look up useful information.

Remember that the best cheatsheets are **visual**—not written—documents. Whenever possible use visual elements to make it easier for readers to find the information they need.

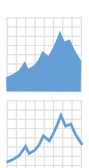
1. Use a **layout** that flows and makes it easy to zero in on specific topics.



2. Use **visualizations** to explain concepts quickly and concisely.

summary function

3. Use visual elements to make the sheet **scannable**.



i + geom_area()
x, y, alpha, color, fill, linetype, size

i + geom_line()
x, y, alpha, color, group, linetype, size

4. Use visual **emphasis** (like color, size, and font weight) to make important information easy to find.

dplyr::**lag()** - Offset elements by 1
dplyr::**lead()** - Offset elements by -1

Layout Suggestions

Use headers, colors, and/or backgrounds to **separate or group together sections**.

Section 1 | **Section 2** | **Section 3**

Create a visual hierarchy. Help users navigate the page with titles, subtitles, and subsubtitles

Title

SUBTITLE

SUBSUBTITLE

Fit sections to content. Try several different layouts.

Use numbers or arrows to link sections if the order/**flow** is confusing.

Quickly identify content with a **package hexsticker** (if available)

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Useful Elements

CODE

Where possible, use **code that works** when run.

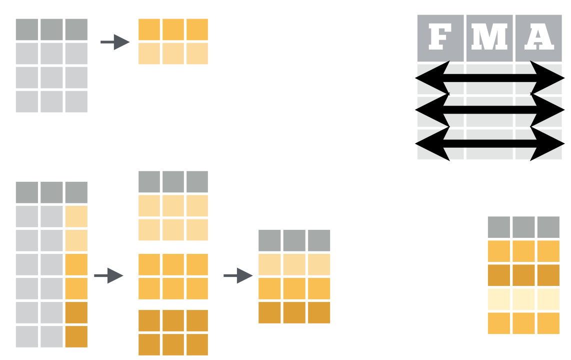
```
ggplot(mpg, aes(hwy, cty)) +
 geom_point(aes(size = fl)) +
 geom_smooth(method ="lm")
```

Word balloons | **can help explain** | **code**

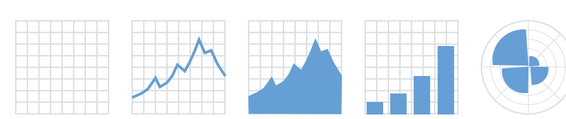
ICONS

These are just **font awesome** characters

MOCK TABLES



MOCK GRAPHS



TABLES

sub-option	description
citation_package	The LaTeX package to process
code_folding	Let readers to toggle the display of R
colortheme	Beamer color theme to use

Logistics

FONTS

This template uses several fonts: **Helvetica Neue, Menlo**, **Source Sans pro**, which you can acquire for free here, www.fontsquirrel.com/fonts/source-sans-pro, and **Font Awesome**, which you can acquire here, fortawesome.github.io/Font-Awesome/get-started/

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KEYNOTE

I make my cheatsheets in **Apple Keynote**, and not latex or R Markdown, because presentation software makes it much easier to tweak the visual appearance of a document

KEYNOTE TIPS

- **Select multiple elements** by holding down shift and then selecting each. Click on a selected element before letting go of shift to unselect it.
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YOUR LOGO
(optional)

Three Column Layout: : CHEAT SHEET

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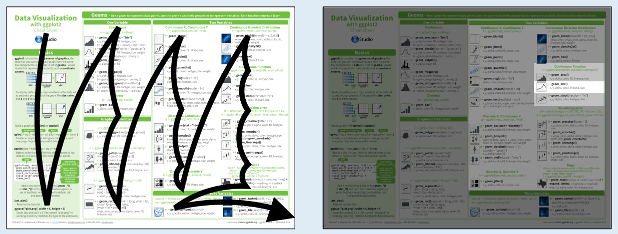

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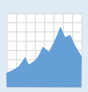

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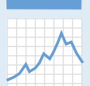

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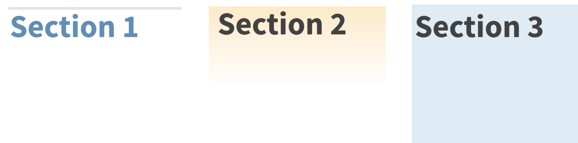

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Manipulate Variables

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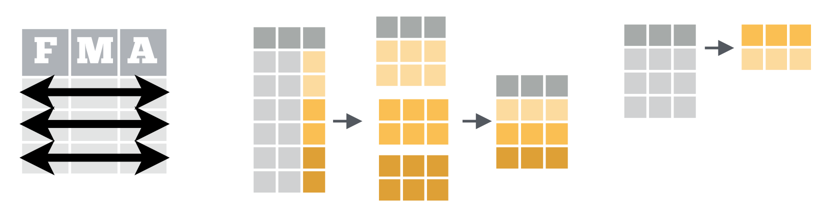

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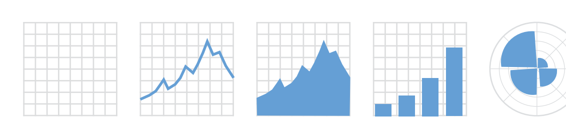

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Machine Learning Modelling in R : : CHEAT SHEET

Supervised & Unsupervised Learning

	ALGORITHM	DESCRIPTION	R PACKAGE::FUNCTION	SAMPLE CODE
SUPERVISED LEARNING	NBC Naïve Bayes classifier	A classification technique based on Bayes' Theorem with an assumption of independence among predictors. In simple terms, a Naive Bayes classifier assumes that the presence of a particular feature in a class is unrelated to the presence of any other feature	e1071::naiveBayes	`naiveBayes(class ~ ., data = x)`
SUPERVISED LEARNING	kNN k–Nearest Neighbours	A non-parametric method used for classification and regression. In both cases, the input consists of the k closest training examples in the feature space. The output depends on whether k-NN is used for classification or regression	class::knn	`knn(train, test, cl, k = 1, l = 0, prob = FALSE, use.all = TRUE)`
SUPERVISED LEARNING	REG Linear Regression	Model the linear relationship between a scalar dependant variable *Y* and one or more explanatory variables (or independent variables) denoted *X*	stats::lm	`lm(dist ~ speed, data=cars)`
SUPERVISED LEARNING	LREG Logistic Regression	Used to predict a binary outcome (1 / 0, Yes / No, True / False) given a set of independent variables.	stats::glm	`glm(Y ~ ., family = binomial (link = 'logit'), data = X)`
SUPERVISED LEARNING	TM Tree-Based Models	The idea is to consecutively divide (branch) the training dataset based on the input features until an assignment criterion with respect to the target variable into a "data bucket" (leaf) is reached	rpart::rpart	`rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)`
SUPERVISED LEARNING	ANN Artificial Neural Network	Neural networks are built from units called perceptrons. Perceptrons have one or more inputs, an activation function and an output. An ANN model is built up by combining perceptrons in structured layers.	neuralnet::neuralnet	`neuralnet(f,data=train_,hidden=c(5,3),linear.output=T)`
SUPERVISED LEARNING	SVM Support Vector Machine	A data classification method that separates data using hyperplanes	e1071::svm	`svm(formula, data = NULL, ..., subset, na.action = na.omit, scale = TRUE)`
UNSUPERVISED LEARNING	PCA Principal Component Analysis	A procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components.	stats::prcomp stats::princomp FactoMineR::PCA ade4::dudi.pca amap::acp	**stats** : `prcomp(formula, data = NULL, subset, na.action, ...)` **stats** : `princomp(formula, data = NULL, subset, na.action, ...)` **FactoMineR** : `PCA(decathlon, quanti.sup = 11:12, quali.sup=13)` **ade4 :** `dudi.pca(deug$tab, center = deug$cent, scale = FALSE, scan = FALSE)` **amap :** `acp(lubisch)`
UNSUPERVISED LEARNING	kMC k-Mean Clustering	Aims at partitioning *n* observations into *k* clusters in which each observation belongs to the cluster with the nearest mean	stats::kmeans	`kmeans(x, centers, iter.max = 10, nstart = 1, algorithm = c("Hartigan-Wong", "Lloyd", "Forgy", "MacQueen"), trace=FALSE)`
UNSUPERVISED LEARNING	HCL Hierarchical Clustering	An approach which builds a hierarchy from the bottom-up, and doesn't require the number of clusters to be specified beforehand.	stats::hclust	`hclust(d, method = "complete", members = NULL)`

Meta-Algorithm, Time Series & Model Validation

	ALGORITHM	DESCRIPTION	R PACKAGE::FUNCTION	SAMPLE CODE
META ALGORITHM	REGU Regularisation L1 (Lasso) L2 (Ridge)	Regularization adds a penalty on the different parameters of a model to reduce the freedom of the model. Hence, the model will be less likely to fit the noise of the training data and will improve the generalization abilities of the model	glmnet::glmnet	**L1 :** `glmnet(myMatrixA, myMatrixB , family = "gaussian", alpha = 1)` **L2 :** `glmnet(myMatrixA, myMatrixB , family = "gaussian", alpha = 0)`
META ALGORITHM	BOO Boosting	A process of iteratively refining, e.g. by reweighting, of estimated regression and classification functions (though it has primarily been applied to the latter), in order to improve predictive ability.	**Paramatric model** - mboost::glmboost	`glmboost(Yen ~ ., data = curr1[trnidxs,])`

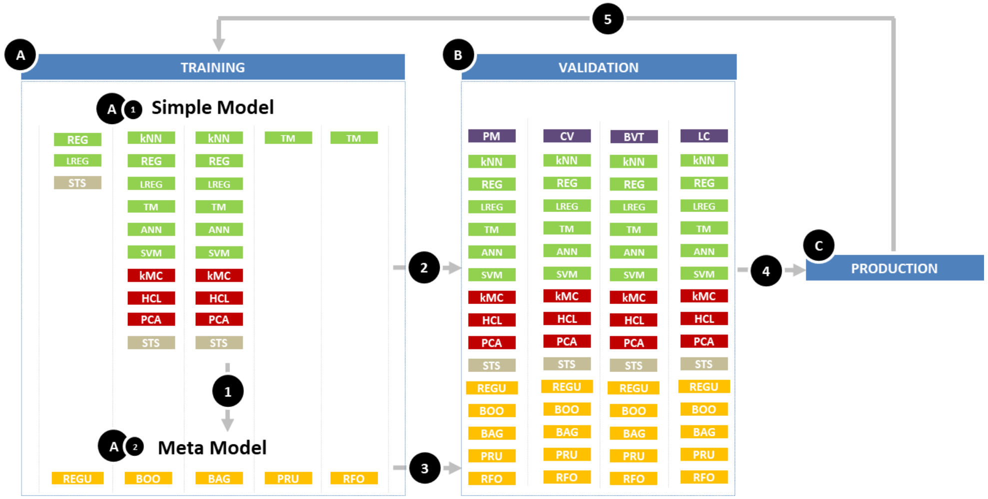
META ALGORITHM	BAG Bagging	Bagging is a way to increase the power of a predictive statistical model by taking multiple random samples (with replacement) of the training data set, and using each of them to construct a separate model and separate predictions for the original test set	**All models**: foreach
			Tree models: ipred::bagging
				foreach : `d <- data.frame(x=1:10, y=rnorm(10))`
				`s <- foreach(d=iter(d, by='row'), .combine=rbind) %dopar%d`
				`identical(s, d)`
				ipred : `bagging(formula, data, subset, na.action=na.rpart, \dots)`

META ALGORITHM	PRU Pruning	Pruning is a technique that reduces the size of decision tree by removing sections of the tree that provide little power to classify instances. Pruning reduces the complexity of the final classifier and hence improves predictive accuracy by reducing overfitting	rpart::prune	`prune(x, cp = 0.1)`
META ALGORITHM	RFO Random Forrest	An ensemble learning method for classification, regression and other tasks, that operate by constructing a multitude of decision trees at training time and outputting the class that is the mode of the classes (classification) or mean prediction (regression)	randomForest::randomForest	`randomForest(X ~ . , data = Y , subset = mySub)`
TIME SERIES	STS Lead-lag analysis, Auto-correlation, Spectral analysis, Time series clustering, Seasonality, Trend....	Random sampling of observations for training and testing a model can be an issue when faced with a times dimension. Random sampling may either destroy serial correlation properties in the data which we would like to exploit	stats xts forecast spectral TTR	**Auto-correlation**: `acf(x, lag.max = NULL, type = c("correlation", "covariance", "partial"))` **Spectral Analysis**: `spec.pgram(myTs, spans = NULL)` **Seasonal Decomposition of Time Series** - `stl(x, s.window = 7, t.window = 50, t.jump = 1)` ......

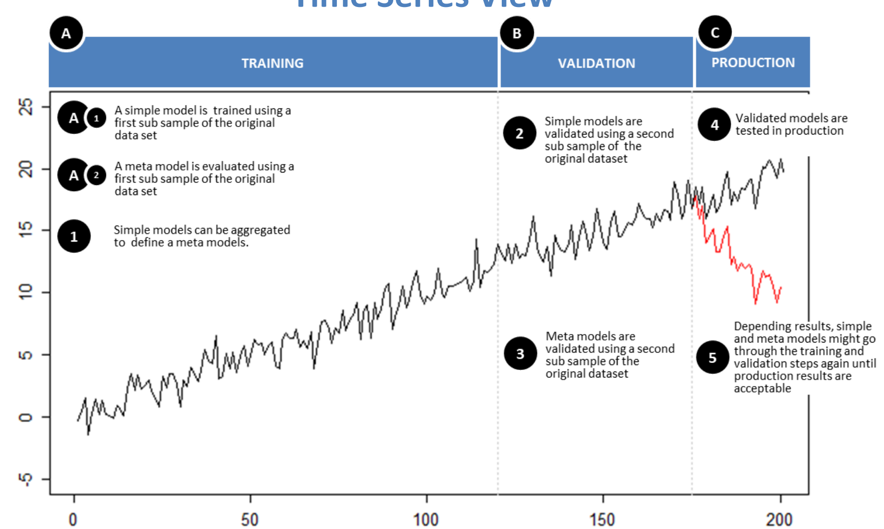
MODEL VALIDATION	PM Performance metrics	Depends on the problem:
		• **Regression**: squared errors, outliers, error rate...
		• **Classification**: Accuracy, precision, recall, F-score...
			Regression-stats::outlierTest, stats:: qqPlot ....
			Classification-ROCR::
			Tree: caret:: confusionMatrix
				Regresion: `fit <- lm(Y~X,data=myData)`
				`outlierTest(fit)`
				`qqPlot(fit, main="QQ Plot")`

MODEL VALIDATION	BVT Biais-Variance Tradeoff	• Simple models with few parameters are easier to compute but may lead to poorer fits (**high bias**). • Complex models may provide more accurate fits but may over-fit the data (**high variance**)	Tailored to the analysis	Tailored to the analysis
MODEL VALIDATION	CV Cross validation	Cross validation compares the test performances of different model realisations with different sets or values of parameters	caret::createDataPartition caret::createFolds	`createDataPartition(classes, p = 0.8, list = FALSE)`
MODEL VALIDATION	LC Learning Curves	Learning curves plot a model's training and test errors, or the chosen performance metric, depending on the training set size	caret:: learing_curve_dat	`learing_curve_dat(dat, outcome = NULL, proportion = (1:10)/10, test_prop = 0, verbose = TRUE, ...)`

Standard Modelling Workflow



Time Series View



 Arnaud Amsellem • thertrader@gmail.com • www.thertrader.com • Updated: 2018-03

SamplingStrata: : CHEAT SHEET

To install last available release:

```
library(devtools)
install_github("barcaroli/SamplingStrata")
```

Optimal stratification

Given a sampling frame, SamplingStrata allows to optimize its stratification when designing a sampling survey, given precision constraints on target estimates.

Three different methods

The optimization can be run by indicating three different methods, on the basis of the following:

A. if stratification variables are categorical (or reduced to) then the method is the "atomic";
B. if stratification variables are continuous, then the method is the "continuous";
C. if stratification variables are continuous, and there is spatial correlation among units in the sampling frame, then the required method is the "spatial".

A. Method "atomic"

Different steps:

1. define the sampling frame;
2. set precision constraints;
3. build atomic strata;
4. run optimization;
5. perform evaluation;
6. select the sample.

Sampling frame

Data on 2896 Swiss municipalities

```
library(SamplingStrata)
data("swissmunicipalities")
swissmunicipalities$id <-
      c(1:nrow(swissmunicipalities))
frame <- buildFrameDF(
          df = swissmunicipalities,
          id = "id",
          domainvalue = "REG",
          X = c("POPTOT","HApoly"),
          Y =c("Surfacesbois", "Airind"))
```

Stratification variables

Target variables

Precision constraints

```
ndom <-
length(unique(frame$domainvalue))
cv <- as.data.frame(list(
           DOM = rep("DOM1",ndom),
           CV1 = rep(0.10,ndom),
           CV2 = rep(0.10,ndom),
           domainvalue = c(1:ndom)))
```

10% of maximum expected CV

Atomic strata

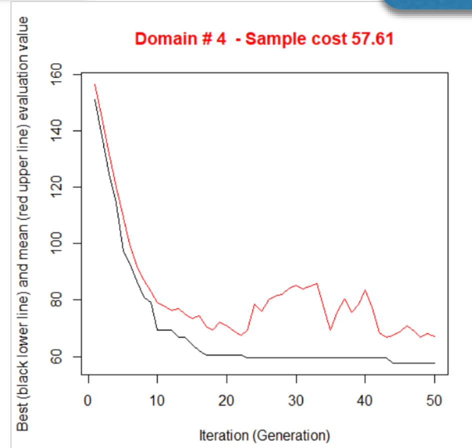
```
strata <- buildStrataDF(frame)
```

Optimization

```
solution <-
optimStrata(method="atomic",
            framesamp = frame,
            errors = cv,
            iter = 50,
            pops = 10)
```

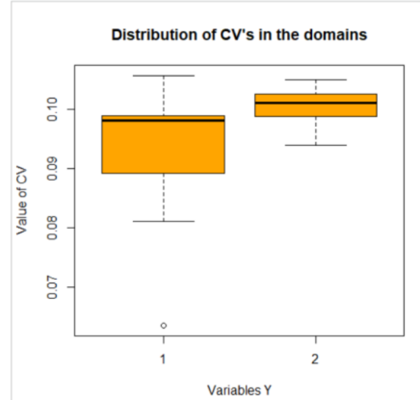
Number of iterations

Number of solutions per iteration



Evaluation

```
outstrata <- solution$aggr_strata
framenew <- solution$framenew
eval <- evalSolution(framenew,outstrata)
eval$coeff_var
```



Sample selection

```
s <- selectSample(framenew,outstrata)
head(s)
```

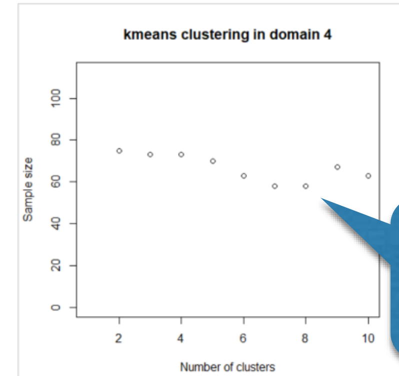
	DOMAINVALUE	STRATO	ID	X1	X2	Y1	Y2	LABEL	WEIGHTS
1	1	1	2398	241	294	101	0	1	21.38462
2	1	1	2331	267	449	215	1	1	21.38462
3	1	1	2410	237	935	471	0	1	21.38462
4	1	1	2112	370	330	98	0	1	21.38462
5	1	1	2563	173	178	16	0	1	21.38462
6	1	1	2091	382	594	338	0	1	21.38462

B. Method "continuous"

Same steps with the exception of strata building, not necessary.
Frame definition and precision constraints settings are done in the same way than in method "atomic".
One more step is in determination of the most promising number of strata with kmeans clustering.

Kmeans clustering

```
kmean <- KmeansSolution2(frame=frame,
                errors=cv,
                maxclusters = 10)
nstrat <- tapply(kmean$suggestions,
                 kmean$domainvalue,
                 FUN=function(x)
                     length(unique(x)))
sugg <- prepareSuggestion(
             kmean = kmean,
             frame = frame,
             nstrat = nstrat)
```

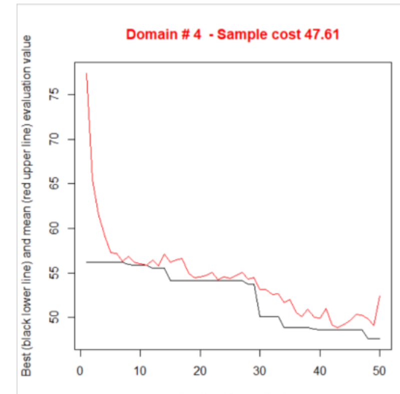


Suggested number of strata (8) for domain 4

Optimization

```
solution <- optimStrata (
             method = "continuous",
             framesamp = frame,
             errors = cv,
             nStrata = nstrat,
             iter = 50,
             pops = 10,
             suggestions = sugg)
```

Suggestion prepared by kmeans clustering



Evaluation

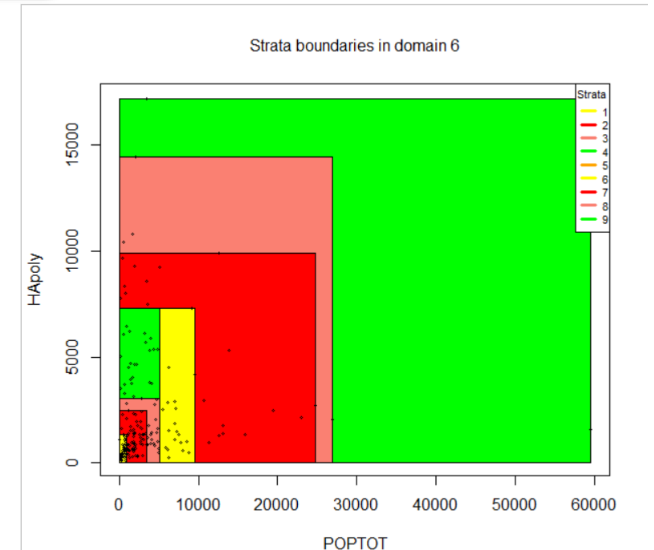
```
framenew <- solution$framenew
outstrata <- solution$aggr_strata
ss <-summaryStrata(framenew,outstrata)
head(ss)
```

	Domain	Stratum	Population	Allocation	SamplingRate
1	1	1	278	13	0.047370
2	1	2	49	6	0.113769
3	1	3	70	5	0.070377
4	1	4	69	10	0.145075
5	1	5	33	6	0.173466
6	1	6	22	9	0.424133

	Lower_X1	Upper_X1	Lower_X2	Upper_X2
1	27	780	32	986
2	65	1422	48	1018
3	95	1562	198	2288
4	78	1963	159	11907
5	1992	2711	107	8925
6	2759	3567	185	11378

```
plotStrata2d(framenew,
             outstrata,
             domain = 6,
             vars = c("X1","X2"),
      labels = c("POPTOT", "HApoly"))
```

Visualization of strata by couples of X's




```
eval <-
evalSolution(framenew,outstrata)
eval$coeff_var
```

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C. Method "spatial"

In cases where units in the sampling frame are geo-referenced and there is spatial correlation among them, it is possible to apply the "spatial" method in the optimization of the frame stratification.

Different steps:

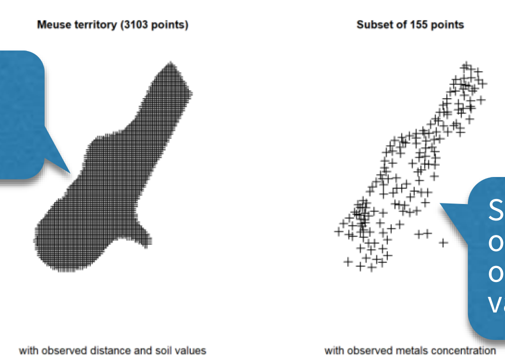
1. perform a preliminary spatial analysis and fit spatial models on target variables
2. define the sampling frame and add predicted values, prediction errors and coordinates;
3. set precision constraints;
4. run optimization;
5. select the sample.

Spatial analysis

We make use of the «Meuse river» datasets, reporting measures of 4 metals concentration.

```
library(sp)
# locations (155 observed points)
data("meuse")
# grid of points (3103)
data("meuse.grid")
meuse.grid$id <- c(1:nrow(meuse.grid))
coordinates(meuse)<-c('x','y')
coordinates(meuse.grid)<-c('x','y')
```

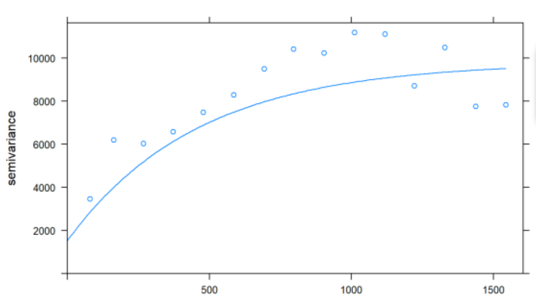
Grid of Meuse river



Sample of observed values

```
library(gstat)
library(automap)
v <- variogram(lead~dist+soil,data=meuse)
fit.vgm.lead <- autofitVariogram(
       lead ~dist+soil,meuse,model="Exp")
plot(v, fit.vgm.lead$var_model)
```

Analysis and fitting



prediction

```
lead.kr <- krige(lead~dist+soil,
          meuse, meuse.grid,
          model=fit.vgm.lead$var_model)
lead.pred <- ifelse(lead.kr[1]$var1.pred<0,
                    0,lead.kr[1]$var1.pred)
lead.var <- ifelse(lead.kr[2]$var1.var < 0,
                    0,lead.kr[2]$var1.var)
```

Sampling frame

```
df <- as.data.frame(list(
       dom=rep(1,nrow(meuse.grid)),
       lead.pred=lead.pred,
       lead.var=lead.var,
       lon=meuse.grid$x,
       lat=meuse.grid$y,
       id=c(1:nrow(meuse.grid))))
frame <- buildFrameSpatial(df=df,
           id="id",
           X=c("lead.pred"),
           Y=c("lead.pred"),
           variance=c ("lead.var"),
           lon="lon",
           lat="lat",
           domainvalue = "dom")
```

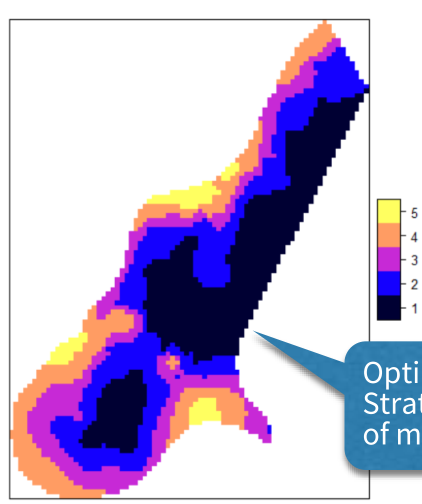
Precision constraints

```
cv2 <- as.data.frame(list(
        DOM=rep("DOM1",1),
        CV1=rep(0.05,1),
        domainvalue=c(1:1) ))
```

Optimization

```
solution <- optimStrata(method="spatial",
   errors=cv2, framesamp=frame, iter=25,
   nStrata=5, fitting=1, kappa=1,
   range=fit.vgm.lead$var_model$range[2])
```

```
framenew <- solution$framenew
outstrata <- solution$aggr_strata
frameres <- SpatialPixelsDataFrame(
     points=framenew[c("LON","LAT")],
     data=framenew)
frameres$LABEL <-
     as.factor(frameres$LABEL)
spplot(frameres,c("LABEL"),
       col.regions=bpy.colors(5))
```



Optimal Stratification of meuse.grid

Use of models

Usually, values of target variables are not available in sampling frames, but only of co-variates. In order to calculate correctly the variance of target variables in strata, we can make use of models. When applying methods 'atomic' and 'continuous', it possible to declare linear or log-linear models linking each target variable to one co-variate available in the sampling frame.

Consider the case with 'swissmunicipalities' dataset. Suppose that for all units we only have values for POPTOT and HApoly, while only on a subset (500) of it the values for Surfacesbois and Airbat are also available.
We fit the following models:

```
k <- sample(c(1:2896),500)
s <- swissmunicipalities[k,]
Airind_POPTOT <-
   lm(Airind~POPTOT, data=s)
Bois_HApoly <-
   lm(Surfacesbois~HApoly,data=s)
```

For both models we calculate heteroscedasticity indexes and variance:

```
airind <-
computeGamma(Airind_POPTOT$residuals,
                 s$POPTOT,nbins = 14)
airind
# gamma     sigma  r.square
# 0.59235109 0.06794055 0.87070106
bois <-
computeGamma(Bois_HApoly$residuals,
                 s$HApoly,nbins = 14)
bois
# gamma     sigma  r.square
# 0.8547931 0.4483606 0.9732122 )
```

We can now instantiate the values in the 'model' dataframe:

```
model <- NULL
model$beta[1] <-
      Airind_POPTOT$coefficients[2]
model$sig2[1] <- airind[2]^2
model$type[1] <- "linear"
model$gamma[1] <- airind[1]
model$beta[2] <-
      Bois_HApoly$coefficients[2]
model$sig2[2] <- bois[2]^2
model$type[2] <- "linear"
model$gamma[2] <- bois[1]
model <- as.data.frame(model)
model
# beta        sig2      type   gamma
# 0.01109583 0.1708807 linear 0.4703953
# 0.26068155 0.2010272 linear 0.8547931
```

Sampling frame

```
frame <- buildFrameDF(
                 df=swissmunicipalities,
                 id="id",
                 X=c("POPTOT","HApoly"),
                 Y=c("POPTOT","HApoly"),
                 domainvalue = "REG")

frame$airind <-
  swissmunicipalities$Airind
frame$surfacesbois <-
  swissmunicipalities$Surfacesbois
```

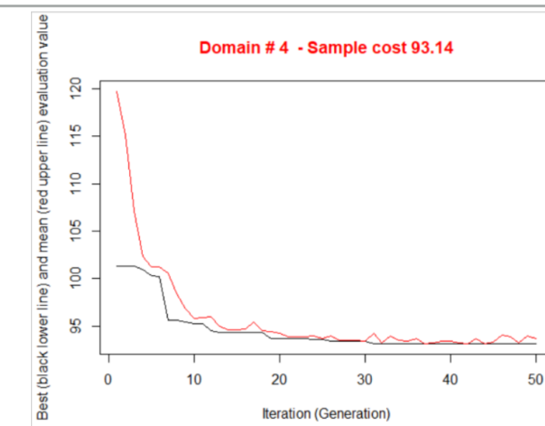
Co-variates as both X's and Y's

Optimization

With the same precision constraints of 10% for both target variables we run the optimization step:

```
solution <-
  optimStrata(
    method = "continuous",
    errors = cv,
    framesamp = frame,
    model = model,
    nStrata = rep(5,7),
    iter = 50,
    pops = 10)
```

'model' dataframe previously defined



Evaluation

```
framenew <- solution$framenew
outstrata <- solution$aggr_strata
framenew$Y3 <- framenew$AIRIND
framenew$Y4 <- framenew$SURFACESBOIS
val <- evalSolution(framenew,outstrata)
val$coeff_var
# CV1    CV2    CV3    CV4   dom
# 0.0107 0.0706 0.0316 0.0603 DOM1
# 0.0073 0.0364 0.0220 0.0426 DOM2
# 0.0062 0.0252 0.0253 0.0332 DOM3
# 0.0071 0.0328 0.0303 0.0572 DOM4
# 0.0055 0.0646 0.0171 0.0541 DOM5
# 0.0037 0.0745 0.0173 0.0606 DOM6
# 0.0036 0.0753 0.0145 0.0541 DOM7
```

Notice that both the CV's of the co-variates (CV1 and CV2) andthe CV's of the real target variables (CV3 and CV4) are compliant to the 10% precision constraints.

Base R
Cheat Sheet

Getting Help

Accessing the help files

?mean
Get help of a particular function.

help.search('weighted mean')
Search the help files for a word or phrase.

help(package = 'dplyr')
Find help for a package.

More about an object

str(iris)
Get a summary of an object's structure.

class(iris)
Find the class an object belongs to.

Using Packages

install.packages('dplyr')
Download and install a package from CRAN.

library(dplyr)
Load the package into the session, making all its functions available to use.

dplyr::select
Use a particular function from a package.

data(iris)
Load a built-in dataset into the environment.

Working Directory

getwd()
Find the current working directory (where inputs are found and outputs are sent).

setwd('C://file/path')
Change the current working directory.

Use projects in RStudio to set the working directory to the folder you are working in.

Vectors

Creating Vectors

c(2, 4, 6)	2 4 6	Join elements into a vector
2:6	2 3 4 5 6	An integer sequence
seq(2, 3, by=0.5)	2.0 2.5 3.0	A complex sequence
rep(1:2, times=3)	1 2 1 2 1 2	Repeat a vector
rep(1:2, each=3)	1 1 1 2 2 2	Repeat elements of a vector

Vector Functions

sort(x)
Return x sorted.

rev(x)
Return x reversed.

table(x)
See counts of values.

unique(x)
See unique values.

Selecting Vector Elements

By Position

x[4]	The fourth element.
x[-4]	All but the fourth.
x[2:4]	Elements two to four.
x[-(2:4)]	All elements except two to four.
x[c(1, 5)]	Elements one and five.

By Value

x[x == 10]	Elements which are equal to 10.
x[x < 0]	All elements less than zero.
x[x %in% c(1, 2, 5)]	Elements in the set 1, 2, 5.

Named Vectors

x['apple']	Element with name 'apple'.

Programming

For Loop

```
for (variable in sequence){
   Do something
}
```

Example

```
for (i in 1:4){
   j <- i + 10
   print(j)
}
```

While Loop

```
while (condition){
   Do something
}
```

Example

```
while (i < 5){
   print(i)
   i <- i + 1
}
```

If Statements

```
if (condition){
   Do something
} else {
   Do something different
}
```

Example

```
if (i > 3){
   print('Yes')
} else {
   print('No')
}
```

Functions

```
function_name <- function(var){
   Do something
   return(new_variable)
}
```

Example

```
square <- function(x){
   squared <- x*x
   return(squared)
}
```

Reading and Writing Data

Also see the **readr** package.

Input	Ouput	Description
df <- read.table('file.txt')	write.table(df, 'file.txt')	Read and write a delimited text file.
df <- read.csv('file.csv')	write.csv(df, 'file.csv')	Read and write a comma separated value file. This is a special case of read.table/write.table.
load('file.RData')	save(df, file = 'file.Rdata')	Read and write an R data file, a file type special for R.

Conditions

a == b	Are equal	a > b	Greater than	a >= b	Greater than or equal to	is.na(a)	Is missing
a != b	Not equal	a < b	Less than	a <= b	Less than or equal to	is.null(a)	Is null

Types

Converting between common data types in R. Can always go from a higher value in the table to a lower value.

`as.logical`	`TRUE, FALSE, TRUE`	Boolean values (TRUE or FALSE).
`as.numeric`	`1, 0, 1`	Integers or floating point numbers.
`as.character`	`'1', '0', '1'`	Character strings. Generally preferred to factors.
`as.factor`	`'1', '0', '1', levels: '1', '0'`	Character strings with preset levels. Needed for some statistical models.

Maths Functions

`log(x)`	Natural log.	`sum(x)`	Sum.
`exp(x)`	Exponential.	`mean(x)`	Mean.
`max(x)`	Largest element.	`median(x)`	Median.
`min(x)`	Smallest element.	`quantile(x)`	Percentage quantiles.
`round(x, n)`	Round to n decimal places.	`rank(x)`	Rank of elements.
`signif(x, n)`	Round to n significant figures.	`var(x)`	The variance.
`cor(x, y)`	Correlation.	`sd(x)`	The standard deviation.

Variable Assignment

```
> a <- 'apple'
> a
[1] 'apple'
```

The Environment

`ls()`	List all variables in the environment.
`rm(x)`	Remove x from the environment.
`rm(list = ls())`	Remove all variables from the environment.

You can use the environment panel in RStudio to browse variables in your environment.

Matrices

`m <- matrix(x, nrow = 3, ncol = 3)`
Create a matrix from x.

`m[2, ]` - Select a row

`m[ , 1]` - Select a column

`m[2, 3]` - Select an element

`t(m)`
Transpose

`m %*% n`
Matrix Multiplication

`solve(m, n)`
Find x in: m * x = n

Lists

`l <- list(x = 1:5, y = c('a', 'b'))`
A list is a collection of elements which can be of different types.

`l[[2]]`	`l[1]`	`l$x`	`l['y']`
Second element of l.	New list with only the first element.	Element named x.	New list with only element named y.

Also see the **dplyr** package.

Data Frames

`df <- data.frame(x = 1:3, y = c('a', 'b', 'c'))`
A special case of a list where all elements are the same length.

x	y
1	a
2	b
3	c

List subsetting

`df$x` `df[[2]]`

Understanding a data frame

`View(df)` See the full data frame.

`head(df)` See the first 6 rows.

Matrix subsetting

`df[ , 2]`

`df[2, ]`

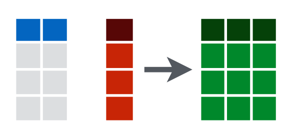
`df[2, 2]`

`nrow(df)`
Number of rows.

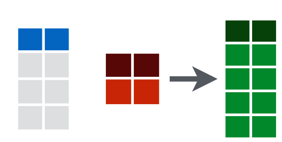
`ncol(df)`
Number of columns.

`dim(df)`
Number of columns and rows.

cbind - Bind columns.



rbind - Bind rows.



Strings

Also see the **stringr** package.

`paste(x, y, sep = ' ')`	Join multiple vectors together.
`paste(x, collapse = ' ')`	Join elements of a vector together.
`grep(pattern, x)`	Find regular expression matches in x.
`gsub(pattern, replace, x)`	Replace matches in x with a string.
`toupper(x)`	Convert to uppercase.
`tolower(x)`	Convert to lowercase.
`nchar(x)`	Number of characters in a string.

Factors

`factor(x)`
Turn a vector into a factor. Can set the levels of the factor and the order.

`cut(x, breaks = 4)`
Turn a numeric vector into a factor by 'cutting' into sections.

Statistics

`lm(y ~ x, data=df)`
Linear model.

`glm(y ~ x, data=df)`
Generalised linear model.

`summary`
Get more detailed information out a model.

`t.test(x, y)`
Perform a t-test for difference between means.

`pairwise.t.test`
Perform a t-test for paired data.

`prop.test`
Test for a difference between proportions.

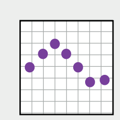
`aov`
Analysis of variance.

Distributions

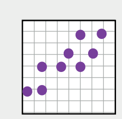
	Random Variates	Density Function	Cumulative Distribution	Quantile
Normal	`rnorm`	`dnorm`	`pnorm`	`qnorm`
Poisson	`rpois`	`dpois`	`ppois`	`qpois`
Binomial	`rbinom`	`dbinom`	`pbinom`	`qbinom`
Uniform	`runif`	`dunif`	`punif`	`qunif`

Plotting

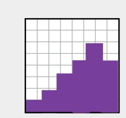
Also see the **ggplot2** package.



`plot(x)`
Values of x in order.



`plot(x, y)`
Values of x against y.



`hist(x)`
Histogram of x.

Dates

See the **lubridate** package.

Bayesplot :: CHEAT SHEET

```r
library("bayesplot")
library("rstanarm")
options(mc.cores = parallel::detectCores())
library("ggplot2")
library("dplyr")
```

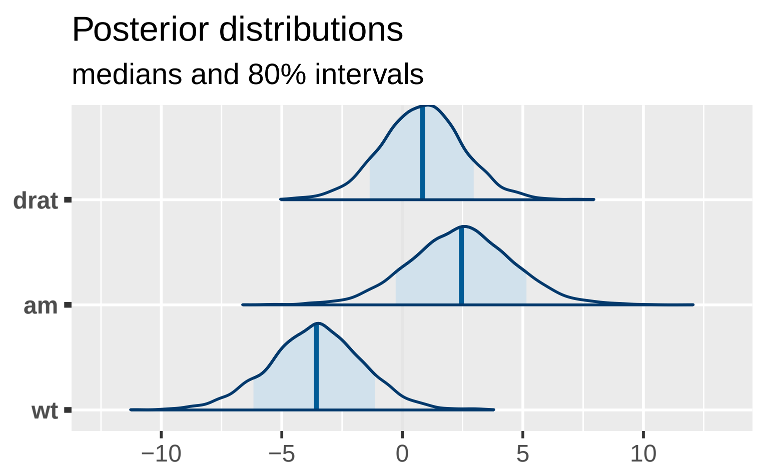
Model Parameters

To showcase bayesplot, we'll fit linear regression using `rstanarm::stan_glm` and use this model throughout.

```r
model <- stan_glm(mpg ~ ., data=mtcars, chains=4)
posterior <- as.matrix(model)
```

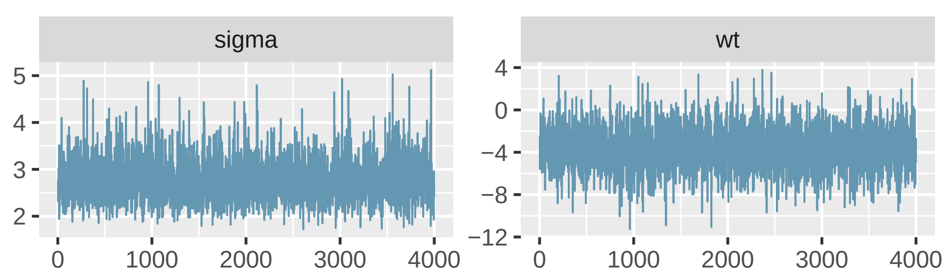
Chances are good you're most interested in the posterior distributions for select parameters.

```r
plot_title <- ggtitle("Posterior distributions",
                      "medians and 80% intervals")
mcmc_areas(posterior,
           pars = c("drat", "am", "wt"),
           prob = 0.8) + plot_title
```



Diagnosing convergence with traceplots is simple.

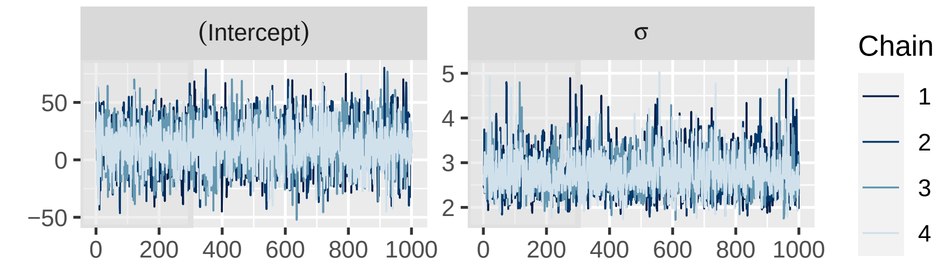
```r
mcmc_trace(posterior, pars=c("sigma", "wt"))
```



Using `as.array`, you can extract each of the four chain's posterior draws, different from above. This allows you to see each chain's traceplot for selected parameters.

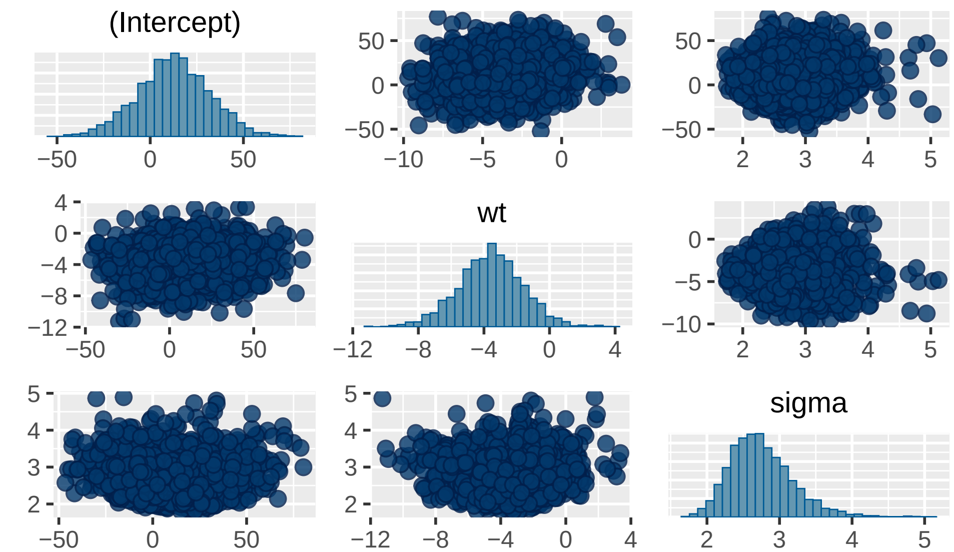
```r
posterior_chains <- as.array(model)
fargs <- list(ncol = 2, labeller = label_parsed)
pars <- c("(Intercept)", "sigma")
chains_trace <- mcmc_trace(posterior_chains, pars = pars,
                           n_warmup = 300, facet_args = fargs)
```

```r
chains_trace
```



The pairs plot is helpful in determining if you have any highly correlated parameters.

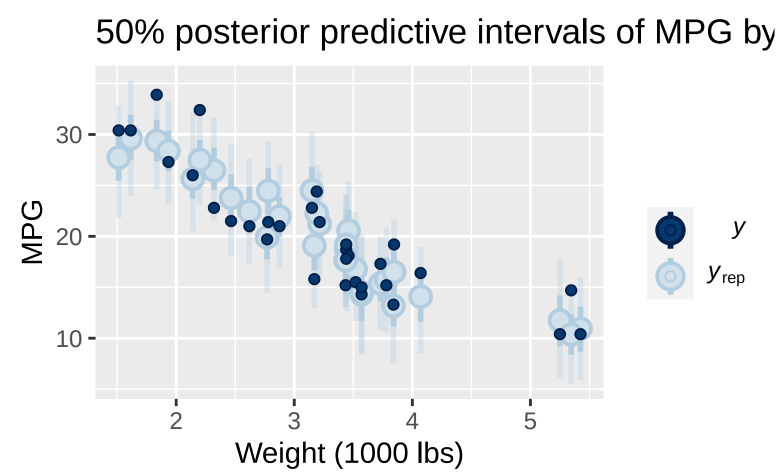
```r
posterior_chains %>%
  mcmc_pairs(pars = c("(Intercept)", "wt", "sigma"))
```



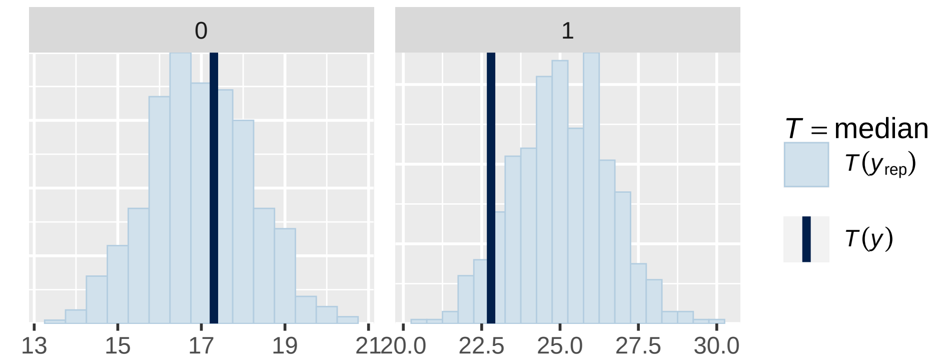
Posterior Predictive Checks

Check how well the model covers your data with draws from the posterior predictive density.

```r
ppd <- posterior_predict(model, draws=500)
ppd %>%
  ppc_intervals(y = mtcars$mpg, yrep = ., x = mtcars$wt, prob = 0.5) +
  labs(x = "Weight (1000 lbs)", y = "MPG",
    title = "50% posterior predictive intervals of MPG by weight")
```



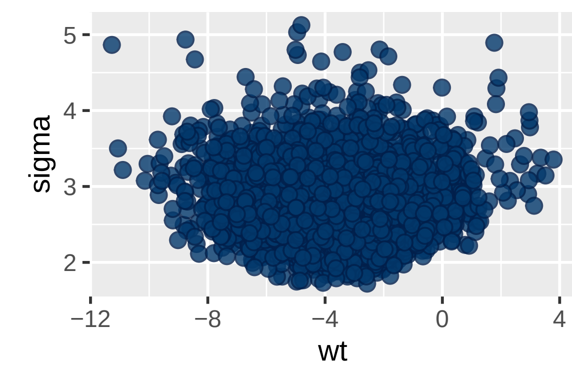

```r
ppd %>%
    ppc_stat_grouped(y = mtcars$mpg,  group = mtcars$am,
                     stat = "median", binwidth=0.5)
```



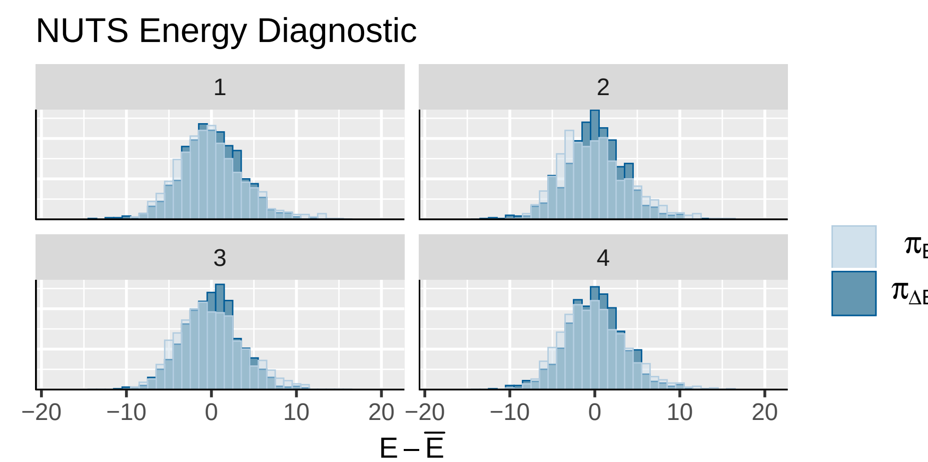
Diagnostics

Bayesplot makes it easy to check diagnostics specific to the NUTS sampling method that `rstanarm` uses by default.

```r
mcmc_scatter(posterior, pars = c("wt", "sigma"),
  np = nuts_params(model$stanfit))
```




```r
np <- nuts_params(model$stanfit)
mcmc_nuts_energy(np, binwidth=1) +
    ggtitle("NUTS Energy Diagnostic")
```



BCEA : : CHEAT SHEET

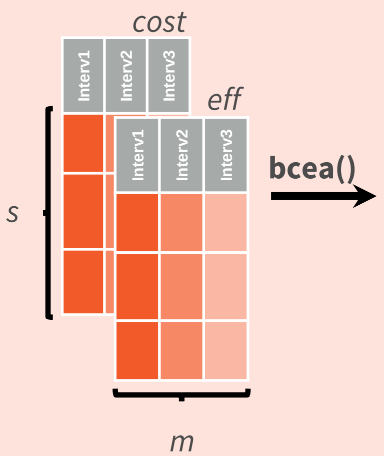
Introduction

Bayesian Cost-Effectiveness Analysis in R

Given a random sample of suitable variables of costs (*cost*) and clinical benefits (*eff*) for two or more interventions produces a health economic evaluation. Inputs may be the results of a Bayesian model (possibly based on MCMC) in the form of simulations from the posterior distributions. For *s* sample points compares one of the *m* interventions (*ref*erence) to the others (*.comparison*).

bcea(eff, cost, ref, .comparison, interventions)

INPUT ARRAY PAIR



CONSTITUENT FUNCTIONS

compute_U() : Expected utility for each WTP & intervention
compute_Ustar() : Maximum 'known-distribution' utility for each WTP
compute_vi() : Value of information for each WTP
compute_ol() : Opportunity Loss for each WTP
compute_ICER() : Incremental cost-effectiveness ratio
compute_IB() : Incremental benefit for each WTP
compute_CEAC() : Cost-effectiveness acceptability for each WTP
compute_EIB() : Expected incremental benefit for each WTP
compute_kstar() : WTP break-even value

bcea() calculates numerous cost-effectiveness analysis statistics. These can be called directly, using the constituent functions, but would require some pre-processing which is already handled by **bcea().**

Plot

Standard cost-effectiveness analysis output plots. Base R, ggplot2 and plotly versions of plots are available and can be called directly but require extra default parameters.

Expected incremental benefit

eib.plot(he, comparison = NULL, pos = c(1, 0), size = NULL, plot.cri = NULL, graph = c("base", "ggplot2", "plotly"), ...)
calls: • **eib_plot_base()**
• **eib_plot_ggplot()**
• **eib_plot_plotly()**

Expected value of information

evi.plot(he, graph = c("base", "ggplot2", "plotly"), ...)

Cost-effectiveness planes with contours

contour[2](he, comparison = 1, scale = 0.5, nlevels = 4, levels = NULL, pos = c(1, 0), xlim = NULL, ylim = NULL, graph = c("base", "ggplot2"), ...)

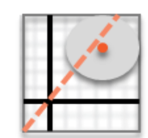
Compare optimal scenario to mixed case

plot.mixedAn(x, y.limits = NULL, pos = c(0, 1), graph = c("base", "ggplot2"), ...)

Cost-effectiveness acceptability curve

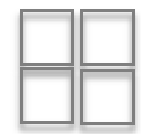
ceac_plot(he, comparison = NULL, pos = c(1, 0), graph = c("base", "ggplot2", "plotly"), ...)
calls: • **ceac_plot_base()**
• **ceac_plot_ggplot()**
• **ceac_plot_plotly()**

Cost-effectiveness plane



ceplane_plot(he, comparison = NULL, pos = c(1, 0), graph = c("base", "ggplot2", "plotly"), ...)
calls: • **ceplane_plot_base()**
• **ceplane_plot_ggplot()**
• **ceplane_plot_plotly()**

Grid of CE plane, EIB, EVI & CEAC



plot.bcea(x, comparison = NULL, pos = c(1, 0), graph = c("base", "ggplot2", "plotly"), ...)

Expected value of perfect partial information

plot.evppi(x, pos = c(0, 0.8), graph = c("base", "ggplot2"), col = NULL, ...)

Value assignment

There are 3 equivalent ways to assign values to analysis parameters.

1. *In Constructor*: When first creating a bcea object.

   he <- **bcea**(eff, cost, ref, .comparison, ...)

2. *Using Setters*: Change directly using replacement functions.

   setComparison(he) <- comparison
   setKmax(he) <- Kmax
   setReference(he) <- ref

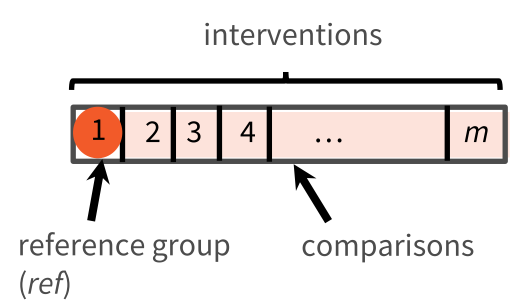
3. *In plotting call*: At the point of making a plot.

   eib.plot(he, comparison, ...)
   ceac.plot(he, comparison, ...)
   ceplane.plot(he, comparison, ...)

SELECTING ANALYSIS INTERVENTIONS

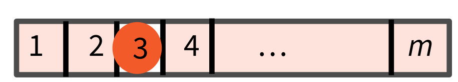
Default

The first columns in (*eff*, *cost*) are the default reference intervention. All other interventions are the comparison interventions unless defined otherwise. E.g. for *m* interventions



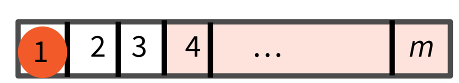
Set reference

Changing the reference group keeps all the other groups as comparison groups e.g. changing to reference group 3



Set comparisons

Changing the comparison groups keeps the reference group the same e.g. changing to comparison groups 4 to *m*



Summarise data

Summary statistics and formatted tables can be used to interrogate a **bcea**() object.

summary.bcea(he, ...)
Prints a table with summary results of the health economic evaluation

summary.mixedAn(he, ...)
Prints summary table for results of mixed analysis

sim.table(he, ...)
Summary table of simulations from the cost-effectiveness analysis

make.report(he, ...)
Constructs the automated report from the output of the BCEA

caret Package
Cheat Sheet

Specifying the Model

Possible syntaxes for specifying the variables in the model:

```
train(y ~ x1 + x2, data = dat, ...)
train(x = predictor_df, y = outcome_vector, ...)
train(recipe_object, data = dat, ...)
```

- `rfe`, `sbf`, `gafs`, and `safs` only have the `x/y` interface.
- The `train` formula method will **always** create dummy variables.
- The `x/y` interface to `train` will not create dummy variables (but the underlying model function might).

Remember to:

- Have column names in your data.
- Use factors for a classification outcome (not 0/1 or integers).
- Have valid R names for class levels (not "0"/"1")
- Set the random number seed prior to calling `train` repeatedly to get the same resamples across calls.
- Use the `train` option `na.action = na.pass` if you will being imputing missing data. Also, use this option when predicting new data containing missing values.

To pass options to the underlying model function, you can pass them to `train` via *the ellipses*:

```
train(y ~ ., data = dat, method = "rf",
      # options to `randomForest`:
      importance = TRUE)
```

Parallel Processing

The `foreach` package is used to run models in parallel. The `train` code does not change but a "`do`" package must be called first.

```
# on MacOS or Linux
library(doMC)
registerDoMC(cores=4)
```

```
# on Windows
library(doParallel)
cl <- makeCluster(2)
registerDoParallel(cl)
```

The function `parallel::detectCores` can help too.

Preprocessing

Transformations, filters, and other operations can be applied to the *predictors* with the `preProc` option.

```
train(, preProc = c("method1", "method2"), ...)
```

Methods include:

- `"center"`, `"scale"`, and `"range"` to normalize predictors.
- `"BoxCox"`, `"YeoJohnson"`, or `"expoTrans"` to transform predictors.
- `"knnImpute"`, `"bagImpute"`, or `"medianImpute"` to impute.
- `"corr"`, `"nzv"`, `"zv"`, and `"conditionalX"` to filter.
- `"pca"`, `"ica"`, or `"spatialSign"` to transform groups.

`train` determines the order of operations; the order that the methods are declared does not matter.

The `recipes` package has a more extensive list of preprocessing operations.

Adding Options

Many `train` options can be specified using the `trainControl` function:

```
train(y ~ ., data = dat, method = "cubist",
      trControl = trainControl(<options>))
```

Resampling Options

`trainControl` is used to choose a resampling method:

```
trainControl(method = <method>, <options>)
```

Methods and options are:

- `"cv"` for K-fold cross-validation (`number` sets the # folds).
- `"repeatedcv"` for repeated cross-validation (`repeats` for # repeats).
- `"boot"` for bootstrap (`number` sets the iterations).
- `"LGOCV"` for leave-group-out (`number` and `p` are options).
- `"LOO"` for leave-one-out cross-validation.
- `"oob"` for out-of-bag resampling (only for some models).
- `"timeslice"` for time-series data (options are `initialWindow`, `horizon`, `fixedWindow`, and `skip`).

Performance Metrics

To choose how to summarize a model, the `trainControl` function is used again.

```
trainControl(summaryFunction = <R function>,
             classProbs = <logical>)
```

Custom R functions can be used but `caret` includes several: `defaultSummary` (for accuracy, RMSE, etc), `twoClassSummary` (for ROC curves), and `prSummary` (for information retrieval). For the last two functions, the option `classProbs` must be set to TRUE.

Grid Search

To let `train` determine the values of the tuning parameter(s), the `tuneLength` option controls how many values **per tuning** parameter to evaluate.

Alternatively, specific values of the tuning parameters can be declared using the `tuneGrid` argument:

```
grid <- expand.grid(alpha = c(0.1, 0.5, 0.9),
                    lambda = c(0.001, 0.01))

train(x = x, y = y, method = "glmnet",
      preProc = c("center", "scale"),
      tuneGrid = grid)
```

Random Search

For tuning, `train` can also generate random tuning parameter combinations over a wide range. `tuneLength` controls the total number of combinations to evaluate. To use random search:

```
trainControl(search = "random")
```

Subsampling

With a large class imbalance, `train` can subsample the data to balance the classes them prior to model fitting.

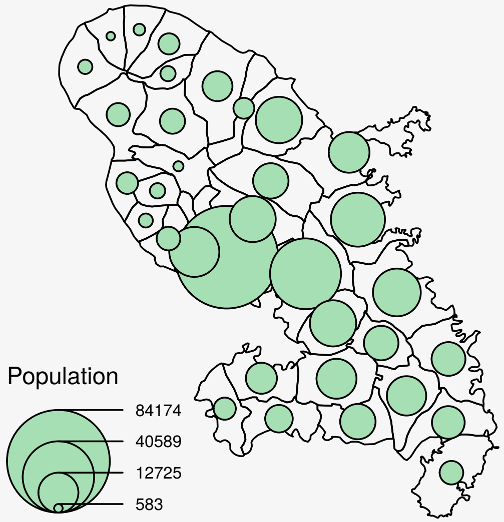
```
trainControl(sampling = "down")
```

Other values are `"up"`, `"smote"`, or `"rose"`. The latter two may require additional package installs.

Thematic maps with cartography : : **CHEAT SHEET**

Use cartography with spatial objects from sf or sp packages to create thematic maps.

```
library(cartography)
library(sf)
mtq <- st_read("martinique.shp")
plot(st_geometry(mtq))
propSymbolsLayer(x = mtq, var = "P13_POP",
 legend.title.txt = "Population",
 col = "#a7dfb4")
```



Classification

Available methods are: quantile, equal, q6, fisher-jenks, mean-sd, sd, geometric progression...

```
bks1 <- getBreaks(v = var, nclass = 6,
 method = "quantile")
bks2 <- getBreaks(v = var, nclass = 6,
 method = "fisher-jenks")
pal <- carto.pal("green.pal",3, "wine.pal", 3)
hist(var, breaks = bks1, col = pal)
```

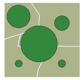

```
hist(var, breaks = bks2, col = pal)
```

Symbology

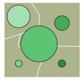
In most functions the x argument should be an sf object. sp objects are handled through spdf and df arguments.

Choropleth
```
choroLayer(x = mtq, var = "myvar",
 method = "quantile", nclass = 8)
```

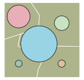
Typology
```
typoLayer(x = mtq, var = "myvar")
```



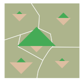
Proportional Symbols
```
propSymbolsLayer(x = mtq, var = "myvar",
 inches = 0.1, symbols = "circle")
```



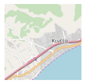
Colorized Proportional Symbols (relative data)
```
propSymbolsChoroLayer(x = mtq, var = "myvar",
 var2 = "myvar2")
```



Colorized Proportional Symbols (qualitative data)
```
propSymbolsTypoLayer(x = mtq, var = "myvar",
 var2 = "myvar2")
```



Double Proportional Symbols
```
propTrianglesLayer(x = mtq, var1 = "myvar",
 var2 = "myvar2")
```

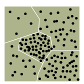


OpenStreetMap Basemap (see rosm package)
```
tiles <- getTiles(x = mtq, type = "osm")
tilesLayer(tiles)
```

Isopleth (see SpatialPosition package)
```
smoothLayer(x = mtq, var = "myvar",
 typefct = "exponential", span = 500,
 beta = 2)
```

Discontinuities
```
discLayer(x = mtq.borders, df = mtq,
 var = "myvar", threshold = 0.5
```

Flows
```
propLinkLayer(x = mtq_link, df = mtq_df,
 var = "fij")
```

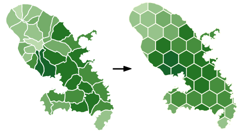


Dot Density
```
dotDensityLayer(x = mtq, var = "myvar")
```

Labels
```
labelLayer(x = mtq, txt = "myvar",
 halo = TRUE, overlap = FALSE)
```

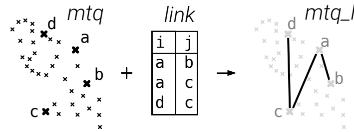
Transformations

Polygons to Grid
```
mtq_grid <- getGridLayer(x = mtq, cellsize = 3.6e+07,
  type = "hexagonal", var = "myvar")
```



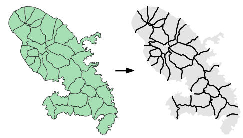
Grids layers can be used by choroLayer() or propSymbolsLayer().

Points to Links
```
mtq_link <- getLinkLayer(x = mtq, df = link)
```



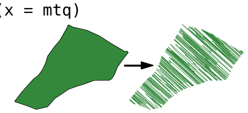
Links layers can be used by *LinkLayer().

Polygons to Borders
```
mtq_border <- getBorders(x = mtq)
```



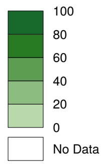
Borders layers can be used by discLayer() function

Polygons to Pencil Lines
```
mtq_pen <- getPencilLayer(x = mtq)
```



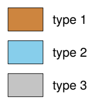
Legends

legendChoro()



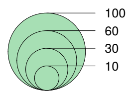

```
legendChoro(pos = "topleft",
 title.txt = "legendChoro()",
 breaks = c(0,20,40,60,80,100),
 col = carto.pal("green.pal", 5),
 nodata = TRUE, nodata.txt = "No Data")
```

legendTypo()




```
legendTypo(title.txt = "legendTypo()",
 col = c("peru", "skyblue", "gray77"),
 categ = c("type 1", "type 2", "type 3"),
 nodata = FALSE)
```

legendCirclesSymbols()




```
legendCirclesSymbols(var = c(10,100),
 title.txt = "legendCirclesSymbols()",
 col = "#a7dfb4ff", inches = 0.3)
```

See also legendSquaresSymbols(), legendBarsSymbols(), legendGradLines(), legendPropLines() and legendPropTriangles().

Map Layout

North Arrow:
```
north(pos = "topright")
```

Scale Bar:
```
barscale(size = 5)
```

Full Layout:
```
layoutLayer(
 title = "Martinique",
 tabtitle = TRUE,
 frame = TRUE,
 author = "Author",
 sources = "Sources",
 north = TRUE,
 scale = 5)
```

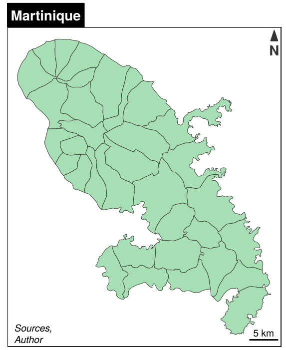
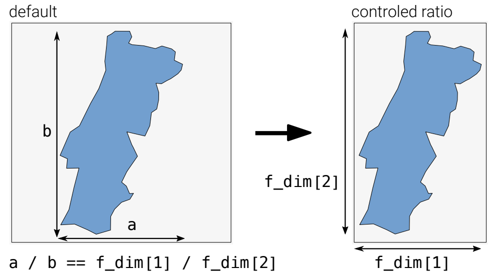


Figure Dimensions

Get figure dimensions based on the dimension ratio of a spatial object, figure margins and output resolution.

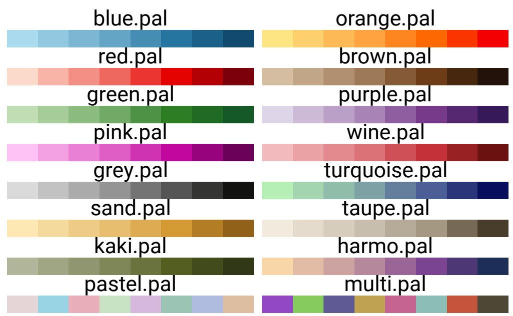
```
f_dim <- getFigDim(x = sf_obj, width = 500,
  mar = c(0,0,0,0))
png("fig.png", width = 500, height = f_dim[2])
par(mar = c(0,0,0,0))
plot(sf_obj, col = "#729fcf")
dev.off()
```



Color Palettes

```
carto.pal(pal1 = "blue.pal", n1 = 5,
 pal2 = sand.pal, n2 = 3)
```

```
display.carto.all(n = 8)
```



Advanced and Fast Data Transformation with collapse : : CHEAT SHEET

Basics

collapse is a powerful (C/C++ based) package supporting advanced (grouped, weighted, time series, panel data and recursive) operations in R.

It also offers a fast, class-agnostic approach to data manipulation - handling matrix and data frame based objects in a uniform, non-destructive way.

It is well integrated with *dplyr* ((grouped) tibbles), *data.table, sf* and *plm* classes for panel data, and can be programmed using pipes (%>%, |>), standard or non-standard evaluation.

Fast Statistical Functions

Fast functions to perform column–wise grouped and weighted computations on matrix-like objects:

```
fmean, fmedian, fmode, fsum, fprod, fsd,
fvar, fmin, fmax, fnth, ffirst, flast,
fnobs, fndistinct
```

Syntax:

```
FUN(x, g = NULL, [w = NULL], TRA = NULL,
    [na.rm = TRUE], use.g.names = TRUE,
    [drop = TRUE])
```

- `x` – vector, matrix, or (grouped) data frame
- `g` – [optional]: (list of) vectors / factors or **GRP()** object
- `w` – [optional]: vector of weights
- `TRA` – [optional]: operation to transform data with computed statistics (can also be done in post, see section below)

Examples:

```
fmean(data[3:5], data$grp1, data$weights)
data %>% fgroup_by(grp1) %>% fmean(weights)
```

Using dplyr grouped tibble & centering on the median:

```
data %>% dplyr::group_by(grp1) %>%
  fmedian(weights, TRA = "-")
```

Transform by (Grouped) Replacing or Sweeping out Statistics

```
TRA(x, STATS, FUN = '-', g = NULL)
```

STATS – statistics matching columns of x (e.g. aggregated matrix or data frame)

FUN – string indicating transformation to perform:

'replace_fill' – overwrite values with statistic
'replace' – same but keep missing values in data,
'-' – center, **'-+'** – center on overall average statistic,
'/' – scale / divide , **'%'** – percentages, **'+'** – add,
'*' – multiply, **'%%'** – modulus, **'-%%'** – flatten

Examples:

```
TRA(mat, fmedian(mat, g), "-", g)
fmedian(mat, g, TRA = "-")
```
– same thing

Advanced Transformations

Fast functions to perform common and specialized data transformations (for panel data econometrics)

Scaling, (Quasi-)Centering and Averaging

```
fscale(x, g = NULL, w = NULL, na.rm = TRUE,
       mean = 0, sd = 1, ...)
fwithin(x, g = NULL, w = NULL, na.rm = TRUE,
        mean = 0, theta = 1, ...)
fbetween(x, g = NULL, w = NULL, na.rm = TRUE,
         fill = FALSE, ...)
```

High-Dimensional Centering and Averaging

```
fhdwithin(x, fl, w = NULL, na.rm = TRUE,
          variable.wise = FALSE, ...)
fhdbetween(x, fl, w = NULL, na.rm = TRUE,
      fill = FALSE, variable.wise = FALSE, )
```

Operators (function shortcuts with extra features):

`STD(), W(), B(), HDW(), HDB()`

Linear Models

```
flm(y, X, w = NULL, add.icpt = FALSE, method =
c('lm','solve','qr','arma','chol','eigen'), )
```
– fast (barebones) linear model fitting with 6 different solvers

```
fFtest(y, exc, X = NULL, w = NULL, ...)
```
– fast F-test of exclusion restrictions for lm's (with HD FE)

Time Series and Panel Series

Fast functions to perform time-based computations on (irregular) time series and (unbalanced) panel data

Lags / Leads, Differences and Growth Rates

```
flag(x, n = 1, g = NULL, t = NULL, fill = NA, )
fdiff(x, n = 1, diff = 1, g = NULL, t = NULL,
      fill = NA, log = FALSE, rho = 1, ...)
fgrowth(x, n = 1, diff = 1, g = NULL, t = NULL,
        fill = NA, logdiff = FALSE,
        scale = 100, power = 1, ...)
```

Operators: `L(), F(), D(), Dlog(), G()`
Cumulative Sums: `fcumsum(x, g, o, na.rm, fill, )`

Panel-ACF/PACF/CCF | Panel-Data → Array

`psacf(), pspacf(), psccf()` | `psmat()`

Other Computations

Apply functions to rows or columns (by groups)

`dapply(x, FUN, ..., MARGIN = 2)` – column/row apply
`BY(x, g, FUN, ...)` – split-apply-combine computing

Advanced Data Aggregation

Fast multi-data-type, multi-function, weighted, parallelized and fully customized data aggregation

```
collap(data, by, FUN = fmean, catFUN = fmode,
       cols = NULL, w = NULL, wFUN = fsum,
       custom = NULL, ...)
```

Where:

- `by` – one- or two-sided formula ([vars] ~ groups) or data (like **g**)
- `FUN` – (list of) functions applied to numeric columns in data
- `catFUN` – (list of) functions applied to categorical columns
- `cols` – [optional]: columns to aggregate (if **by** is one-sided)
- `w` – [optional]: one-sided formula or vector giving weights
- `wFUN` – (list of) functions to aggregate weights passed to **w**
- `custom` – [alternatively]: list mapping functions to columns e.g. `list(fmean = 1:3, fsum = 4:5, ...)`

Examples:

```
collap(data, var1 + var2 ~ grp1 + grp2)
collap(data, ~ grp1, fmedian, w = ~ weights)
```

collapg supports grouped data frames and NS eval:

```
data %>% gby(grp1) %>% collapg(w = weights)
```

Grouping and Ordering

Optimized functions for grouping, ordering, unique values, and for creating and interacting factors

`GRP(data, ~ grp1 + grp2)` – create a grouping object (class 'GRP') from grp1 and grp2 – can be passed to **g** argument – useful for programming and C/C++ development

`fgroup_by(data, grp1, grp2)` – attach 'GRP' object to **data** – a flexible grouped data frame that preserves the attributes of **data** and supports fast computations

`fgroup_vars(), fungroup()` – get group vars & ungroup

`qF(), qG()` – quick conversion to factor and vector grouping object (a factor-light class 'qG')

`groupid()` – fast run-length-type group id (class 'qG')

`seqid()` – group-id from integer-sequences (class 'qG')

`radixorder[v]()` – fast Radix-based ordering

`finteraction()` – fast factor interactions

`fdroplevels()` – fast removal of unused factor levels

`funique()` – fast unique values / rows (by `cols`)

Quick Conversions

`qDF(), qDT(), qTBL(),` – convert vectors, arrays, data.frames or lists to data.frame, data.table or tibble

`qM()` – to matrix, `m[r/c]tl()` – matrix rows/cols to list

`as_numeric_factor(), as_character_factor()` – convert factors or all factors in a list / data.frame

Fast Data Manipulation

- `fselect[<-]()` – select/replace cols
- `fsubset()` – subset data (rows and cols)
- `colorder[v]()` – reorder cols ('v FUN's aid programming)
- `roworder[v]()` – sort (reorder) rows
- `[f/set]transform[v][<-]()` – transform cols (by reference)
- `fcompute[v]()` – compute new cols dropping existing ones
- `[f/set]rename()` – rename (any object with 'names' attr.)
- `get_vars[<-]()` – select/replace cols (standard evaluation)
- `num_vars[<-](), cat_vars[<-](), char_vars[<-](), fact_vars[<-](), logi_vars[<-](), date_vars[<-]()` – select/replace cols by data type
- `add_vars[<-]()` – add (column - bind) cols

List-Processing

Functions to process (nested) lists (of data objects)

- `ldepth()` – level of nesting of list
- `is_unlistable()` – is list composed of atomic objects
- `has_elem()` – search if list contains certain elements
- `get_elem()` – pull out elements from list / subset list
- `atomic_elem[<-](), list_elem[<-]()` – get list with atomic / sub-list elements, examining only first level of list
- `reg_elem(), irreg_elem()` – get full list tree leading to atomic ('regular') or non-atomic ('irregular') elements
- `rsplit()` – efficient (recursive) splitting
- `rapply2d()` – recursive apply to lists of data objects
- `unlist2d()` – recursive row-binding to data.frame

Summary Statistics

`qsu()` – fast (grouped, weighted, panel-decomposed) summary statistics for cross-sectional and panel data

`descr()` – detailed statistical description of data.frame

`varying()` – check variation within groups (panel-id's)

`pwcor(), pwcov(), pwnobs()` – pairwise correlations, covariance and obs. (with P-value and pretty printing)

Recode and Replace Values

`recode_num(), recode_char()` – recode numeric / character values (+ regex recoding) in matrix-like objects

`replace_NA(), replace_Inf(), replace_outliers()`
– replace special values `pad()` – add observations / rows.

Utility Functions

`.c, Vlabels[<-], namlab, na_rm, na_omit, allNA, missing_cases, ckmatch, add_stub, rm_stub, fnrow, seq_row, %!in%, unattrib` etc...

Data import with the tidyverse : : CHEAT SHEET

readr

Read Tabular Data with readr

read_*(file, col_names = TRUE, col_types = NULL, col_select = NULL, id = NULL, locale, n_max = Inf, skip = 0, na = c("", "NA"), guess_max = min(1000, n_max), show_col_types = TRUE) See **?read_delim**

```
A|B|C
1|2|3
4|5|NA
```

A	B	C
1	2	3
4	5	NA

read_delim("file.txt", delim = "|"**)** Read files with any delimiter. If no delimiter is specified, it will automatically guess.
To make file.txt, run: write_file("A|B|C\n1|2|3\n4|5|NA", file = "file.txt")

```
A,B,C
1,2,3
4,5,NA
```

A	B	C
1	2	3
4	5	NA

read_csv("file.csv"**)** Read a comma delimited file with period decimal marks.
write_file("A,B,C\n1,2,3\n4,5,NA", file = "file.csv")

```
A;B;C
1,5;2;3
4,5;5;NA
```

A	B	C
1.5	2	3
4.5	5	NA

read_csv2("file2.csv"**)** Read semicolon delimited files with comma decimal marks.
write_file("A;B;C\n1,5;2;3\n4,5;5;NA", file = "file2.csv")

```
A B C
1 2 3
4 5 NA
```

A	B	C
1	2	3
4	5	NA

read_tsv("file.tsv"**)** Read a tab delimited file. Also **read_table()**.
read_fwf("file.tsv", fwf_widths(c(2, 2, NA))**)** Read a fixed width file.
write_file("A\tB\tC\n1\t2\t3\n4\t5\tNA\n", file = "file.tsv")

USEFUL READ ARGUMENTS

A	B	C
1	2	3
4	5	NA

No header
read_csv("file.csv", col_names = FALSE)

x	y	z
A	B	C
1	2	3
4	5	NA

Provide header
read_csv("file.csv",
col_names = c("x", "y", "z"))

Read multiple files into a single table
read_csv(c("f1.csv", "f2.csv", "f3.csv"),
id = "origin_file")

1	2	3
4	5	NA

Skip lines
read_csv("file.csv", skip = 1)

A	B	C
1	2	3

Read a subset of lines
read_csv("file.csv", n_max = 1)

A	B	C
NA	2	3
4	5	NA

Read values as missing
read_csv("file.csv", na = c("1"))

```
A;B;C
1,5;2;3,0
```

Specify decimal marks
read_delim("file2.csv", locale =
locale(decimal_mark = ","))

Save Data with readr

write_*(x, file, na = "NA", append, col_names, quote, escape, eol, num_threads, progress)

A	B	C
1	2	3
4	5	NA

```
A,B,C
1,2,3
4,5,NA
```

write_delim(x, file, delim = " "**)** Write files with any delimiter.

write_csv(x, file**)** Write a comma delimited file.

write_csv2(x, file**)** Write a semicolon delimited file.

write_tsv(x, file**)** Write a tab delimited file.

One of the first steps of a project is to import outside data into R. Data is often stored in tabular formats, like csv files or spreadsheets.

The front page of this sheet shows how to import and save text files into R using **readr**.

The back page shows how to import spreadsheet data from Excel files using **readxl** or Google Sheets using **googlesheets4**.

OTHER TYPES OF DATA

Try one of the following packages to import other types of files:

- **haven** - SPSS, Stata, and SAS files
- **DBI** - databases
- **jsonlite** - json
- **xml2** - XML
- **httr** - Web APIs
- **rvest** - HTML (Web Scraping)
- **readr::read_lines()** - text data

Column Specification with readr

Column specifications define what data type each column of a file will be imported as. By default readr will generate a column spec when a file is read and output a summary.

spec(x**)** Extract the full column specification for the given imported data frame.

```
spec(x)
# cols(
#   age = col_integer(),
#   sex = col_character(),
#   earn = col_double()
# )
```

age is an integer
sex is a character
earn is a double (numeric)

USEFUL COLUMN ARGUMENTS

Hide col spec message
read_*(file, show_col_types = FALSE)

Select columns to import
Use names, position, or selection helpers.
read_*(file, col_select = c(age, earn))

Guess column types
To guess a column type, read_*() looks at the first 1000 rows of data. Increase with **guess_max**.
read_*(file, guess_max = Inf)

COLUMN TYPES

Each column type has a function and corresponding string abbreviation.

- **col_logical()** - "l"
- **col_integer()** - "i"
- **col_double()** - "d"
- **col_number()** - "n"
- **col_character()** - "c"
- **col_factor(**levels, ordered = FALSE**)** - "f"
- **col_datetime(**format = ""**)** - "T"
- **col_date(**format = ""**)** - "D"
- **col_time(**format = ""**)** - "t"
- **col_skip()** - "-", "_"
- **col_guess()** - "?"

DEFINE COLUMN SPECIFICATION

Set a default type
```
read_csv(
  file,
  col_type = list(.default = col_double())
)
```

Use column type or string abbreviation
```
read_csv(
  file,
  col_type = list(x = col_double(), y = "l", z = "_")
)
```

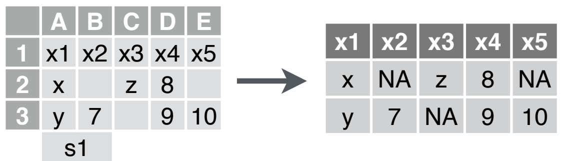
Use a single string of abbreviations
```
# col types: skip, guess, integer, logical, character
read_csv(
  file,
  col_type = "_?ilc"
)
```

RStudio

Import Spreadsheets

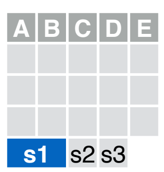
with readxl

READ EXCEL FILES



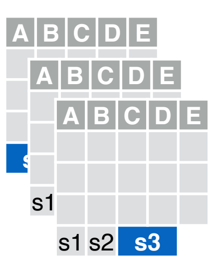
read_excel(path, sheet = NULL, range = NULL)
Read a .xls or .xlsx file based on the file extension. See front page for more read arguments. Also **read_xls()** and **read_xlsx()**.
read_excel("excel_file.xlsx")

READ SHEETS



read_excel(path, **sheet = NULL)** Specify which sheet to read by position or name.
read_excel(path, sheet = 1)
read_excel(path, sheet = "s1")

excel_sheets(path) Get a vector of sheet names.
excel_sheets("excel_file.xlsx")



To **read multiple sheets:**

1. Get a vector of sheet names from the file path.
2. Set the vector names to be the sheet names.
3. Use purrr::map_dfr() to read multiple files into one data frame.

```
path <- "your_file_path.xlsx"

path %>% excel_sheets() %>%
  set_names() %>%
  map_dfr(read_excel, path = path)
```

OTHER USEFUL EXCEL PACKAGES

For functions to write data to Excel files, see:

- **openxlsx**
- **writexl**

For working with non-tabular Excel data, see:

- **tidyxl**

READXL COLUMN SPECIFICATION

Column specifications define what data type each column of a file will be imported as.

Use the **col_types** argument of **read_excel()** to set the column specification.

Guess column types
To guess a column type, read_ excel() looks at the first 1000 rows of data. Increase with the **guess_max** argument.
read_excel(path, **guess_max** = Inf)

Set all columns to same type, e.g. character
read_excel(path, col_types = "text")

Set each column individually

```
read_excel(
  path,
  col_types = c("text", "guess", "guess","numeric")
)
```

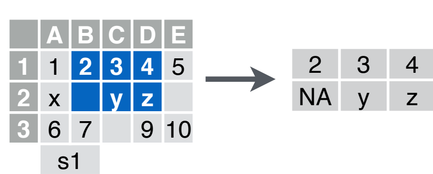
COLUMN TYPES

logical	numeric	text	date	list
TRUE	2	hello	1947-01-08	hello
FALSE	3.45	world	1956-10-21	1

- skip
- guess
- logical
- numeric
- text
- date
- list

Use **list** for columns that include multiple data types. See **tidyr** and **purrr** for list-column data.

CELL SPECIFICATION FOR READXL AND GOOGLESHEETS4

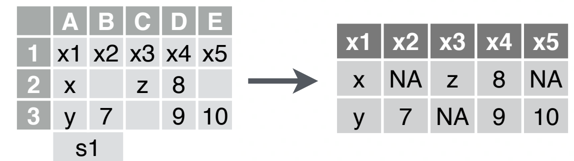


Use the **range** argument of **readxl::read_excel()** or **googlesheets4::read_sheet()** to read a subset of cells from a sheet.
read_excel(path, range = "Sheet1!B1:D2")
read_sheet(ss, range = "B1:D2")

Also use the range argument with cell specification functions **cell_limits()**, **cell_rows()**, **cell_cols()**, and **anchored().**

with googlesheets4

READ SHEETS



read_sheet(ss, sheet = NULL, range = NULL**)**
Read a sheet from a URL, a Sheet ID, or a dribble from the googledrive package. See front page for more read arguments. Same as **range_read()**.

SHEETS METADATA

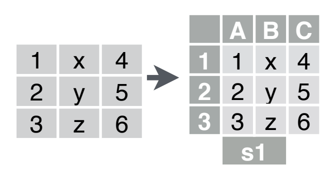
URLs are in the form:
https://docs.google.com/spreadsheets/d/
SPREADSHEET_ID/edit#gid=**SHEET_ID**

gs4_get(ss) Get spreadsheet meta data.

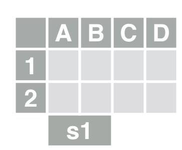
gs4_find(...) Get data on all spreadsheet files.

sheet_properties(ss) Get a tibble of properties for each worksheet. Also **sheet_names()**.

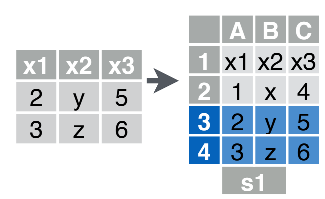
WRITE SHEETS



write_sheet(data, ss = NULL, sheet = NULL**)**
Write a data frame into a new or existing Sheet.



gs4_create(name, ..., sheets = NULL) Create a new Sheet with a vector of names, a data frame, or a (named) list of data frames.



sheet_append(ss, data, sheet = 1) Add rows to the end of a worksheet.

GOOGLESHEETS4 COLUMN SPECIFICATION

Column specifications define what data type each column of a file will be imported as.

Use the **col_types** argument of **read_sheet()/ range_read()** to set the column specification.

Guess column types
To guess a column type read_sheet()/ range_read() looks at the first 1000 rows of data. Increase with **guess_max**.
read_sheet(path, **guess_max** = Inf)

Set all columns to same type, e.g. character
read_sheet(path, col_types = "c")

Set each column individually
# col types: skip, guess, integer, logical, character
read_sheets(ss, col_types = "_?ilc")

COLUMN TYPES

l	n	c	D	L
TRUE	2	hello	1947-01-08	hello
FALSE	3.45	world	1956-10-21	1

- skip - "_" or "-"
- guess - "?"
- logical - "l"
- integer - "i"
- double - "d"
- numeric - "n"
- date - "D"
- datetime - "T"
- character - "c"
- list-column - "L"
- cell - "C" Returns list of raw cell data.

Use list for columns that include multiple data types. See **tidyr** and **purrr** for list-column data.

FILE LEVEL OPERATIONS

googlesheets4 also offers ways to modify other aspects of Sheets (e.g. freeze rows, set column width, manage (work)sheets). Go to **googlesheets4.tidyverse.org** to read more.

For whole-file operations (e.g. renaming, sharing, placing within a folder), see the tidyverse package **googledrive** at **googledrive.tidyverse.org**.

Data transformation with dplyr : : CHEAT SHEET

dplyr functions work with pipes and expect **tidy data**. In tidy data:

Each **variable** is in its own **column** & Each **observation**, or **case**, is in its own **row**

pipes

x %>% f(y) becomes **f(x, y)**

Summarise Cases

Apply **summary functions** to columns to create a new table of summary statistics. Summary functions take vectors as input and return one value (see back).

summary function

summarise(.data, …**)**
Compute table of summaries.
summarise(mtcars, avg = mean(mpg))

count(.data, …, wt = NULL, sort = FALSE, name = NULL**)** Count number of rows in each group defined by the variables in … Also **tally()**.
count(mtcars, cyl)

Group Cases

Use **group_by(**.data, …, .add = FALSE, .drop = TRUE**)** to create a "grouped" copy of a table grouped by columns in ... dplyr functions will manipulate each "group" separately and combine the results.

```
mtcars %>%
  group_by(cyl) %>%
  summarise(avg = mean(mpg))
```

Use **rowwise(**.data, …**)** to group data into individual rows. dplyr functions will compute results for each row. Also apply functions to list-columns. See tidyr cheat sheet for list-column workflow.

```
starwars %>%
  rowwise() %>%
  mutate(film_count = length(films))
```

ungroup(x, …**)** Returns ungrouped copy of table.
ungroup(g_mtcars)

Manipulate Cases

EXTRACT CASES

Row functions return a subset of rows as a new table.

filter(.data, …, .preserve = FALSE**)** Extract rows that meet logical criteria.
filter(mtcars, mpg > 20)

distinct(.data, …, .keep_all = FALSE**)** Remove rows with duplicate values.
distinct(mtcars, gear)

slice(.data, …, .preserve = FALSE**)** Select rows by position.
slice(mtcars, 10:15)

slice_sample(.data, …, n, prop, weight_by = NULL, replace = FALSE**)** Randomly select rows. Use n to select a number of rows and prop to select a fraction of rows.
slice_sample(mtcars, n = 5, replace = TRUE)

slice_min(.data, order_by, …, n, prop, with_ties = TRUE**)** and **slice_max()** Select rows with the lowest and highest values.
slice_min(mtcars, mpg, prop = 0.25)

slice_head(.data, …, n, prop**)** and **slice_tail()** Select the first or last rows.
slice_head(mtcars, n = 5)

Logical and boolean operators to use with filter()

==	<	<=	is.na()	%in%	|	xor()
!=	>	>=	!is.na()	!	&	

See **?base::Logic** and **?Comparison** for help.

ARRANGE CASES

arrange(.data, …, .by_group = FALSE**)** Order rows by values of a column or columns (low to high), use with **desc()** to order from high to low.
arrange(mtcars, mpg)
arrange(mtcars, desc(mpg))

ADD CASES

add_row(.data, …, .before = NULL, .after = NULL**)** Add one or more rows to a table.
add_row(cars, speed = 1, dist = 1)

Manipulate Variables

EXTRACT VARIABLES

Column functions return a set of columns as a new vector or table.

pull(.data, var = -1, name = NULL, …**)** Extract column values as a vector, by name or index.
pull(mtcars, wt)

select(.data, …**)** Extract columns as a table.
select(mtcars, mpg, wt)

relocate(.data, …, .before = NULL, .after = NULL**)** Move columns to new position.
relocate(mtcars, mpg, cyl, .after = last_col())

Use these helpers with select() and across()
e.g. select(mtcars, mpg:cyl)

contains(match**)**	**num_range(**prefix, range**)**	**:**, e.g. mpg:cyl
ends_with(match**)**	**all_of(**x**)/any_of(**x, …, vars**)**	**-**, e.g, -gear
starts_with(match**)**	**matches(**match**)**	**everything()**

MANIPULATE MULTIPLE VARIABLES AT ONCE

across(.cols, .funs, …, .names = NULL**)** Summarise or mutate multiple columns in the same way.
summarise(mtcars, across(everything(), mean))

c_across(.cols**)** Compute across columns in row-wise data.
transmute(rowwise(UKgas), total = sum(c_across(1:2)))

MAKE NEW VARIABLES

Apply **vectorized functions** to columns. Vectorized functions take vectors as input and return vectors of the same length as output (see back).

vectorized function

mutate(.data, …, .keep = "all", .before = NULL, .after = NULL**)** Compute new column(s). Also **add_column(), add_count(),** and **add_tally().**
mutate(mtcars, gpm = 1 / mpg)

transmute(.data, …**)** Compute new column(s), drop others.
transmute(mtcars, gpm = 1 / mpg)

rename(.data, …**)** Rename columns. Use **rename_with()** to rename with a function.
rename(cars, distance = dist)

RStudio

Vectorized Functions

TO USE WITH MUTATE ()

mutate() and **transmute()** apply vectorized functions to columns to create new columns. Vectorized functions take vectors as input and return vectors of the same length as output.

vectorized function

OFFSET

dplyr::**lag()** - offset elements by 1
dplyr::**lead()** - offset elements by -1

CUMULATIVE AGGREGATE

dplyr::**cumall()** - cumulative all()
dplyr::**cumany()** - cumulative any()
cummax() - cumulative max()
dplyr::**cummean()** - cumulative mean()
cummin() - cumulative min()
cumprod() - cumulative prod()
cumsum() - cumulative sum()

RANKING

dplyr::**cume_dist()** - proportion of all values <=
dplyr::**dense_rank()** - rank w ties = min, no gaps
dplyr::**min_rank()** - rank with ties = min
dplyr::**ntile()** - bins into n bins
dplyr::**percent_rank()** - min_rank scaled to [0,1]
dplyr::**row_number()** - rank with ties = "first"

MATH

+, - , *, /, ^, %/%, %% - arithmetic ops
log(), log2(), log10() - logs
<, <=, >, >=, !=, == - logical comparisons
dplyr::**between()** - x >= left & x <= right
dplyr::**near()** - safe == for floating point numbers

MISCELLANEOUS

dplyr::**case_when()** - multi-case if_else()

```
starwars %>%
  mutate(type = case_when(
    height > 200 | mass > 200 ~ "large",
      species == "Droid"        ~ "robot",
      TRUE                      ~ "other")
  )
```

dplyr::**coalesce()** - first non-NA values by element across a set of vectors
dplyr::**if_else()** - element-wise if() + else()
dplyr::**na_if()** - replace specific values with NA
pmax() - element-wise max()
pmin() - element-wise min()

Summary Functions

TO USE WITH SUMMARISE ()

summarise() applies summary functions to columns to create a new table. Summary functions take vectors as input and return single values as output.

summary function

COUNT

dplyr::**n()** - number of values/rows
dplyr::**n_distinct()** - # of uniques
sum(!is.na()) - # of non-NA's

POSITION

mean() - mean, also **mean(!is.na())**
median() - median

LOGICAL

mean() - proportion of TRUE's
sum() - # of TRUE's

ORDER

dplyr::**first()** - first value
dplyr::**last()** - last value
dplyr::**nth()** - value in nth location of vector

RANK

quantile() - nth quantile
min() - minimum value
max() - maximum value

SPREAD

IQR() - Inter-Quartile Range
mad() - median absolute deviation
sd() - standard deviation
var() - variance

Row Names

Tidy data does not use rownames, which store a variable outside of the columns. To work with the rownames, first move them into a column.

tibble::**rownames_to_column()**
Move row names into col.
a <- rownames_to_column(mtcars, var = "C")

tibble::**column_to_rownames()**
Move col into row names.
column_to_rownames(a, var = "C")

Also tibble::**has_rownames()** and tibble::**remove_rownames()**.

Combine Tables

COMBINE VARIABLES

bind_cols(..., .name_repair) Returns tables placed side by side as a single table. Column lengths must be equal. Columns will NOT be matched by id (to do that look at Relational Data below), so be sure to check that both tables are ordered the way you want before binding.

COMBINE CASES

bind_rows(..., .id = NULL) Returns tables one on top of the other as a single table. Set .id to a column name to add a column of the original table names (as pictured).

RELATIONAL DATA

Use a "**Mutating Join**" to join one table to columns from another, matching values with the rows that they correspond to. Each join retains a different combination of values from the tables.

left_join(x, y, by = NULL, copy = FALSE, suffix = c(".x", ".y"), ..., keep = FALSE, na_matched = "na") Join matching values from y to x.

right_join(x, y, by = NULL, copy = FALSE, suffix = c(".x", ".y"), ..., keep = FALSE, na_matches = "na") Join matching values from x to y.

inner_join(x, y, by = NULL, copy = FALSE, suffix = c(".x", ".y"), ..., keep = FALSE, na_matches = "na") Join data. Retain only rows with matches.

full_join(x, y, by = NULL, copy = FALSE, suffix = c(".x", ".y"), ..., keep = FALSE, na_matches = "na") Join data. Retain all values, all rows.

Use a "**Filtering Join**" to filter one table against the rows of another.

semi_join(x, y, by = NULL, copy = FALSE, ..., na_matches = "na") Return rows of x that have a match in y. Use to see what will be included in a join.

anti_join(x, y, by = NULL, copy = FALSE, ..., na_matches = "na") Return rows of x that do not have a match in y. Use to see what will not be included in a join.

Use a "**Nest Join**" to inner join one table to another into a nested data frame.

nest_join(x, y, by = NULL, copy = FALSE, keep = FALSE, name = NULL, ...) Join data, nesting matches from y in a single new data frame column.

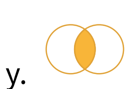
COLUMN MATCHING FOR JOINS

Use **by = c("col1", "col2", ...)** to specify one or more common columns to match on.
left_join(x, y, by = "A")

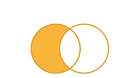
Use a named vector, **by = c("col1" = "col2")**, to match on columns that have different names in each table.
left_join(x, y, by = c("C" = "D"))

Use **suffix** to specify the suffix to give to unmatched columns that have the same name in both tables.
left_join(x, y, by = c("C" = "D"), suffix = c("1", "2"))

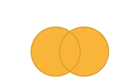
SET OPERATIONS



intersect(x, y, ...)
Rows that appear in both x and y.



setdiff(x, y, ...)
Rows that appear in x but not y.



union(x, y, ...)
Rows that appear in x or y. (Duplicates removed). **union_all()** retains duplicates.

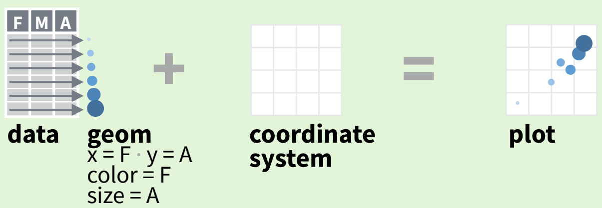
Use **setequal()** to test whether two data sets contain the exact same rows (in any order).

Data visualization with ggplot2 : : CHEAT SHEET

Basics

ggplot2 is based on the **grammar of graphics**, the idea that you can build every graph from the same components: a **data** set, a **coordinate system**, and **geoms**—visual marks that represent data points.

To display values, map variables in the data to visual properties of the geom (**aesthetics**) like **size**, **color**, and **x** and **y** locations.



Complete the template below to build a graph.

ggplot (data = <DATA> **) +** — required
<GEOM_FUNCTION> **(mapping = aes(** <MAPPINGS> **),**
stat = <STAT>, position = <POSITION>) +
<COORDINATE_FUNCTION> +
<FACET_FUNCTION> +
<SCALE_FUNCTION> +
<THEME_FUNCTION>

Not required, sensible defaults supplied

ggplot(data = mpg, **aes**(x = cty, y = hwy)) Begins a plot that you finish by adding layers to. Add one geom function per layer.

last_plot() Returns the last plot.

ggsave("plot.png", width = 5, height = 5) Saves last plot as 5' x 5' file named "plot.png" in working directory. Matches file type to file extension.

Aes

Common aesthetic values.

color and **fill** - string ("red", "#RRGGBB")

linetype - integer or string (0 = "blank", 1 = "solid", 2 = "dashed", 3 = "dotted", 4 = "dotdash", 5 = "longdash", 6 = "twodash")

lineend - string ("round", "butt", or "square")

linejoin - string ("round", "mitre", or "bevel")

size - integer (line width in mm)

shape - integer/shape name or a single character ("a")

0 1 2 3 4 5 6 7 8 9 10 11 12
13 14 15 16 17 18 19 20 21 22 23 24 25

Geoms

Use a geom function to represent data points, use the geom's aesthetic properties to represent variables. Each function returns a layer.

GRAPHICAL PRIMITIVES

a <- ggplot(economics, aes(date, unemploy))
b <- ggplot(seals, aes(x = long, y = lat))

a + geom_blank() and **a + expand_limits()**
Ensure limits include values across all plots.

b + geom_curve(aes(yend = lat + 1, xend = long + 1), curvature = 1) - x, xend, y, yend, alpha, angle, color, curvature, linetype, size

a + geom_path(lineend = "butt", linejoin = "round", linemitre = 1)
x, y, alpha, color, group, linetype, size

a + geom_polygon(aes(alpha = 50)) - x, y, alpha, color, fill, group, subgroup, linetype, size

b + geom_rect(aes(xmin = long, ymin = lat, xmax = long + 1, ymax = lat + 1)) - xmax, xmin, ymax, ymin, alpha, color, fill, linetype, size

a + geom_ribbon(aes(ymin = unemploy - 900, ymax = unemploy + 900)) - x, ymax, ymin, alpha, color, fill, group, linetype, size

LINE SEGMENTS

common aesthetics: x, y, alpha, color, linetype, size

b + geom_abline(aes(intercept = 0, slope = 1))
b + geom_hline(aes(yintercept = lat))
b + geom_vline(aes(xintercept = long))

b + geom_segment(aes(yend = lat + 1, xend = long + 1))
b + geom_spoke(aes(angle = 1:1155, radius = 1))

ONE VARIABLE continuous

c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)

c + geom_area(stat = "bin")
x, y, alpha, color, fill, linetype, size

c + geom_density(kernel = "gaussian")
x, y, alpha, color, fill, group, linetype, size, weight

c + geom_dotplot()
x, y, alpha, color, fill

c + geom_freqpoly()
x, y, alpha, color, group, linetype, size

c + geom_histogram(binwidth = 5)
x, y, alpha, color, fill, linetype, size, weight

c2 + geom_qq(aes(sample = hwy))
x, y, alpha, color, fill, linetype, size, weight

discrete

d <- ggplot(mpg, aes(fl))

d + geom_bar()
x, alpha, color, fill, linetype, size, weight

TWO VARIABLES

both continuous

e <- ggplot(mpg, aes(cty, hwy))

e + geom_label(aes(label = cty), nudge_x = 1, nudge_y = 1) - x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

e + geom_point()
x, y, alpha, color, fill, shape, size, stroke

e + geom_quantile()
x, y, alpha, color, group, linetype, size, weight

e + geom_rug(sides = "bl")
x, y, alpha, color, linetype, size

e + geom_smooth(method = lm)
x, y, alpha, color, fill, group, linetype, size, weight

e + geom_text(aes(label = cty), nudge_x = 1, nudge_y = 1) - x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

one discrete, one continuous

f <- ggplot(mpg, aes(class, hwy))

f + geom_col()
x, y, alpha, color, fill, group, linetype, size

f + geom_boxplot()
x, y, lower, middle, upper, ymax, ymin, alpha, color, fill, group, linetype, shape, size, weight

f + geom_dotplot(binaxis = "y", stackdir = "center")
x, y, alpha, color, fill, group

f + geom_violin(scale = "area")
x, y, alpha, color, fill, group, linetype, size, weight

both discrete

g <- ggplot(diamonds, aes(cut, color))

g + geom_count()
x, y, alpha, color, fill, shape, size, stroke

e + geom_jitter(height = 2, width = 2)
x, y, alpha, color, fill, shape, size

continuous bivariate distribution

h <- ggplot(diamonds, aes(carat, price))

h + geom_bin2d(binwidth = c(0.25, 500))
x, y, alpha, color, fill, linetype, size, weight

h + geom_density_2d()
x, y, alpha, color, group, linetype, size

h + geom_hex()
x, y, alpha, color, fill, size

continuous function

i <- ggplot(economics, aes(date, unemploy))

i + geom_area()
x, y, alpha, color, fill, linetype, size

i + geom_line()
x, y, alpha, color, group, linetype, size

i + geom_step(direction = "hv")
x, y, alpha, color, group, linetype, size

visualizing error

df <- data.frame(grp = c("A", "B"), fit = 4:5, se = 1:2)
j <- ggplot(df, aes(grp, fit, ymin = fit - se, ymax = fit + se))

j + geom_crossbar(fatten = 2) - x, y, ymax, ymin, alpha, color, fill, group, linetype, size

j + geom_errorbar() - x, ymax, ymin, alpha, color, group, linetype, size, width
Also **geom_errorbarh()**.

j + geom_linerange()
x, ymin, ymax, alpha, color, group, linetype, size

j + geom_pointrange() - x, y, ymin, ymax, alpha, color, fill, group, linetype, shape, size

maps

data <- data.frame(murder = USArrests$Murder,
state = tolower(rownames(USArrests)))
map <- map_data("state")
k <- ggplot(data, aes(fill = murder))

k + geom_map(aes(map_id = state), map = map)
+ expand_limits(x = map$long, y = map$lat)
map_id, alpha, color, fill, linetype, size

THREE VARIABLES

seals$z <- with(seals, sqrt(delta_long^2 + delta_lat^2)); l <- ggplot(seals, aes(long, lat))

l + geom_contour(aes(z = z))
x, y, z, alpha, color, group, linetype, size, weight

l + geom_contour_filled(aes(fill = z))
x, y, alpha, color, fill, group, linetype, size, subgroup

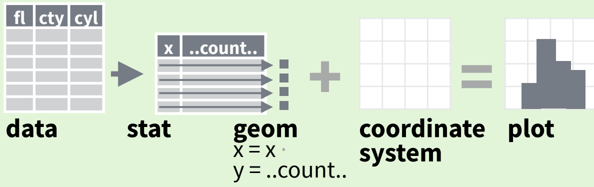
l + geom_raster(aes(fill = z), hjust = 0.5, vjust = 0.5, interpolate = FALSE)
x, y, alpha, fill

l + geom_tile(aes(fill = z))
x, y, alpha, color, fill, linetype, size, width

R Studio

Stats
An alternative way to build a layer.

A stat builds new variables to plot (e.g., count, prop).



Visualize a stat by changing the default stat of a geom function, **geom_bar(stat="count")** or by using a stat function, **stat_count(geom="bar")**, which calls a default geom to make a layer (equivalent to a geom function). Use **..name..** syntax to map stat variables to aesthetics.

geom to use | stat function | geommappings

i + stat_density_2d(aes(fill = ..level..), geom = "polygon")

variable created by stat

c + stat_bin(binwidth = 1, boundary = 10)
x, y | ..count.., ..ncount.., ..density.., ..ndensity..

c + stat_count(width = 1) **x, y** | ..count.., ..prop..

c + stat_density(adjust = 1, kernel = "gaussian")
x, y | ..count.., ..density.., ..scaled..

e + stat_bin_2d(bins = 30, drop = T)
x, y, fill | ..count.., ..density..

e + stat_bin_hex(bins = 30) **x, y, fill** | ..count.., ..density..

e + stat_density_2d(contour = TRUE, n = 100)
x, y, color, size | ..level..

e + stat_ellipse(level = 0.95, segments = 51, type = "t")

l + stat_contour(aes(z = z)) **x, y, z, order** | ..level..

l + stat_summary_hex(aes(z = z), bins = 30, fun = max)
x, y, z, fill | ..value..

l + stat_summary_2d(aes(z = z), bins = 30, fun = mean)
x, y, z, fill | ..value..

f + stat_boxplot(coef = 1.5)
x, y | ..lower.., ..middle.., ..upper.., ..width.. , ..ymin.., ..ymax..

f + stat_ydensity(kernel = "gaussian", scale = "area") **x, y**
| ..density.., ..scaled.., ..count.., ..n.., ..violinwidth.., ..width..

e + stat_ecdf(n = 40) **x, y** | ..x.., ..y..

e + stat_quantile(quantiles = c(0.1, 0.9), formula = y ~ log(x), method = "rq") **x, y** | ..quantile..

e + stat_smooth(method = "lm", formula = y ~ x, se = T, level = 0.95) **x, y** | ..se.., ..x.., ..y.., ..ymin.., ..ymax..

ggplot() + xlim(-5, 5) **+ stat_function**(fun = dnorm, n = 20, geom = "point") **x** | ..x.., ..y..

ggplot() + stat_qq(aes(sample = 1:100))
x, y, sample | ..sample.., ..theoretical..

e + stat_sum() x, y, size | ..n.., ..prop..

e + stat_summary(fun.data = "mean_cl_boot")

h + stat_summary_bin(fun = "mean", geom = "bar")

e + stat_identity()

e + stat_unique()

Scales
Override defaults with **scales** package.

Scales map data values to the visual values of an aesthetic. To change a mapping, add a new scale.

n <- d + geom_bar(aes(fill = fl))

scale_ | aesthetic to adjust | prepackaged scale to use | scale-specific arguments

n + scale_fill_manual(
values = c("skyblue", "royalblue", "blue", "navy"),
limits = c("d", "e", "p", "r"), breaks =c("d", "e", "p", "r"),
name = "fuel", labels = c("D", "E", "P", "R"))

range of values to include in mapping | title to use in legend/axis | labels to use in legend/axis | breaks to use in legend/axis

GENERAL PURPOSE SCALES
Use with most aesthetics

scale_*_continuous() - Map cont' values to visual ones.
scale_*_discrete() - Map discrete values to visual ones.
scale_*_binned() - Map continuous values to discrete bins.
scale_*_identity() - Use data values as visual ones.
scale_*_manual(values = c()) - Map discrete values to manually chosen visual ones.
scale_*_date(date_labels = "%m/%d"), date_breaks = "2 weeks") - Treat data values as dates.
scale_*_datetime() - Treat data values as date times. Same as scale_*_date(). See ?strptime for label formats.

X & Y LOCATION SCALES
Use with x or y aesthetics (x shown here)

scale_x_log10() - Plot x on log10 scale.
scale_x_reverse() - Reverse the direction of the x axis.
scale_x_sqrt() - Plot x on square root scale.

COLOR AND FILL SCALES (DISCRETE)

n + scale_fill_brewer(palette = "Blues")
For palette choices:
RColorBrewer::display.brewer.all()

n + scale_fill_grey(start = 0.2, end = 0.8, na.value = "red")

COLOR AND FILL SCALES (CONTINUOUS)

o <- c + geom_dotplot(aes(fill = ..x..))

o + scale_fill_distiller(palette = "Blues")

o + scale_fill_gradient(low="red", high="yellow")

o + scale_fill_gradient2(low = "red", high = "blue", mid = "white", midpoint = 25)

o + scale_fill_gradientn(colors = topo.colors(6))
Also: rainbow(), heat.colors(), terrain.colors(), cm.colors(), RColorBrewer::brewer.pal()

SHAPE AND SIZE SCALES

p <- e + geom_point(aes(shape = fl, size = cyl))

p + scale_shape() + scale_size()
p + scale_shape_manual(values = c(3:7))

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25

p + scale_radius(range = c(1,6))
p + scale_size_area(max_size = 6)

Coordinate Systems

r <- d + geom_bar()

r + coord_cartesian(xlim = c(0, 5)) - xlim, ylim
The default cartesian coordinate system.

r + coord_fixed(ratio = 1/2)
ratio, xlim, ylim - Cartesian coordinates with fixed aspect ratio between x and y units.

ggplot(mpg, aes(y = fl)) **+ geom_bar()**
Flip cartesian coordinates by switching x and y aesthetic mappings.

r + coord_polar(theta = "x", direction=1)
theta, start, direction - Polar coordinates.

r + coord_trans(y = "sqrt") - x, y, xlim, ylim
Transformed cartesian coordinates. Set xtrans and ytrans to the name of a window function.

π + coord_quickmap()
π + coord_map(projection = "ortho", orientation = c(41, -74, 0)) - projection, xlim, ylim
Map projections from the mapproj package (mercator (default), azequalarea, lagrange, etc.).

Position Adjustments

Position adjustments determine how to arrange geoms that would otherwise occupy the same space.

s <- ggplot(mpg, aes(fl, fill = drv))

s + geom_bar(position = "dodge")
Arrange elements side by side.

s + geom_bar(position = "fill")
Stack elements on top of one another, normalize height.

e + geom_point(position = "jitter")
Add random noise to X and Y position of each element to avoid overplotting.

e + geom_label(position = "nudge")
Nudge labels away from points.

s + geom_bar(position = "stack")
Stack elements on top of one another.

Each position adjustment can be recast as a function with manual **width** and **height** arguments:
s + geom_bar(position = position_dodge(width = 1))

Themes

r + theme_bw()
White background with grid lines.

r + theme_gray()
Grey background (default theme).

r + theme_dark()
Dark for contrast.

r + theme_classic()

r + theme_light()

r + theme_linedraw()

r + theme_minimal()
Minimal theme.

r + theme_void()
Empty theme.

r + theme() Customize aspects of the theme such as axis, legend, panel, and facet properties.
r + ggtitle("Title") + theme(plot.title.postion = "plot")
r + theme(panel.background = element_rect(fill = "blue"))

Faceting

Facets divide a plot into subplots based on the values of one or more discrete variables.

t <- ggplot(mpg, aes(cty, hwy)) + geom_point()

t + facet_grid(cols = vars(fl))
Facet into columns based on fl.

t + facet_grid(rows = vars(year))
Facet into rows based on year.

t + facet_grid(rows = vars(year), cols = vars(fl))
Facet into both rows and columns.

t + facet_wrap(vars(fl))
Wrap facets into a rectangular layout.

Set **scales** to let axis limits vary across facets.

t + facet_grid(rows = vars(drv), cols = vars(fl), scales = "free")
x and y axis limits adjust to individual facets:
"free_x" - x axis limits adjust
"free_y" - y axis limits adjust

Set **labeller** to adjust facet label:

t + facet_grid(cols = vars(fl), labeller = label_both)

fl: c	fl: d	fl: e	fl: p	fl: r

t + facet_grid(rows = vars(fl), labeller = label_bquote(alpha ^ .(fl)))

α^c	α^d	α^e	α^p	α^r

Labels and Legends

Use **labs()** to label the elements of your plot.

t + labs(x = "New x axis label", **y** = "New y axis label",
title ="Add a title above the plot",
subtitle = "Add a subtitle below title",
caption = "Add a caption below plot",
alt = "Add alt text to the plot",
<AES> = "New <AES> legend title")

t + annotate(geom = "text", x = 8, y = 9, label = "A")
Places a geom with manually selected aesthetics.

p + guides(x = guide_axis(n.dodge = 2)) Avoid crowded or overlapping labels with guide_axis(n.dodge or angle).

n + guides(fill = "none") Set legend type for each aesthetic: colorbar, legend, or none (no legend).

n + theme(legend.position = "bottom")
Place legend at "bottom", "top", "left", or "right".

n + scale_fill_discrete(name = "Title", labels = c("A", "B", "C", "D", "E"))
Set legend title and labels with a scale function.

Zooming

Without clipping (preferred):
t + coord_cartesian(xlim = c(0, 100), ylim = c(10, 20))

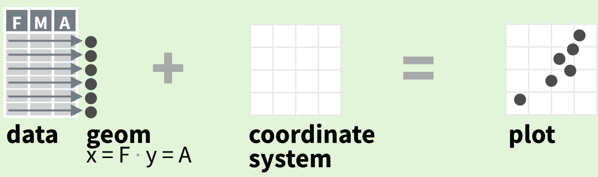
With clipping (removes unseen data points):
t + xlim(0, 100) **+ ylim**(10, 20)

t + scale_x_continuous(limits = c(0, 100)) **+ scale_y_continuous**(limits = c(0, 100))

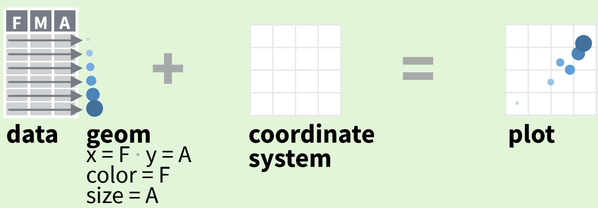
Data visualization with ggplot2 : : CHEAT SHEET

Basics

ggplot2 is based on the **grammar of graphics**, the idea that you can build every graph from the same components: a **data** set, a **coordinate system**, and **geoms**—visual marks that represent data points.



To display values, map variables in the data to visual properties of the geom (**aesthetics**) like **size**, **color**, and **x** and **y** locations.



Complete the template below to build a graph.

ggplot (data = <DATA> **) +** — required
<GEOM_FUNCTION>**(mapping = aes(**<MAPPINGS>**),**
stat = <STAT>, position = <POSITION>) +
<COORDINATE_FUNCTION> +
<FACET_FUNCTION> +
<SCALE_FUNCTION> +
<THEME_FUNCTION>

Not required, sensible defaults supplied

ggplot(data = mpg, **aes**(x = cty, y = hwy)) Begins a plot that you finish by adding layers to. Add one geom function per layer.

last_plot() Returns the last plot.

ggsave("plot.png", width = 5, height = 5) Saves last plot as 5' x 5' file named "plot.png" in working directory. Matches file type to file extension.

Aes

Common aesthetic values.

color and **fill** - string ("red", "#RRGGBB")

linetype - integer or string (0 = "blank", 1 = "solid", 2 = "dashed", 3 = "dotted", 4 = "dotdash", 5 = "longdash", 6 = "twodash")

lineend - string ("round", "butt", or "square")

linejoin - string ("round", "mitre", or "bevel")

size - integer (line width in mm)

shape - integer/shape name or a single character ("a")

0 1 2 3 4 5 6 7 8 9 10 11 12
13 14 15 16 17 18 19 20 21 22 23 24 25

Geoms

Use a geom function to represent data points, use the geom's aesthetic properties to represent variables. Each function returns a layer.

GRAPHICAL PRIMITIVES

a <- ggplot(economics, aes(date, unemploy))
b <- ggplot(seals, aes(x = long, y = lat))

a + geom_blank() and **a + expand_limits()**
Ensure limits include values across all plots.

b + geom_curve(aes(yend = lat + 1, xend = long + 1), curvature = 1**)** - x, xend, y, yend, alpha, angle, color, curvature, linetype, size

a + geom_path(lineend = "butt", linejoin = "round", linemitre = 1**)**
x, y, alpha, color, group, linetype, size

a + geom_polygon(aes(alpha = 50)**)** - x, y, alpha, color, fill, group, subgroup, linetype, size

b + geom_rect(aes(xmin = long, ymin = lat, xmax = long + 1, ymax = lat + 1)**)** - xmax, xmin, ymax, ymin, alpha, color, fill, linetype, size

a + geom_ribbon(aes(ymin = unemploy - 900, ymax = unemploy + 900)**)** - x, ymax, ymin, alpha, color, fill, group, linetype, size

LINE SEGMENTS

common aesthetics: x, y, alpha, color, linetype, size

b + geom_abline(aes(intercept = 0, slope = 1)**)**
b + geom_hline(aes(yintercept = lat)**)**
b + geom_vline(aes(xintercept = long)**)**

b + geom_segment(aes(yend = lat + 1, xend = long + 1)**)**
b + geom_spoke(aes(angle = 1:1155, radius = 1)**)**

ONE VARIABLE continuous

c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)

c + geom_area(stat = "bin"**)**
x, y, alpha, color, fill, linetype, size

c + geom_density(kernel = "gaussian"**)**
x, y, alpha, color, fill, group, linetype, size, weight

c + geom_dotplot()
x, y, alpha, color, fill

c + geom_freqpoly()
x, y, alpha, color, group, linetype, size

c + geom_histogram(binwidth = 5**)**
x, y, alpha, color, fill, linetype, size, weight

c2 + geom_qq(aes(sample = hwy)**)**
x, y, alpha, color, fill, linetype, size, weight

discrete

d <- ggplot(mpg, aes(fl))

d + geom_bar()
x, alpha, color, fill, linetype, size, weight

TWO VARIABLES

both continuous

e <- ggplot(mpg, aes(cty, hwy))

e + geom_label(aes(label = cty), nudge_x = 1, nudge_y = 1**)** - x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

e + geom_point()
x, y, alpha, color, fill, shape, size, stroke

e + geom_quantile()
x, y, alpha, color, group, linetype, size, weight

e + geom_rug(sides = "bl"**)**
x, y, alpha, color, linetype, size

e + geom_smooth(method = lm**)**
x, y, alpha, color, fill, group, linetype, size, weight

e + geom_text(aes(label = cty), nudge_x = 1, nudge_y = 1**)** - x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

one discrete, one continuous

f <- ggplot(mpg, aes(class, hwy))

f + geom_col()
x, y, alpha, color, fill, group, linetype, size

f + geom_boxplot()
x, y, lower, middle, upper, ymax, ymin, alpha, color, fill, group, linetype, shape, size, weight

f + geom_dotplot(binaxis = "y", stackdir = "center"**)**
x, y, alpha, color, fill, group

f + geom_violin(scale = "area"**)**
x, y, alpha, color, fill, group, linetype, size, weight

both discrete

g <- ggplot(diamonds, aes(cut, color))

g + geom_count()
x, y, alpha, color, fill, shape, size, stroke

e + geom_jitter(height = 2, width = 2**)**
x, y, alpha, color, fill, shape, size

continuous bivariate distribution

h <- ggplot(diamonds, aes(carat, price))

h + geom_bin2d(binwidth = c(0.25, 500)**)**
x, y, alpha, color, fill, linetype, size, weight

h + geom_density_2d()
x, y, alpha, color, group, linetype, size

h + geom_hex()
x, y, alpha, color, fill, size

continuous function

i <- ggplot(economics, aes(date, unemploy))

i + geom_area()
x, y, alpha, color, fill, linetype, size

i + geom_line()
x, y, alpha, color, group, linetype, size

i + geom_step(direction = "hv"**)**
x, y, alpha, color, group, linetype, size

visualizing error

df <- data.frame(grp = c("A", "B"), fit = 4:5, se = 1:2)
j <- ggplot(df, aes(grp, fit, ymin = fit - se, ymax = fit + se))

j + geom_crossbar(fatten = 2**)** - x, y, ymax, ymin, alpha, color, fill, group, linetype, size

j + geom_errorbar() - x, ymax, ymin, alpha, color, group, linetype, size, width
Also **geom_errorbarh()**.

j + geom_linerange()
x, ymin, ymax, alpha, color, group, linetype, size

j + geom_pointrange() - x, y, ymin, ymax, alpha, color, fill, group, linetype, shape, size

maps

data <- data.frame(murder = USArrests$Murder,
state = tolower(rownames(USArrests)))
map <- map_data("state")
k <- ggplot(data, aes(fill = murder))

k + geom_map(aes(map_id = state), map = map**)**
+ expand_limits(x = map$long, y = map$lat**)**
map_id, alpha, color, fill, linetype, size

THREE VARIABLES

seals$z <- with(seals, sqrt(delta_long^2 + delta_lat^2)); l <- ggplot(seals, aes(long, lat))

l + geom_contour(aes(z = z)**)**
x, y, z, alpha, color, group, linetype, size, weight

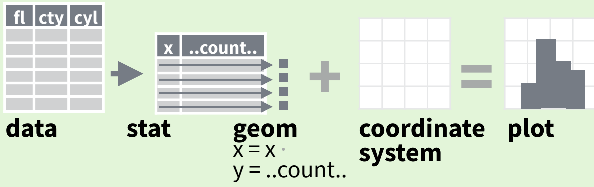
l + geom_contour_filled(aes(fill = z)**)**
x, y, alpha, color, fill, group, linetype, size, subgroup

l + geom_raster(aes(fill = z), hjust = 0.5, vjust = 0.5, interpolate = FALSE**)**
x, y, alpha, fill

l + geom_tile(aes(fill = z)**)**
x, y, alpha, color, fill, linetype, size, width

Stats
An alternative way to build a layer.

A stat builds new variables to plot (e.g., count, prop).



Visualize a stat by changing the default stat of a geom function, **geom_bar(stat="count")** or by using a stat function, **stat_count(geom="bar")**, which calls a default geom to make a layer (equivalent to a geom function). Use **..name..** syntax to map stat variables to aesthetics.

geom to use | stat function | geommappings

i + stat_density_2d(aes(fill = ..level..), geom = "polygon")

variable created by stat

c + stat_bin(binwidth = 1, boundary = 10)
x, y | ..count.., ..ncount.., ..density.., ..ndensity..

c + stat_count(width = 1) **x, y** | ..count.., ..prop..

c + stat_density(adjust = 1, kernel = "gaussian")
x, y | ..count.., ..density.., ..scaled..

e + stat_bin_2d(bins = 30, drop = T)
x, y, fill | ..count.., ..density..

e + stat_bin_hex(bins = 30) **x, y, fill** | ..count.., ..density..

e + stat_density_2d(contour = TRUE, n = 100)
x, y, color, size | ..level..

e + stat_ellipse(level = 0.95, segments = 51, type = "t")

l + stat_contour(aes(z = z)) **x, y, z, order** | ..level..

l + stat_summary_hex(aes(z = z), bins = 30, fun = max)
x, y, z, fill | ..value..

l + stat_summary_2d(aes(z = z), bins = 30, fun = mean)
x, y, z, fill | ..value..

f + stat_boxplot(coef = 1.5)
x, y | ..lower.., ..middle.., ..upper.., ..width.. , ..ymin.., ..ymax..

f + stat_ydensity(kernel = "gaussian", scale = "area") **x, y**
| ..density.., ..scaled.., ..count.., ..n.., ..violinwidth.., ..width..

e + stat_ecdf(n = 40) **x, y** | ..x.., ..y..

e + stat_quantile(quantiles = c(0.1, 0.9), formula = y ~ log(x), method = "rq") **x, y** | ..quantile..

e + stat_smooth(method = "lm", formula = y ~ x, se = T, level = 0.95) **x, y** | ..se.., ..x.., ..y.., ..ymin.., ..ymax..

ggplot() + xlim(-5, 5) **+ stat_function(**fun = dnorm, n = 20, geom = "point") **x** | ..x.., ..y..

ggplot() + stat_qq(aes(sample = 1:100))
x, y, sample | ..sample.., ..theoretical..

e + stat_sum() x, y, size | ..n.., ..prop..

e + stat_summary(fun.data = "mean_cl_boot")

h + stat_summary_bin(fun = "mean", geom = "bar")

e + stat_identity()

e + stat_unique()

Scales
Override defaults with **scales** package.

Scales map data values to the visual values of an aesthetic. To change a mapping, add a new scale.

n <- d + geom_bar(aes(fill = fl))

scale_ | aesthetic to adjust | prepackaged scale to use | scale-specific arguments

n + scale_fill_manual(
values = c("skyblue", "royalblue", "blue", "navy"),
limits = c("d", "e", "p", "r"), **breaks** =c("d", "e", "p", "r"),
name = "fuel", **labels** = c("D", "E", "P", "R"))

range of values to include in mapping | title to use in legend/axis | labels to use in legend/axis | breaks to use in legend/axis

GENERAL PURPOSE SCALES
Use with most aesthetics

scale_*_continuous() - Map cont' values to visual ones.
scale_*_discrete() - Map discrete values to visual ones.
scale_*_binned() - Map continuous values to discrete bins.
scale_*_identity() - Use data values as visual ones.
scale_*_manual(values = c()) - Map discrete values to manually chosen visual ones.
scale_*_date(date_labels = "%m/%d"), date_breaks = "2 weeks") - Treat data values as dates.
scale_*_datetime() - Treat data values as date times. Same as scale_*_date(). See ?strptime for label formats.

X & Y LOCATION SCALES
Use with x or y aesthetics (x shown here)

scale_x_log10() - Plot x on log10 scale.
scale_x_reverse() - Reverse the direction of the x axis.
scale_x_sqrt() - Plot x on square root scale.

COLOR AND FILL SCALES (DISCRETE)

n + scale_fill_brewer(palette = "Blues")
For palette choices:
RColorBrewer::display.brewer.all()

n + scale_fill_grey(start = 0.2, end = 0.8, na.value = "red")

COLOR AND FILL SCALES (CONTINUOUS)

o <- c + geom_dotplot(aes(fill = ..x..))

o + scale_fill_distiller(palette = "Blues")

o + scale_fill_gradient(low="red", high="yellow")

o + scale_fill_gradient2(low = "red", high = "blue", mid = "white", midpoint = 25)

o + scale_fill_gradientn(colors = topo.colors(6))
Also: rainbow(), heat.colors(), terrain.colors(), cm.colors(), RColorBrewer::brewer.pal()

SHAPE AND SIZE SCALES

p <- e + geom_point(aes(shape = fl, size = cyl))

p + scale_shape() + scale_size()
p + scale_shape_manual(values = c(3:7))

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25

p + scale_radius(range = c(1,6))
p + scale_size_area(max_size = 6)

Coordinate Systems

r <- d + geom_bar()

r + coord_cartesian(xlim = c(0, 5)) - xlim, ylim
The default cartesian coordinate system.

r + coord_fixed(ratio = 1/2)
ratio, xlim, ylim - Cartesian coordinates with fixed aspect ratio between x and y units.

ggplot(mpg, aes(y = fl)) **+ geom_bar()**
Flip cartesian coordinates by switching x and y aesthetic mappings.

r + coord_polar(theta = "x", direction=1)
theta, start, direction - Polar coordinates.

r + coord_trans(y = "sqrt") - x, y, xlim, ylim
Transformed cartesian coordinates. Set xtrans and ytrans to the name of a window function.

π + coord_quickmap()
π + coord_map(projection = "ortho", orientation = c(41, -74, 0)) - projection, xlim, ylim
Map projections from the mapproj package (mercator (default), azequalarea, lagrange, etc.).

Position Adjustments

Position adjustments determine how to arrange geoms that would otherwise occupy the same space.

s <- ggplot(mpg, aes(fl, fill = drv))

s + geom_bar(position = "dodge")
Arrange elements side by side.

s + geom_bar(position = "fill")
Stack elements on top of one another, normalize height.

e + geom_point(position = "jitter")
Add random noise to X and Y position of each element to avoid overplotting.

e + geom_label(position = "nudge")
Nudge labels away from points.

s + geom_bar(position = "stack")
Stack elements on top of one another.

Each position adjustment can be recast as a function with manual **width** and **height** arguments:
s + geom_bar(position = position_dodge(width = 1))

Themes

r + theme_bw()
White background with grid lines.

r + theme_gray()
Grey background (default theme).

r + theme_dark()
Dark for contrast.

r + theme_classic()

r + theme_light()

r + theme_linedraw()

r + theme_minimal()
Minimal theme.

r + theme_void()
Empty theme.

r + theme() Customize aspects of the theme such as axis, legend, panel, and facet properties.
r + ggtitle("Title") + theme(plot.title.postion = "plot")
r + theme(panel.background = element_rect(fill = "blue"))

Faceting

Facets divide a plot into subplots based on the values of one or more discrete variables.

t <- ggplot(mpg, aes(cty, hwy)) + geom_point()

t + facet_grid(cols = vars(fl))
Facet into columns based on fl.

t + facet_grid(rows = vars(year))
Facet into rows based on year.

t + facet_grid(rows = vars(year), cols = vars(fl))
Facet into both rows and columns.

t + facet_wrap(vars(fl))
Wrap facets into a rectangular layout.

Set **scales** to let axis limits vary across facets.

t + facet_grid(rows = vars(drv), cols = vars(fl), scales = "free")
x and y axis limits adjust to individual facets:
"free_x" - x axis limits adjust
"free_y" - y axis limits adjust

Set **labeller** to adjust facet label:

t + facet_grid(cols = vars(fl), labeller = label_both)

fl: c	fl: d	fl: e	fl: p	fl: r

t + facet_grid(rows = vars(fl), labeller = label_bquote(alpha ^ .(fl)))

α^c	α^d	α^e	α^p	α^r

Labels and Legends

Use **labs()** to label the elements of your plot.

t + labs(x = "New x axis label", **y** = "New y axis label",
title ="Add a title above the plot",
subtitle = "Add a subtitle below title",
caption = "Add a caption below plot",
alt = "Add alt text to the plot",
<AES> = "New <AES> legend title")

t + annotate(geom = "text", x = 8, y = 9, label = "A")
Places a geom with manually selected aesthetics.

p + guides(x = guide_axis(n.dodge = 2)) Avoid crowded or overlapping labels with guide_axis(n.dodge or angle).

n + guides(fill = "none") Set legend type for each aesthetic: colorbar, legend, or none (no legend).

n + theme(legend.position = "bottom")
Place legend at "bottom", "top", "left", or "right".

n + scale_fill_discrete(name = "Title", labels = c("A", "B", "C", "D", "E"))
Set legend title and labels with a scale function.

Zooming

Without clipping (preferred):
t + coord_cartesian(xlim = c(0, 100), ylim = c(10, 20))

With clipping (removes unseen data points):
t + xlim(0, 100) **+ ylim(**10, 20)

t + scale_x_continuous(limits = c(0, 100)) **+ scale_y_continuous(**limits = c(0, 100))

Data Transformation with data.table : : CHEAT SHEET

Basics

data.table is an extremely fast and memory efficient package for transforming data in R. It works by converting R's native data frame objects into data.tables with new and enhanced functionality. The basics of working with data.tables are:

dt[i, j, by]

Take data.table **dt**,
subset rows using **i**
and manipulate columns with **j**,
grouped according to **by**.

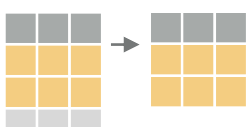
data.tables are also data frames – functions that work with data frames therefore also work with data.tables.

Create a data.table

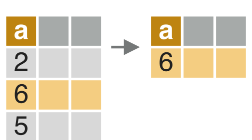
data.table(a = c(1, 2), b = c("a", "b")**)** – create a data.table from scratch. Analogous to data.frame().

setDT(df**)*** or **as.data.table(**df**)** – convert a data frame or a list to a data.table.

Subset rows using i



dt[**1:2**,] – subset rows based on row numbers.



dt[**a > 5**,] – subset rows based on values in one or more columns.

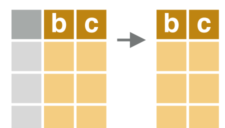
LOGICAL OPERATORS TO USE IN i

<	<=	is.na()	%in%	|	**%like%**
>	>=	!is.na()	!	&	**%between%**

Manipulate columns with j

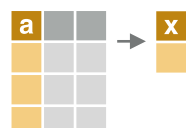
EXTRACT

dt[, **c(2)**] – extract columns by number. Prefix column numbers with "-" to drop.



dt[, **.(b, c)**] – extract columns by name.

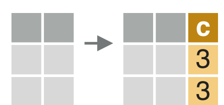
SUMMARIZE



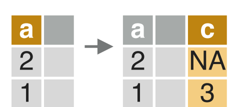
dt[, **.(x = sum(a))**] – create a data.table with new columns based on the summarized values of rows.

Summary functions like mean(), median(), min(), max(), etc. can be used to summarize rows.

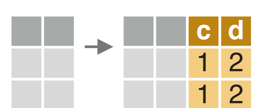
COMPUTE COLUMNS*



dt[, **c := 1 + 2**] – compute a column based on an expression.

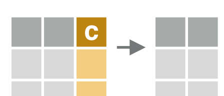


dt[**a == 1, c := 1 + 2**] – compute a column based on an expression but only for a subset of rows.



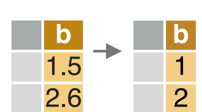
dt[, **`:=`(c = 1 , d = 2)**] – compute multiple columns based on separate expressions.

DELETE COLUMN



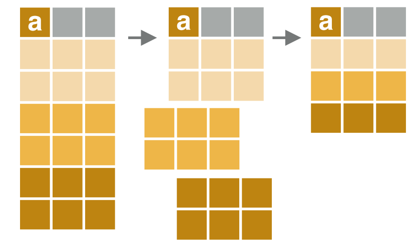
dt[, **c := NULL**] – delete a column.

CONVERT COLUMN TYPE



dt[, **b := as.integer(b)**] – convert the type of a column using as.integer(), as.numeric(), as.character(), as.Date(), etc..

Group according to by



dt[, j, **by = .(a)**] – group rows by values in specified columns.

dt[, j, **keyby = .(a)**] – group *and simultaneously sort* rows by values in specified columns.

COMMON GROUPED OPERATIONS

dt[, **.(c = sum(b)), by = a**] – summarize rows within groups.

dt[, **c := sum(b), by = a**] – create a new column and compute rows within groups.

dt[, **.SD[1], by = a**] – extract first row of groups.

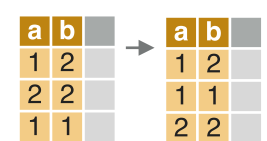
dt[, **.SD[.N], by = a**] – extract last row of groups.

Chaining

dt[…][…] – perform a sequence of data.table operations by *chaining* multiple "[]".

Functions for data.tables

REORDER

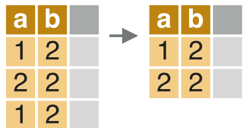


setorder(dt, a, -b**)** – reorder a data.table according to specified columns. Prefix column names with "**-**" for descending order.

* SET FUNCTIONS AND :=

data.table's functions prefixed with "set" and the operator ":=" work without "<-" to alter data without making copies in memory. E.g., the more efficient "setDT(df)" is analogous to "df <- as.data.table(df)".

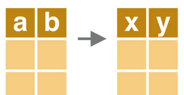
UNIQUE ROWS



unique(dt, by = c("a", "b")) – extract unique rows based on columns specified in "by". Leave out "by" to use all columns.

uniqueN(dt, by = c("a", "b")) – count the number of unique rows based on columns specified in "by".

RENAME COLUMNS



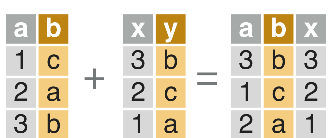
setnames(dt, c("a", "b"), c("x", "y")) – rename columns.

SET KEYS

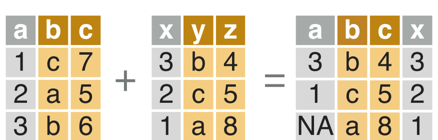
setkey(dt, a, b) – set keys to enable fast repeated lookup in specified columns using "dt[.(value),]" or for merging without specifying merging columns using "dt_a[dt_b]".

Combine data.tables

JOIN

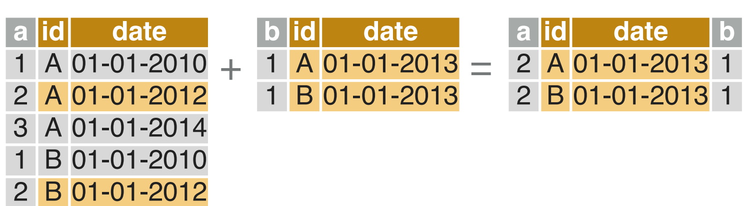


dt_a[dt_b, **on = .(b = y)**] – join data.tables on rows with equal values.



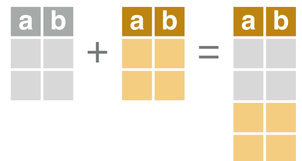
dt_a[dt_b, **on = .(b = y, c > z)**] – join data.tables on rows with equal *and unequal* values.

ROLLING JOIN

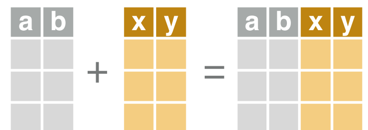


dt_a[dt_b, **on = .(id = id, date = date), roll = TRUE**] – join data.tables on matching rows in id columns but only keep the most recent preceding match with the left data.table according to date columns. "roll = -Inf" reverses direction.

BIND



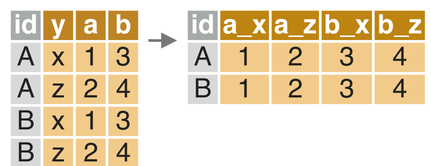
rbind(dt_a, dt_b) – combine rows of two data.tables.



cbind(dt_a, dt_b) – combine columns of two data.tables.

Reshape a data.table

RESHAPE TO WIDE FORMAT

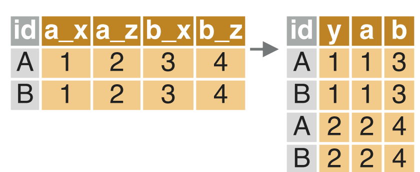


dcast(dt,
id ~ y,
value.var = c("a", "b"))

Reshape a data.table from long to wide format.

dt	A data.table.
id ~ y	Formula with a LHS: ID columns containing IDs for multiple entries. And a RHS: columns with values to spread in column headers.
value.var	Columns containing values to fill into cells.

RESHAPE TO LONG FORMAT



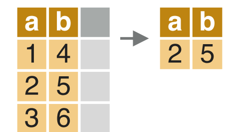
melt(dt,
id.vars = c("id"),
measure.vars = patterns("^a", "^b"),
variable.name = "y",
value.name = c("a", "b"))

Reshape a data.table from wide to long format.

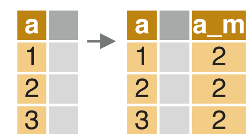
dt	A data.table.
id.vars	ID columns with IDs for multiple entries.
measure.vars	Columns containing values to fill into cells (often in pattern form).
variable.name, value.name	Names of new columns for variables and values derived from old headers.

Apply function to cols.

APPLY A FUNCTION TO MULTIPLE COLUMNS



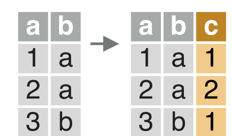
dt[, **lapply(.SD, mean)**, **.SDcols = c("a", "b")**] – apply a function – e.g. mean(), as.character(), which.max() – to columns specified in .SDcols with lapply() and the .SD symbol. Also works with groups.



cols <- c("a")
dt[, **paste0(cols, "_m") := lapply(.SD, mean)**,
.SDcols = cols] – apply a function to specified columns and assign the result with suffixed variable names to the original data.

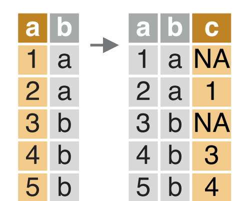
Sequential rows

ROW IDS



dt[, **c := 1:.N, by = b**] – within groups, compute a column with sequential row IDs.

LAG & LEAD



dt[, **c := shift(a, 1), by = b**] – within groups, duplicate a column with rows *lagged* by specified amount.

dt[, **c := shift(a, 1, type = "lead"), by = b**] – within groups, duplicate a column with rows *leading* by specified amount.

read & write files

IMPORT

fread("file.csv") – read data from a flat file such as .csv or .tsv into R.

fread("file.csv", select = c("a", "b")) – read specified columns from a flat file into R.

EXPORT

fwrite(dt, "file.csv") – write data to a flat file from R.

DeclareDesign: : CHEAT SHEET

Model

What is your model of the world, including how outcomes respond to interventions in the world?

Population

Define the size of the population, hierarchical structure (if any), and background variables.

Simple dataset with no background variables

```
pop <- declare_population(N = 100)
pop()
```

Simple dataset with background variables

```
declare_population(N = 100,
                   X = rnorm(N))
```

Two-level dataset

```
declare_population(
  schools =
    add_level(N = 10,
              funding = rnorm(N)),
  students =
    add_level(N = 100,
              scores = rnorm(N))
)
```

Outcomes

Outcomes that depend on a treatment (Z)

Using a formula

```
declare_potential_outcomes(
  Y ~ .5 * Z + rnorm(N))
```

As separate variables

```
declare_potential_outcomes(
  Y_Z_0 = rnorm(N),
  Y_Z_1 = Y_Z_0 + .5)
```

Outcomes that do not depend on treatment

```
declare_potential_outcomes(
  Y = rnorm(N))
```

Inquiry

What is the research question you want to answer?

Causal inquiries

```
declare_estimand(
  ATE = mean(Y_Z_1 - Y_Z_0))
```

Descriptive inquiries

```
declare_estimand(
  Y_median = median(Y))
```

Conditional estimands

```
declare_estimand(
  LATE = mean(Y_Z_1 - Y_Z_0),
  subset = complier == TRUE)
```

Data Strategy

How will you generate data to answer your inquiry?

Sampling

```
declare_sampling(n = 100)

declare_sampling(
  strata_n = 20,
  strata = urban_area)
```

Treatment assignment

```
declare_assignment(m = 100)

declare_assignment(
  clusters = villages,
  m = 10)
```

Answer Strategy

How will you generate an answer to your inquiry?

OLS with robust standard errors

```
declare_estimator(
  Y ~ Z, model = lm_robust)
```

2SLS instrumental variables regression with robust SEs

```
declare_estimator(
  Y ~ D | Z, model = iv_robust)
```

Difference-in-means

```
declare_estimator(
  Y ~ Z,
  model = difference_in_means)
```

DeclareDesign is a software implementation of the MIDA framework, according to which research designs have a **M**odel of the world, an **I**nquiry about that model, a **D**ata strategy that generates information about the world, and an **A**nswer strategy that uses data to make a guess about the **I**nquiry. Declared designs can be “diagnosed” to calculate the properties of the design such as power and bias using Monte Carlo simulation.

All `declare_*` functions return *functions*. Most functions take a data.frame and return a data.frame.

Design Declaration

Put together all the steps into a declared design using the + operator

```
design <-
  declare_population(N = 200, X = rnorm(N)) +
  declare_potential_outcomes(Y ~ .5 * Z + X) +
  declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0)) +
  declare_sampling(n = 100) +
  declare_assignment(m = 50) +
  declare_estimator(Y ~ Z, model = lm_robust)
```

```
draw_data(design)
draw_estimates(design)
get_estimates(design, data = real_data)
draw_estimands(design)
run_design(design)
summary(design)
compare_designs(design_1, design_2)
```

Design Diagnosis

Diagnose the properties of your design

```
diagnosis <- diagnose_design(
  design, sims = 100, bootstrap_sims = 100)
```

```
summary(diagnosis)
get_diagnosands(diagnosis)
get_simulations(diagnosis)
```

Custom diagnosands

```
diagnose_design(
  design,
  diagnosands = declare_diagnosands(
    sig_pos = mean(p.value < .05 & estimate > 0)))
```

Create, query and manipulate distributions with distr6 : : CHEAT SHEET

Introduction

distr6 is an object-oriented interface for probability distributions. Including distributions as objects, statistical properties of distributions, composite modelling and decorators for numerical imputation. As well as this cheat sheet, see:

- GitHub for an issue tracker and latest development branch
- CRAN for package meta-data
- The distr6 website for more complete tutorials.

R6 Classes

`Distribution` The parent class to most distr6 classes.	Distribution
`SDistribution` Class given to all probability distributions implemented in distr6.	Distribution ↑ SDistribution
`Kernel` Class given to all kernel-like probability distributions.	Distribution ↑ Kernel
`Decorator` Used to add or impute methods to a Distribution.	
`Wrapper` Create composite distributions by adapting class properties	
`ParameterSet` Class used to add parameters to a distribution.	

R6 Basics

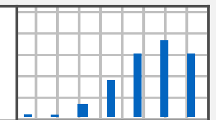
$ All methods are called using dollar-sign notation	`N <- Normal$new()`
	`N$mean()`
	`N$pdf(2)`

clone Objects are copied using the clone method	`N1 <- Normal$new()` `N2 <- N1$clone()`
Method chaining Call one method after another	`Normal$new()$pdf(2)`

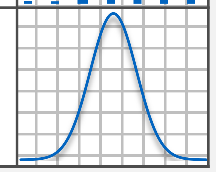
Construct a Distribution

Each distribution has a default parameterisation, and all common parameterisations are available.

```
Binomial$new()
Binomial$new(size=5,prob=0.6)
Binomial$new(size=5,qprob=0.4)
```



```
Normal$new()
Normal$new(mean=0,sd=1)
Normal$new(mean=0,var=1)
Normal$new(mean=0,prec=1)
```



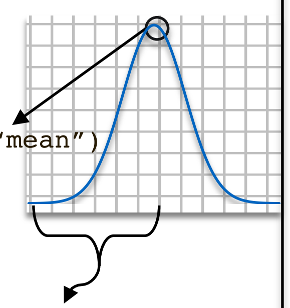
You can list all the implemented probability distributions and kernels

```
listDistributions()

listKernels()
```

Get and Set Parameters

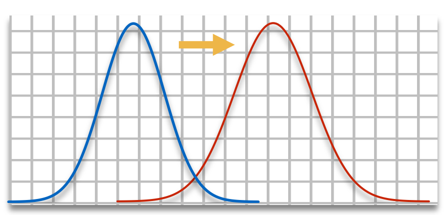
```
N <- Normal$new()
N$parameters()
N$getParameterValue("mean")
```



```
N$getParameterValue("variance")
```

Any parameter can be set, even if it wasn't used in construction. And multiple can be updated at the same time.

```
N$setParameterValue(mean = 2)
N$setParameterValue(prec = 2)
N$setParameterValue(mean = 3, sd = 3)
```



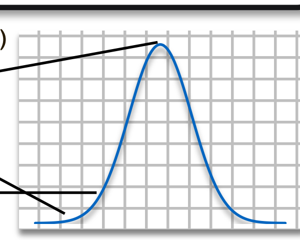
Properties and Traits

Property	Class attribute. Distribution property is dependent on parameterisation.
Trait	Class attribute. Distribution trait is independent of parameterisation.

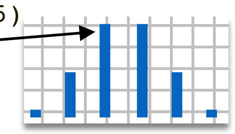
`$properties()`	`$traits()`
`$support()` values in which distribution pdf is non-zero	`$valueSupport()` discrete/continuous/mixture
`$symmetry()` symmetric/asymmetric	`$variateForm()` univariate/multi-variate/matrixvariate
`$kurtosis()` leptokurtic/mesokurtic/platykurtic	`$type()` Mathematical set, class *SetInterval*
`$skewness()` negative/no/positive	

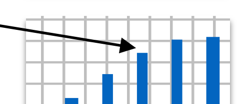
Statistical Methods

```
N <- Normal$new()
N$mean()
N$variance()
N$skewness()
N$kurtosis()
N$entropy()
```



```
B <- Binomial$new(size = 5)
B$pdf(0:5)
B$cdf(0:5)
B$quantile(0.42)
B$rand(5)
```





Use ?SDistribution, ?Normal (or any other distribution) to see available methods.

S3 and Piping

distr6 uses 'R62S3' so every R6 method has an S3 dispatch available.

`N <- Normal$new()`	
`N$mean()`	→ `mean(N)`
`N$getParameterValue("mean")`	→ `getParameterValue(N, "mean")`
`N$pdf(1:5)`	→ `pdf(N, 1:5)`

Use the 'magrittr' package for method chaining and piping (%>%).

```
> N <- Normal$new()
> N$setParameterValue(sd=2)$getParameterValue("var")
```

↓ `library(magrittr)`

```
> N <- Normal$new()
> N %>% setParameterValue(sd=2) %>%
    getParameterValue("var")
```

Multivariate Distributions

Multivariate distributions are handled just like univariate distributions, except the pdf/cdf functions take multiple arguments, as do cf and mgf where available.

```
> MN <- MultivariateNormal$new(mean =
c(0,0,0), cov = c(3,-1,-1,-1,1,0,-1,0,1))

> MN <- MultivariateNormal$new(mean =
c(0,0,0), prec = c(3,-1,-1,-1,1,0,-
1,0,1))

> MN$pdf(1, 2, 3)
> MN$cdf(1, 1, 1)
```

Once again vectorization is available

```
> MN$pdf(1:2, 2:3, 1:2)
> MN$cdf(c(0.45, 0.65),
    c(0.12, 0.99), c(0, 1))
```

Create, query and manipulate distributions with distr6 : : CHEAT SHEET

Decorators

Decorators are a design pattern (Gamma et al., 1994) used to add methods to objects.

Distribution
- Method A - Method B

Decorator
- Method C

`decorate(distribution, decorator)`

Decorated Distribution
- Method A - Method B - Method C

Available Decorators

`CoreStatistics`	Imputes common numeric statistical results, adds generalised expectation and moments function.
`ExoticStatistics`	Adds methods for survival analysis and statistical modelling.
`FunctionImputation`	Uses numerical methods to impute missing pdf/cdf/quantile/rand functions

Remember to decorate first before using a method from a decorator

```
> N <- Normal$new()
> N$survival(1)
Error: attempt to apply non-function
> decorate(N, ExoticStatistics)
> N$survival(1)
[1] 0.1586553
```

S3 methods will now work too

```
> N <- Normal$new(decorators = ExoticStatistics)
> pdfPNorm(N, 3, -1, 1)
[1] 0.4383636
```

Use listing to see which decorators are currently implemented.

`listDecorators()`

Wrappers

*Wrappers are based on the **Adapter** design pattern (Gamma et al., 1994) and are used to change the interface of an object.*

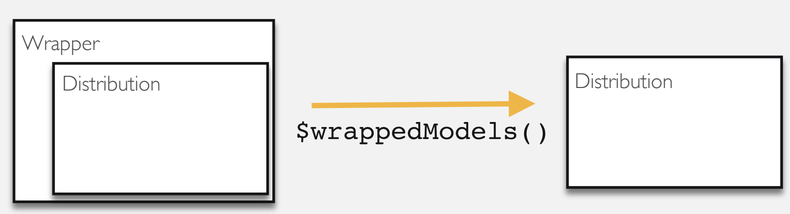
Distribution
- Method A - Method B

`Wrapper$new(distribution, ...)`

Wrapped Distribution
- Method A - Method C

Available Wrappers

`ProductDistribution` Product of two or more distributions.	**`VectorDistribution`** Vectorizes two or more distributions.
`Convolution` Addition (or subtraction) of two distributions	**`MixtureDistribution`** Weighted mixture of two or more distributions
`HuberizedDistribution` Huberizes a distribution between limits.	**`TruncatedDistribution`** Truncates a distribution between limits.




```
> TruncatedDistribution$new(Normal$new(),
        lower = -1, upper = 1)
> MixtureDistribution$new(list(Binomial$new(),
        Normal$new()), weights = c(0.4, 0.6))
> ProductDistribution$new(list(Exponential$new(),
        Normal$new()))$pdf(1,1)
```

Use listing to see which wrappers are currently implemented.

`listWrappers()`

Custom Distributions

Custom distributions can be created using **`Distribution$new`**, *this is not the same as implementing a new* **`SDistribution`**!

```
pdf <-
function(x1)return(1/(self$getParameterValue("upper
")-self$getParameterValue("lower")))
```

The **`self`** *argument tells the object to call the method on itself.*

All **`pdf/cdf`** *methods in distr6 use* **`'x1,x2,...'`** *as their arguments*

```
cdf <- function(x1)return((x1 -
self$getParameterValue("lower")) /
(self$getParameterValue("upper") -
self$getParameterValue("lower")))
```

`ParameterSet` *is the class used for distr6 parameters.*

```
ps <- ParameterSet$new(id = list("lower","upper"),
value = c(1,10), support =
list(Reals$new(),Reals$new()), settable =
list(TRUE, TRUE))
```

The argument **`support`** *is of type* **`SetInterval`**.
See **`listSpecialSets()`**

Unique distribution **`name`** *and one-word* **`short_name`** *(ID)*

```
dist <- Distribution$new(name = "Uniform",
short_name = "unif", type = Reals$new(), support =
Interval$new(1, 10), symmetric = TRUE, pdf = pdf,
cdf = cdf, parameters = ps, description = "Custom
uniform distribution", decorators = CoreStatistics)
```

Distribution **`type`** *and* **`support`** *is of type* **`SetInterval`**.

`CoreStatistics` *decorator is optionally used to impute numeric results.*

`log` *and* **`lower.tail`** *arguments are added automatically*

```
> dist$pdf(1, log = TRUE)
[1] -2.197225
> dist$cdf(2, lower.tail = FALSE)
[1] 0.8888889
> decorate(dist, FunctionImputation)
> dist$mean()
[1] 5.5
> dist$quantile(0.42)
[1] 4.78
```

impute missing **`quantile`** *and* **`rand`** *methods*

estimatr : : CHEAT SHEET

OLS with lm_robust()

`lm_robust()` is `lm()` with robust SEs. HC2 is the default.

```
lm_robust(mpg ~ hp, data = mtcars)
lm_robust(mpg ~ hp, se_type = "HC1",
          data = mtcars)
lm_robust(mpg ~ hp, se_type = "classical",
          data = mtcars)
```

Indicate `clusters` to get clustered SEs. CR2 is the default.

```
lm_robust(mpg ~ hp, clusters = carb,
          data = mtcars)
lm_robust(mpg ~ hp, clusters = carb,
          se_type = "stata", data = mtcars)
```

Fixed effects two ways:

```
# FEs as "dummies"
lm_robust(mpg ~ hp + as.factor(am),
          data = mtcars)

# "Absorbing" FEs (substantially faster)
lm_robust(mpg ~ hp,
          fixed_effects = ~ am,
          data = mtcars)
```

post-estimation commands:

```
fit <- lm_robust(mpg ~ hp, data = mtcars)
summary(fit)
print(fit)
tidy(fit)
vcov(fit)
confint(fit)
nobs(fit)
predict(fit, newdata = mtcars)
```

2SLS with iv_robust()

`iv_robust()` is `AER::ivreg()` with robust SEs.

```
iv_robust(mpg ~ hp | am, data = mtcars)
iv_robust(mpg ~ hp | am,
          clusters = carb, data = mtcars)
```

Two-group estimators

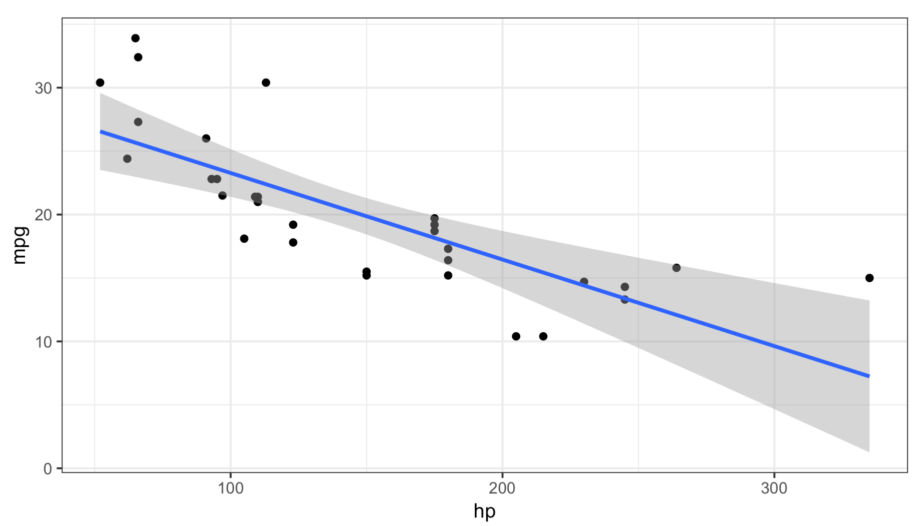
`difference_in_means()` and `horvitz_thompson()` compare two groups

```
difference_in_means(mpg ~ am, data = mtcars)
horvitz_thompson(mpg ~ am, data = mtcars)
```

ggplot2 integration

Use robust variance estimates for drawing confidence intervals:

```
library(ggplot2)
ggplot(mtcars, aes(mpg, hp)) +
  geom_point() +
  stat_smooth(method = "lm_robust") +
  theme_bw()
```



estimatr is part of the DeclareDesign suite of packages for designing, implementing, and analyzing social science research designs.

Multiple models

Same outcome, different subsets:

```
library(tidyverse)
mtcars %>%
  split(.$cyl) %>%
  map(~lm_robust(mpg ~ hp, data = .)) %>%
  map(tidy) %>%
  bind_rows(.id = "cyl")
```

Different outcomes, same subset:

```
c("mpg", "disp") %>%
  map(~formula(paste0(., " ~ hp"))) %>%
  map(~lm_robust(., data = mtcars)) %>%
  map(tidy) %>%
  bind_rows
```

Extras

```
# Lin (2013) covariate adjustment
lm_lin(mpg ~ am, covariates = ~ hp,
       data = mtcars)

# regression tables with texreg
fit <- lm_robust(mpg ~ hp, data = mtcars)
texreg::texreg(fit, include.ci = FALSE)
```

estimatr-to-Stata dictionary

estimatr	Stata
`lm_robust(y ~ z, data = dat)`	`reg y z, vce(hc2)`
`lm_robust(y ~ z, clusters = cl, se_type = "stata", data = dat)`	`reg y z, vce(cluster cl)`
`lm_robust(mpg ~ hp, fixed_effects = ~ am, se_type = "stata", data = mtcars)`	`areg mpg hp, absorb(am) vce(robust)`
`iv_robust(mpg ~ hp | am, se_type = "HC1", data = mtcars)`	`ivregress 2sls mpg (hp = am), vce(robust) small`

Access Eurostat data with eurostat::**cheat sheet**

Search and download

Data in the Eurostat database is stored in tables.
Each table has an identifier, a short table_code, and
a description (e.g. tps00199 - Total fertility rate).

Key eurostat functions allow to find the table_code,
download the eurostat table and polish labels in the table.

Find the table code

The **search_eurostat(pattern, ...)** function scans the directory
of Eurostat tables and returns codes and descriptions of
tables that match pattern.

```
library("eurostat")
query <- search_eurostat(pattern = "fertility rate",
                         type = "table", fixed = FALSE)
query[,1:2]
## title                                   code
## <chr>                                   <chr>
## Total fertility rate by NUTS 2 region tgs00100
## Total fertility rate                    tps00199
## Total fertility rate by NUTS 2 region tgs00100
```

Download the table

The **get_eurostat(id, time_format = "date", filters = "none", type = "code", cache = TRUE, ...)** function downloads the
requested table from the Eurostat bulk download facility or
from The Eurostat Web Services JSON API (if filters are defined).
Downloaded data is cached (if cache=TRUE).
Additional arguments define how to read the time column
(time_format) and if table dimensions shall be kept as
codes or converted to labels (type).

```
ct <- c("AT","BE","BG","CH","CY","CZ","DE","DK","EE","EL","ES",
        "FI","FR","HR","HU","IE","IS","IT","LI","LT","LU","LV",
        "MT","NL","NO","PL","PT","RO","SE","SI","SK","UK")
dat <- get_eurostat(id="tps00199", time_format="num",
                    filters = list(geo = ct))
dat[1:2,]
## indic_de geo    time values
## TOTFERRT AT     2006   1.41
## TOTFERRT AT     2007   1.38
```

Add labels

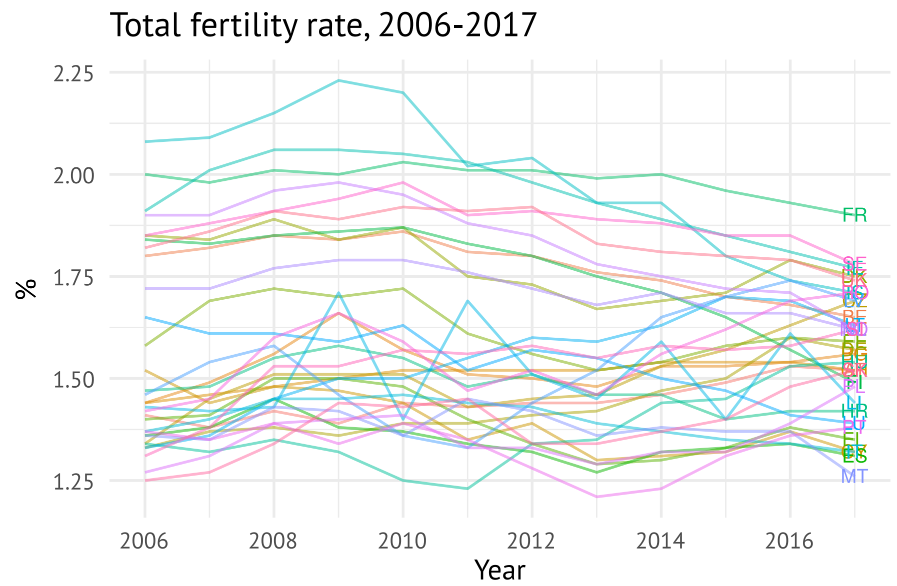
The **label_eurostat(x, lang = "en", ...)** gets definitions for Eurostat
codes and replace them with labels in given language ("en", "fr" or "de")

```
dat <- label_eurostat(dat)
dat[1:3,]
## indic_de             geo      time  values
## <fct>                <fct>   <dbl>  <dbl>
## Total fertility rate Andorra  2006   1.24
## Total fertility rate Albania  2006   1.67
## Total fertility rate Armenia  2006   1.34
```

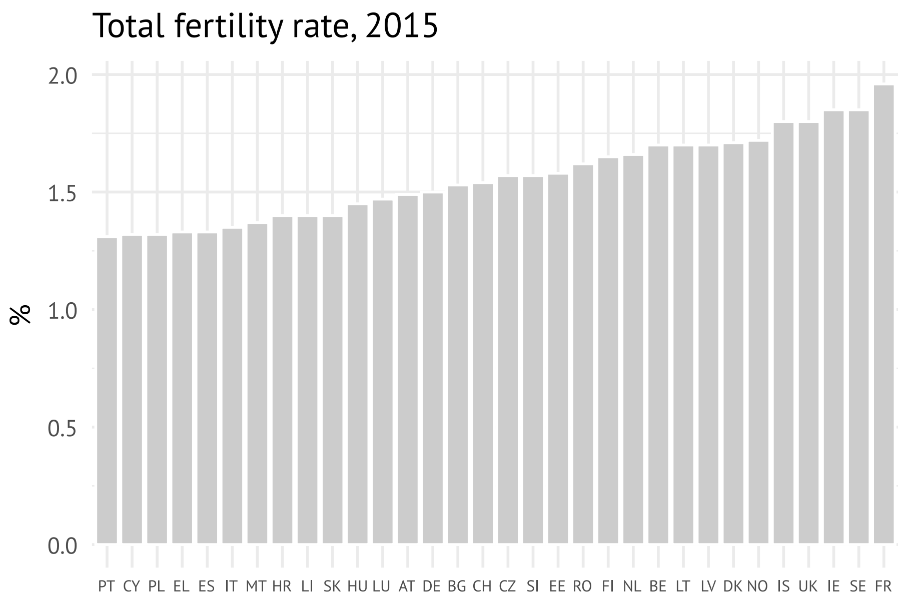

eurostat and plots

The **get_eurostat()** function returns tibbles in the long format. Packages
dplyr and tidyr are well suited to transform these objects. The **ggplot2**
-package is well suited to plot these objects.

```
dat <- get_eurostat(id="tps00199", filters = list(geo = ct))
library(ggplot2)
library(dplyr)
ggplot(dat,
       aes(x = time, y = values, color = geo, label = geo)) +
  geom_line(alpha = .5) +
  geom_text(data = dat %>% group_by(geo) %>%
              filter(time == max(time)),
            size = 2.6) +
  theme(legend.position = "none") +
  labs(title = "Total fertility rate, 2006-2017",
       x = "Year", y = "%")
```




```
dat_2015 <- dat %>%
  filter(time == "2015-01-01")
ggplot(dat_2015, aes(x = reorder(geo, values), y = values)) +
  geom_col(color = "white", fill = "grey80") +
  theme(axis.text.x = element_text(size = 6)) +
  labs(title = "Total fertility rate, 2015",
       y = "%", x = NULL)
```



eurostat and maps

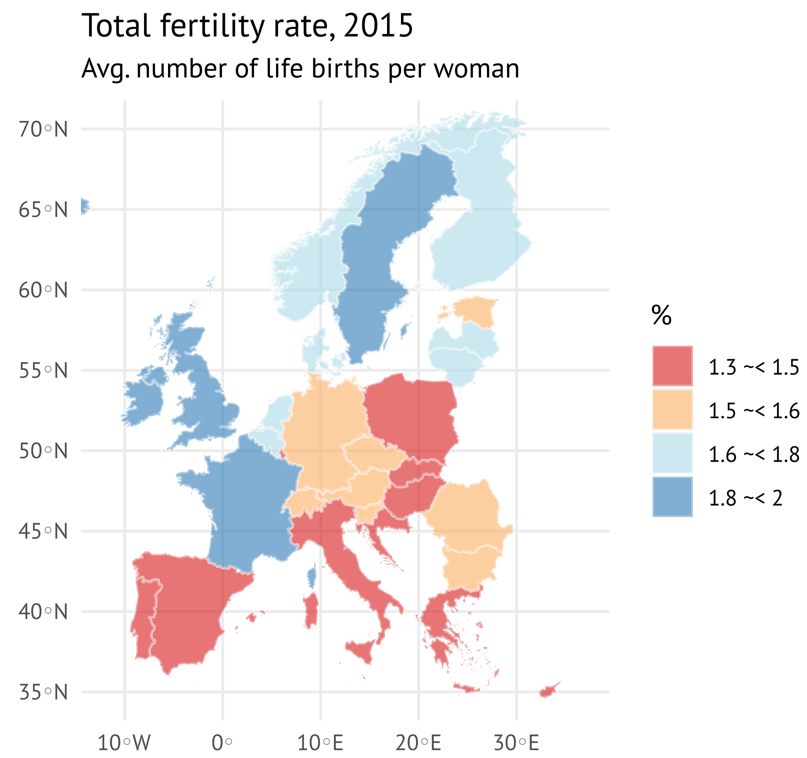
There are two function to work with geospatial data from GISCO. The
get_eurostat_geospatial() returns spatial data as sf-object.
Object can me merged with data.frames using **dplyr::*_join()**-functions.
The **cut_to_classes()** is a wrapper for cut() - function and
is used for categorizing data for maps with tidy labels.

```
mapdata <- get_eurostat_geospatial(nuts_level = 0) %>%
  right_join(dat_2015) %>%
  mutate(cat = cut_to_classes(values, n=4, decimals=1))
head(select(mapdata,geo,values,cat), 3)
## geo values       cat                      geometry
## AT   1.49 1.5 ~< 1.6 MULTIPOLYGON (((15.54245 48...
## BE   1.70 1.6 ~< 1.8 MULTIPOLYGON (((5.10218 51....
## BG   1.53 1.5 ~< 1.6 MULTIPOLYGON (((22.99717 43...
```

Plot a Map

The **sf**-object returned are ready to be plotted with
ggplot::geom_sf()-function.

```
ggplot(mapdata, aes(fill = cat)) +
  scale_fill_brewer(palette = "RdYlBu") +
  geom_sf(color = alpha("white",1/3), alpha = .6) +
  xlim(c(-12,44)) + ylim(c(35,70)) +
  labs(title = "Total fertility rate, 2015",
       subtitle = "Avg. number of life births per woman",
       fill = "%")
```



This onepager presents the eurostat package 2014-2019
Leo Lahti, Janne Huovari, Markus Kainu, Przemyslaw Biecek
package version 3.3.55 URL: https://github.com/rOpenGov/eurostat

Retrieval and Analysis of Eurostat Open Data with the eurostat Package.
Leo Lahti, Janne Huovari, Markus Kainu, and Przemysław Biecek.
The R Journal, 9(1):385–392, 2017.

rOpenGov

Factors with forcats : : CHEAT SHEET

The **forcats** package provides tools for working with factors, which are R's data structure for categorical data.

Factors

R represents categorical data with factors. A **factor** is an integer vector with a **levels** attribute that stores a set of mappings between integers and categorical values. When you view a factor, R displays not the integers, but the levels associated with them.

Create a factor with factor()

factor(x = character(), levels, labels = levels, exclude = NA, ordered = is.ordered(x), nmax = NA**)** Convert a vector to a factor. Also **as_factor()**.
f <- factor(c("a", "c", "b", "a"), levels = c("a", "b", "c"))

Return its levels with levels()

levels(x**)** Return/set the levels of a factor. levels(f); levels(f) <- c("x","y","z")

Use unclass() to see its structure

Inspect Factors

fct_count(f, sort = FALSE, prop = FALSE**)** Count the number of values with each level. fct_count(f)

fct_match(f, lvls**)** Check for lvls in f. fct_match(f, "a")

fct_unique(f**)** Return the unique values, removing duplicates. fct_unique(f)

Combine Factors

fct_c(…**)** Combine factors with different levels. Also **fct_cross()**.
f1 <- factor(c("a", "c"))
f2 <- factor(c("b", "a"))
fct_c(f1, f2)

fct_unify(fs, levels = lvls_union(fs)**)** Standardize levels across a list of factors. fct_unify(list(f2, f1))

Change the order of levels

fct_relevel(.f, ..., after = 0L**)** Manually reorder factor levels. fct_relevel(f, c("b", "c", "a"))

fct_infreq(f, ordered = NA**)** Reorder levels by the frequency in which they appear in the data (highest frequency first). Also **fct_inseq()**.
f3 <- factor(c("c", "c", "a"))
fct_infreq(f3)

fct_inorder(f, ordered = NA**)** Reorder levels by order in which they appear in the data. fct_inorder(f2)

fct_rev(f**)** Reverse level order.
f4 <- factor(c("a","b","c"))
fct_rev(f4)

fct_shift(f**)** Shift levels to left or right, wrapping around end. fct_shift(f4)

fct_shuffle(f, n = 1L**)** Randomly permute order of factor levels. fct_shuffle(f4)

fct_reorder(.f, .x, .fun = median, ..., .desc = FALSE**)** Reorder levels by their relationship with another variable.
boxplot(data = PlantGrowth, weight ~ reorder(group, weight))

fct_reorder2(.f, .x, .y, .fun = last2, ..., .desc = TRUE**)** Reorder levels by their final values when plotted with two other variables.
ggplot(diamonds,aes(carat, price, color = fct_reorder2(color, carat, price))) + geom_smooth()

Change the value of levels

fct_recode(.f, ...**)** Manually change levels. Also **fct_relabel()** which obeys purrr::map syntax to apply a function or expression to each level.
fct_recode(f, v = "a", x = "b", z = "c")
fct_relabel(f, ~ paste0("x", .x))

fct_anon(f, prefix = ""**)** Anonymize levels with random integers. fct_anon(f)

fct_collapse(.f, …, other_level = NULL**)** Collapse levels into manually defined groups. fct_collapse(f, x = c("a", "b"))

fct_lump_min(f, min, w = NULL, other_level = "Other"**)** Lumps together factors that appear fewer than min times. Also **fct_lump_n()**, **fct_lump_prop()**, and **fct_lump_lowfreq()**.
fct_lump_min(f, min = 2)

fct_other(f, keep, drop, other_level = "Other"**)** Replace levels with "other." fct_other(f, keep = c("a", "b"))

Add or drop levels

fct_drop(f, only**)** Drop unused levels.
f5 <- factor(c("a","b"),c("a","b","x"))
f6 <- fct_drop(f5)

fct_expand(f, …**)** Add levels to a factor. fct_expand(f6, "x")

fct_explicit_na(f, na_level="(Missing)"**)** Assigns a level to NAs to ensure they appear in plots, etc. fct_explicit_na(factor(c("a", "b", NA)))

RStudio

Animate ggplots with gganimate : : CHEAT SHEET

Core Concepts

gganimate builds on ggplot2's grammar of graphics to provide functions for animation. You add them to plots created with `ggplot()` the same way you add a geom.

Main Function Groups

- **`transition_*()`**: What variable controls change and how?
- **`view_*()`**: Should the axes change with the data?
- **`enter/exit_*()`**: How does new data get added the plot? How does old data leave?
- **`shadow_*()`**: Should previous data be "remembered" and shown with current data?
- **`ease_aes()`**: How do you want to handle the pace of change between transition values?

Note: you only need a `transition_*()` or `view_*()` to make an animation. The other function groups enable you to add features or alter gganimate's default settings .

Starting Plots

```
library(tidyverse)
library(gganimate)

a <- ggplot(diamonds,
            aes(carat, price)) +
  geom_point()

b <- ggplot(txhousing,
            aes(month, sales)) +
  geom_col()

c <- ggplot(economics,
            aes(date, psavert)) +
  geom_line()
```

transition_*()

transition_states()

We're cycling between values of **color**, ...

```
a + transition_states(color, transition_length = 3, state_length = 1)
```

… and spending **3** times as long going to the next cut as we do pausing there.

transition_time()

We're cycling through each **year** of the data...

```
b + transition_time(year, range = c(2002L,2006L))
```

...from **2002** to **2006** (range is optional; default is the whole time frame). Unlike `transition_states()`, `transition_time()` treats the data as continuous and so the transition length is based on the actual values. Using **2002L** instead of **2002** because the underlying data is an integer.

transition_reveal()

```
c + transition_reveal(date)
```

We're adding each **date** of the data on top of 'old' data

transition_filters()

`transition_length` and `filter_length` work the same as `transition/state_length()` in `transition_states()`...

```
a + transition_filter(transition_length = 3,
                      filter_length = 1,
                      cut == "Ideal",
                      Deep = depth >= 60)
```

… but now we're cycling between these two filtering conditions. **Names** are optional, but can be useful (see "Label variables" on next page).

Other transitions

- **`transition_manual()`**: Similar to transition_states(), but without intermediate states.
- **`transition_layers()`**: Add layers (geoms) one at time.
- **`transition_components()`**: Transition elements independently from each other.
- **`transition_events()`**: Each element's duration can be controlled individually.

Baseline Animation

```
anim_a <- a + transition_states(color, transition_length = 3, state_length = 1)
```

view_*()

view_follow()

```
anim_a +
  view_follow(fixed_x = TRUE,
              fixed_y = c(2500, NA))
```

x-axis shows **full range**, y shows **[2500, as much is needed for that frame]**. Default is for both axis to vary as needed.

view_step()

We're spending **twice** as long moving between views as staying at them...

```
anim_a  +
  view_step(pause_length = 2,
            step_length = 1,
            nstep = 7)
```

… and we're cycling between **seven** views. Seven is the number of steps in the transition, so the view is changing when the points are static, and visa versa. Views are determined by what data is in the current frame.

view_zoom()

`view_zoom()` works similarly to `view_step()`, except it changes the view by zooming and panning.

Note: both `view_step()` and `view_zoom()` have `view_*_manual()` versions for setting views directly instead of inferring it from frame data.

Animate ggplots with gganimate : : CHEAT SHEET

gganimate

enter/exit_*()

Every `enter_*()` function has a corresponding `exit_*()` function, and visa versa.

enter/exit_fade()
```
anim_a + enter_fade()
```
When new points need to be added, they will start transparent and become opaque.

enter_grow()/exit_shrink()
```
anim_a + exit_shrink()
```
When extra points need to be removed, they will shrink in size before disappearing.

enter/exit_fly()
```
anim_a + enter_fly(x_loc = 0,
                   y_loc = 0)
```
When new points need to be added, they will fly in from **(0, 0)**.

enter/exit_drift()
```
anim_a + exit_drift(x_mod = 3, y_mod = -2)
```
When extra points need to be removed, They drift **3** units to the right and down 2 units before disappearing.

enter/exit_recolour() (or enter/exit_recolor())
```
anim_a + enter_recolour(color = "red")
```
When new points need to be added, they start as **red** before transitioning to their correct color.

Note: `enter/exit_*()` functions can be combined so that you can have old data fade away and shrink to nothing by adding `exit_fade()` and `exit_shrink()` to the plot.

shadow_*()

shadow_wake()
```
anim_a + shadow_wake(wake_length = 0.05)
```
Points have a wake of points with the data from the last **5%** of frames.

shadow_trail()
```
anim_a + shadow_trail(distance = 0.05)
```
Animation will keep the points from **5%** of the frames, spaced as evenly as possible.

shadow_mark()
```
anim_a + shadow_mark(color = "red")
```
Animation will keep past states plotted in **red** (but not the intermediate frames).

ease_aes()

`ease_aes()` allows you to set an easing function to control the rate of change between transition states. See `?ease_aes` for the full list.

Compare:
```
anim_a
anim_a + ease_aes("cubic-in") # Change easing of all aesthetics
anim_a + ease_aes(x = "elastic-in") # Only change `x` (others remain "linear")
```

Saving animations

```
animation_to_save <- anim_a  + exit_shrink()
anim_save("first_saved_animation.gif", animation = animation_to_save)
```

Since the `animation` argument uses your last rendered animation by default, this also works:
```
anim_a  + exit_shrink()
anim_save("second_saved_animation.gif")
```

`anim_save()` uses gifski to render the animation as a .gif file by default. You can use the `renderer` argument for other output types including video files (`av_renderer()` or `ffmeg_renderer()`) or spritesheets (`sprite_renderer()`):
```
# requires you to have the av package installed
anim_save("third_saved_animation.mp4",
          renderer =  av_renderer())
```

Label variables

gganimate's `transition_*()` functions create label variables you can pass to (sub)titles and other labels with the glue package. For example, `transition_states()` has `next_state`, which is the name of the state the animation is transitioning towards. Label variables are different between transitions, and details are included in the documentation of each.

```
anim_a + labs(subtitle = "Moving to {next_state}")
```
We're using the **next_state** label variable to tell the viewer where we're going.

Label variable	Description	Transitions
`transitioning`	TRUE if the current frame is an transition frame, FALSE otherwise	states, layers, filter
`previous_state/layer`	Last shown state/layer	states, layers
`next_state/layer`	State/layer that will been shown next	states, layers
`closest_state/layer`	State/layer that current frame is closest to (if between states/layers, either next or closest).	states, layers
`previous/closest/ next_filter/ expression`	Similar to their state/layer analogs. `*_filter` variables return the name of the filter, `*_expression` variables return the condition.	filter
`frame_time`	Time of current frame	time, components, events
`frame_along`	Current frame's value for the dimension we're transitioning over	reveal
`nlayers`	Number of layers (total, not just currently shown)	layer

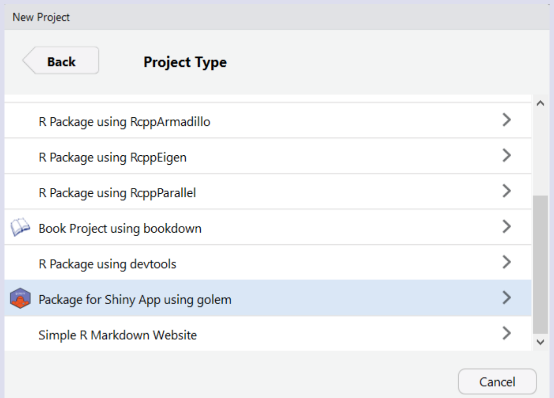
golem :: A Framework for Building Robust Shiny Apps

Create, maintain & deploy a packaged Shiny Application

1. Create a golem

With RStudio:

File ➡ New Project ➡ New Directory ➡ Package for Shiny App using golem



Using the command line:

golem::create_golem(path = "~/appdemo")
Creates a golem at '~/appdemo'.

2. Set up your golem with dev/01_start.R

golem::fill_desc(pkg_name = "appdemo", …)
Fills the package DESCRIPTION with the author information, the application title & description, links…

golem::set_golem_options()
Sets {golem} global options.

golem::use_recommended_tests()
Creates a test template for your app.

golem::use_recommended_deps()
Adds {shiny}, {DT}, {attempt}, {glue}, {htmltools}, and {golem} as dependencies.

golem::use_favicon(path = "path/to/favicon.ico")
Changes the default favicon.

golem::use_utils_ui()
Creates 'R/golem_utils_ui.R', with UI-related helper functions.

golem::use_utils_server()
Creates 'R/golem_utils_server.R', with server-related helper functions.

3. Day-to-day dev with golem

A. Look at your golem

- **Launch your app with *dev/run_dev.R*:**

options(golem.app.prod = FALSE)
Sets the prod or dev mode. (see ?golem::app_dev)

golem::detach_all_attached()
Detaches all loaded packages and cleans your environment.

golem::document_and_reload()
Documents and reloads your package.

appdemo::run_app()
Launches your application.

B. Customise your golem with dev/02_dev.R

- **Edit R/app_ui.R & R/app_server.R**

'R/app_ui.R' & 'R/app_server.R' hold the UI and server logic of your app. You can edit them directly, or add elements created with golem (e.g, modules).

- **Add shiny modules**

golem::add_module(name = "example")
Creates 'R/mod_example.R', with mod_example_ui and mod_example_server functions inside.

- **Add external files**

golem::add_js_file("script")
Creates 'inst/app/www/script.js'.

golem::add_js_handler("script")
Creates 'inst/app/www/script.js' with a skeleton for shiny custom handlers.

golem::add_css_file("custom")
Creates 'inst/app/www/custom.css'.

- **Use golem built-in JavaScript functions**

golem::activate_js()
Activates the built-in JavaScript functions. To be inserted in the UI.

golem::invoke_js("jsfunction", ns("ref_ui"))
Invokes from the server any JS function: built-in golem JS functions or custom ones created with add_js_handler()

4. Exhibit your golem

Locally

remotes::install_local()
Installs your golem locally like any other package.

To Rstudio products

golem::add_rstudioconnect_file()
Creates an app.R file, ready to be deployed to RStudio Connect.

golem::add_shinyappsio_file()
Creates an app.R file, ready to be deployed to shinyapps.io.

golem::add_shinyserver_file()
Creates an app.R file, ready to be deployed to Shiny Server.

With Docker

golem::add_dockerfile()
Creates a Dockerfile that can launch your app.

golem::add_dockerfile_shinyproxy()
Creates a Dockerfile for ShinyProxy.

golem::add_dockerfile_heroku()
Creates a Dockerfile for Heroku.

Tips and tricks

golem::print_dev("text")
Prints *text* in your console if *golem::app_dev()* is *TRUE*.

golem::make_dev(function)
Makes function depend on *golem::app_dev()* being *TRUE*.

golem::browser_button()
Creates a backdoor to your app (see ?golem::browser_button).

- How to make a *run_dev* script for a specific module:

```
golem::detach_all_attached()
golem::document_and_reload()

ui <- mod_example_ui( "my_module" )
server <- function(input,output,session){
  callModule( mod_example_server, "my_module", session )
}
shinyApp(ui, server)
```

Keep in mind that a golem is a package. Everything you know about package development works with your packaged Shiny App created with {golem}! (documentation, tests, CI & CD, …)

GWAS Catalog access with gwasrapidd

Introduction

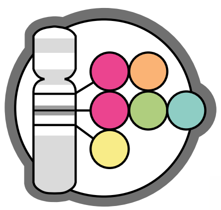
The **GWAS Catalog** is a service provided by the EMBL-EBI and NHGRI that offers a manually curated and freely available database of published genome-wide association studies (GWAS).

The GWAS Catalog data provided by the **RESTful API** is organized around four core entities:

- **studies**
- **associations**
- **variants**
- **traits**

Get GWAS Catalog Entities

gwasrapidd facilitates the access to the Catalog via the RESTful API, allowing you to programmatically retrieve data directly into R. Each of the four entities is mapped to an S4 object of a class of the same name.



GWAS CATALOG	RETRIEVAL FUNCTIONS	S4 CLASSES
	`get_studies()`	S studies
	`get_associations()`	A associations
	`get_variants()`	V variants
	`get_traits()`	T traits

Search by	Example	S	A	V	T
study_id	"GCST000858"	●	●	●	●
association_id	"24300113"	●	●	●	●
variant_id	"rs12752552"	●	●	●	
efo_id	"EFO_0005543"	●	●	●	●
pubmed_id	"21626137"	●	●	●	●
user_requested	TRUE	●			
full_pvalue_set	FALSE	●			
efo_uri	"http://www.ebi.ac.uk/efo/EFO_0004761"	●			●
genomic_range	list(chromosome = "22", start = 1L, end = 15473564L)			●	
gene_name	"BRCA1"			●	
efo_trait	"lung adenocarcinoma"	●	●	●	●
reported_trait	"Breast cancer"	●		●	
cytogenetic_band	"1p36.33"			●	

S4 Representation of GWAS Catalog Entities

S4 class studies

The **`studies`** object consists of eight slots, each a table (tibble). Each study is an observation (row) in the `studies` table — main table. All tables have the column `study_id` as primary key.

For details about the studies S4 class: `class?studies`.

`studies`
- study_id
- reported_trait
- initial_sample_size
- replication_sample_size
- gxe
- gxg
- snp_count
- qualifier
- imputed
- pooled
- study_design_comment
- full_pvalue_set
- user_requested

`genotyping_techs`
- study_id
- genotyping technology

`platforms`
- study_id
- manufacturer

`ancestries`
- study_id
- ancestry_id
- type
- number_of_individuals

`ancestral_groups`
- study_id
- ancestry_id
- ancestral_group

`countries_of_recruitment`
- study_id
- ancestry_id
- country_name
- major_area
- region

`countries_of_origin`
- study_id
- ancestry_id
- country_name
- major_area
- region

`publications`
- study_id
- pubmed_id
- publication_date
- publication
- title
- author_fullname
- author_orcid

S

S4 class associations

The **`associations`** object consists of six slots, each a table (tibble). Each association is an observation (row) in the `associations` table — main table. All tables have the column `association_id` as primary key.

For details about the associations S4 class: `class?associations`.

`associations`
- association_id
- pvalue
- pvalue_description
- pvalue_mantissa
- pvalue_exponent
- multiple_snp_haplotype
- snp_interaction
- snp_type
- standard_error
- range
- or_per_copy_number
- beta_number
- beta_unit
- beta_direction
- beta_description
- last_mapping_date
- last_update_date

`loci`
- association_id
- locus_id
- haplotype_snp_count
- description

`risk_alleles`
- association_id
- locus_id
- variant_id
- risk_allele
- risk_frequency
- genome_wide
- limited_list

`genes`
- association_id
- locus_id
- gene_name

`ensembl_ids`
- association_id
- locus_id
- gene_name
- ensembl_id

`entrez_ids`
- association_id
- locus_id
- gene_name
- entrez_id

A

S4 class variants

The **`variants`** object consists of four slots, each a table (tibble). Each variant is an observation (row) in the `variants` table — main table. All tables have the column `variant_id` as primary key.

For details about the variants S4 class: `class?variants`.

`variants`
- variant_id
- merged
- functional_class
- chromosome_name
- chromosome_position
- chromosome_region
- last_update_date

`genomic_contexts`
- variant_id
- gene_name
- chromosome_name
- chromosome_position
- distance
- is_closest_gene
- is_intergenic
- is_upstream
- is_downstream
- source
- mapping_method

`ensembl_ids`
- variant_id
- gene_name
- ensembl_id

`entrez_ids`
- variant_id
- gene_name
- entrez_id

V

S4 class traits

The **`traits`** object consists of one slot only, a table (tibble) of GWAS Catalog EFO traits. Each EFO trait is an observation (row) in the traits table — main table.

For details about the traits S4 class: `class?traits`.

`traits`
- efo_id
- trait
- uri

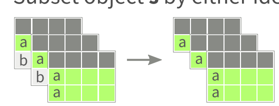
T

Manipulate Cases

Get a **`studies`** object **s** of two GWAS studies:

```
s <- get_studies(study_id = c('a', 'b'))
```

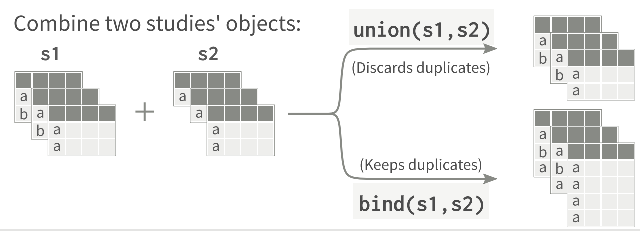
Subset object **s** by either identifier or position using `` `[` ``:



```
s['a'] # Subset by identifier
```

```
s[1] # Subset by position
```

Combine two studies' objects:



h2o: : CHEAT SHEET

H2O.ai

Dataset Operations

DATA IMPORT / EXPORT

h2o.uploadFile: Upload a file into H2O from a client-side path, and parse it.

h2o.downloadCSV: Download a H2O dataset to a client-side CSV file.

h2o.importFile: Import a file into H2O from a server-side path, and parse it.

h2o.exportFile: Export an H2O Data Frame to a server-side file.

h2o.parseRaw: Parse a raw data file.

NATIVE R TO H2O COERCION

as.h2o: Convert a R object to an H2O object

H2O TO NATIVE R COERCION

as.data.frame: Check if an object is a data frame, and coerce it if possible.

DATA GENERATION

h2o.createFrame: Creates a data frame in H2O with real-valued, categorical, integer, and binary columns specified by the user, with optional randomization.

h2o.runif: Produce a vector of random uniform numbers.

h2o.interaction: Create interaction terms between categorical features of an H2O Frame.

h2o.target_encode_apply: Target encoding map to an H2O Data Frame, which can improve performance of supervised learning models for high cardinality categorical columns.

DATA SAMPLING / SPLITTING

h2o.splitFrame: Split an existing H2O dataset according to user-specified ratios.

MISSING DATA HANDLING

h2o.impute: Impute a column of data using the mean, median, or mode.

h2o.insertMissingValues: Replaces a user-specified fraction of entries in an H2O dataset with missing values.

h2o.na_omit: Remove Rows With NAs.

General Operations

SUBSCRIPTING

Subscripting example to pull (/push) pieces from (/to) a H2O Parsed Data object.

```
x[j]  ## column J
x[i, j]
x[[i]]
x$name
```

Selection

```
x[i]  <- value
x[i, j, ...] <- value
x[[i]] <- value
x$i <- value
```

Value Assignation

SUBSETTING

h2o.head, h2o.tail: Object's Start or End.

DATA ATTRIBUTES

h2o.names: Return column names for an H2O Frame. Also: **h2o.colnames**

names<-: Set the row or column names of a H2O Frame. Also: **colnames<-**

h2o.dim: Retrieve object dimensions.

h2o.length: Length of vector, list or factor.

h2o.nrow: Number of H2O Frame rows.

h2o.ncol: Number of H2O Frame columns.

h2o.anyFactor: Check if an H2O Frame object has any categorical data columns.

is.factor, is.character, is.numeric: Check Column's Data Type.

DATA TYPE COERCION: Convert to:

h2o.asfactor, as.factor: Factor.

h2o.as_date, as.Date: Date.

h2o.ascharacter, as.character: Character.

h2o.asnumeric, as.numeric: Numeric.

BASIC DATA MANIPULATION

c: Combine Values into a Vector or List.

h2o.cbind; h2o.rbind: Combine a sequence of H2O datasets by column (cbind) or rows (rbind).

h2o.merge: Merges 2 H2OFrames.

h2o.arrange: Sorts an H2OFrame by columns.

ELEMENT INDEX SELECTION

h2o.which: True Condition's Row Numbers

CONDITIONAL VALUE SELECTION

h2o.ifelse: Apply conditional statements to numeric vectors in an H2O Frame.

Math Operations

(math) vectorized function

MATH

h2o.abs: Compute the absolute value of x.

h2o.sqrt: Principal Square Root of x, √x.

h2o.ceiling: Take a single numeric argument x and return a numeric vector containing the smallest integers not less than the corresponding elements of x.

h2o.floor: Take a single numeric argument x and return a numeric vector containing the largest integers not greater than the corresponding elements of x.

h2o.trunc: Take a single numeric argument x and return a numeric vector containing the integers formed by truncating the values in x toward 0.

h2o.log: Compute natural logarithms. See also: **h2o.log10, h2o.log2, h2o.log1p**

h2o.exp: Compute the exponential function

h2o.cos, h2o.cosh, h2o.acos, h2o.sin, h2o.tan, h2o.tanh, Math: ?groupGeneric

sign: Return a vector with the signs of the corresponding elements of x (the sign of a real number is 1, 0, or -1 if the number is positive, zero, or negative, respectively).

&& (Vectorized AND), **||** (Vectorized OR), **!x, %in%,** Ops: **+, -, *, /, ^, %%, %/%, ==, !=, <, <=, >=, >, &, |, !**

CUMULATIVE

h2o.cummax: Vector of the cumulative maxima of the elements of the argument.

h2o.cummin: Vector of the cumulative minima of the elements of the argument.

h2o.cumprod: Vector of the cumulative products of the elements of the argument.

h2o.cumsum: Vector of the cumulative sums of the elements of the argument.

PRECISION

h2o.round: Round values to the specified number of decimal places. The default is 0.

h2o.signif: Round values to the specified number of significant digits.

Group By Summaries

(group by) summary function

nrow: Count the number of rows.

max: All input argument's Maximum.

min: All input argument's Minimum.

sum: All argument values Sum.

mean: (Trimmed) arithmetic mean.

sd: Calculate the standard deviation of a column of continuous real valued data.

var: Compute the variance of x.

Generic Summaries

NON-GROUP_BY SUMMARIES

h2o.median: Calculate the median of x.

h2o.range: Input argument's Min/Max Vector

h2o.cor: Correlation Matrix of H2O Frames.

h2o.quantile: Obtain and display quantiles for an H2O Frame Column.

h2o.hist: Compute a histogram over a numeric H2O Frame Column.

h2o.prod: Product of all arguments values.

h2o.any: Given a set of logical vectors, determine if at least one of the values is true.

h2o.all: Given a set of logical vectors, determine if all of the values are true.

NON-GROUP_BY SUMMARIES: GENERIC

h2o.summary: Produce result summaries of the results of various model fitting functions.

Aggregations

ROW / COLUMN AGGREGATION

or

By Rows By Cols

apply: Apply a function over an H2O parsed data object (an array) margins.

GROUP BY AGGREGATION

h2o.group_by: Apply an aggregate function to each group of an H2O dataset.

TABULATION

h2o.table: Use the cross-classifying factors to build a table of counts at each combination of factor levels.

h2o: : CHEAT SHEET

H2O.ai

Data Modeling

MODEL TRAINING: SUPERVISED LEARNING

h2o.deeplearning: Perform Deep Learning Neural Networks on an H2OFrame.

h2o.gbm: Build Gradient Boosted Regression Trees or Classification Trees.

h2o.glm: Fit a Generalized Linear Model, specified by a response variable, a set of predictors, and the error distribution.

h2o.naiveBayes: Compute Naive Bayes classification probabilities on an H2O Frame.

h2o.randomForest: Perform Random Forest Classification on an H2O Frame.

h2o.xgboost: Build an Extreme Gradient Boosted Model using the XGBoost backend.

h2o.stackedEnsemble: Build a stacked ensemble (aka. Super Learner) using the specified H2O base learning algorithms.

h2o.automl: Automates the Supervised Machine Learning Model Training Process: Automatically Trains and Cross-validates a set of Models, and trains a Stacked Ensemble.

MODEL TRAINING: UNSUPERVISED LEARNING

h2o.prcomp: Perform Principal Components Analysis on the given H2O Frame.

h2o.kmeans: Perform k-means Clustering on the given H2O Frame.

h2o.anomaly: Detect anomalies in a H2O Frame using a H2O Deep Learning Model with Auto-Encoding.

h2o.deepfeatures: Extract the non-linear features from a H2O Frame using a H2O Deep Learning Model.

h2o.glrm: Builds a Generalized Low Rank Decomposition of an H2O Frame.

h2o.svd: Singular value decomposition of an H2O Frame using the power method.

h2o.word2vec: Trains a word2vec model on a String column of an H2O data frame.

SURVIVAL MODELS: TIME-TO-EVENT

h2o.coxph: Trains a Cox Proportional Hazards Model (CoxPH) on an H2O Frame.

GRID SEARCH

h2o.grid: Efficient method to build multiple models with different hyperparameters.

h2o.getGrid: Get a grid object from H2O distributed K/V store.

MODEL SCORING

h2o.predict: Obtain predictions from various fitted H2O model objects.

h2o.scoreHistory: Get Model Score History.

MODEL METRICS

h2o.make_metrics: Given predicted values (target for regression, class-1 probabilities, or binomial or per-class probabilities for multinomial), compute a model metrics object.

GENERAL MODEL HELPER

h2o.performance: Evaluate the predictive performance of a Supervised Learning Regression or Classification Model via various metrics. Set **xval = TRUE** for retrieving the training cross-validation metrics.

REGRESSION MODEL HELPER

h2o.mse: Display the mean squared error calculated from "Predicted Responses" and "Actual (Reference) Responses". Set **xval = TRUE** for retrieving the cross-validation MSE.

CLASSIFICATION MODEL HELPERS

h2o.accuracy: Get Model Accuracy metric.

h2o.auc: Retrieve the AUC (area under ROC curve). Set **xval = TRUE** for retrieving the cross-validation AUC.

h2o.confusionMatrix: Display prediction errors for classification data ("Predicted" vs "Reference : Real Values").

h2o.hit_ratio_table: Retrieve the Hit Ratios. Set **xval = TRUE** for retrieving the cross-validation Hit Ratio.

CLUSTERING MODEL HELPER

h2o.betweenss: Get the between cluster Sum of Squares.

h2o.centers: Retrieve the Model Centers.

PREDICTOR VARIABLE IMPORTANCE

h2o.varimp: Retrieve the variable importance

h2o.varimp_plot: Plot Variable Importances.

Data Munging

GENERAL COLUMN MANIPULATION

is.na: Display missing elements.

FACTOR LEVEL MANIPULATIONS

h2o.levels: Display a list of the unique values found in a categorical data column.

h2o.relevel: Reorders levels of an H2O factor, similarly to standard R's relevel.

h2o.setLevels: Set Levels of H2O Factor.

NUMERIC COLUMN MANIPULATIONS

h2o.cut: Convert H2O Numeric Data to Factor by breaking it into Intervals.

CHARACTER COLUMN MANIPULATIONS

h2o.strsplit: **"**String Split": Splits the given factor column on the input split.

h2o.tolower: Convert the characters of a character vector to lower case.

h2o.toupper: Convert the characters of a character vector to upper case.

h2o.trim: **"**Trim spaces": Remove leading and trailing white space.

h2o.gsub: Match a pattern & replace ***all*** instances (occurrences) of the matched pattern with the replacement string globally.

h2o.sub: Match a pattern & replace the ***first*** instance (occurrence) of the matched pattern with the replacement string.

DATE MANIPULATIONS

h2o.month: Convert Milliseconds to Months in H2O Datasets (Scale: 0 to 11).

h2o.year: Convert Milliseconds to Years in H2O Datasets, indexed starting from 1900.

h2o.day: Convert Milliseconds to Day of Month in H2O Datasets (Scale: 1 to 31).

h2o.hour: Convert Milliseconds to Hour of Day in H2O Datasets (Scale: 0 to 23).

h2o.dayOfWeek: Convert Milliseconds to Day of Week in a H2OFrame (Scale: 0 to 6)

MATRIX OPERATIONS

%*%: Multiply two conformable matrices.

t: Returns the transpose of an H2OFrame.

Cluster Operations

H2O KEY VALUE STORE ACCESS

h2o.assign: Assign H2O hex.keys to R objects.

h2o.getFrame: Get H2O dataset Reference.

h2o.getModel: Get H2O model reference.

h2o.ls: Display a list of object keys in the running instance of H2O.

h2o.rm: Remove specified H2O Objects from the H2O server, but not from the R environment.

h2o.removeAll: Remove All H2O Objects from the H2O server, but not from the R environment.

H2O MODEL IMPORT / EXPORT

h2o.loadModel: Load H2OModel from disk.

h2o.saveModel: Save H2OModel object to disk.

h2o.download_pojo: Download the Scoring POJO (Plain Old Java Object) of an H2O Model.

h2o.download_mojo: Download the model in MOJO format.

H2O CLUSTER CONNECTION

h2o.init: Connect to a running H2O instance using all CPUs on the host.

h2o.shutdown: Shut down the specified H2O instance. All data on the server will be lost!

H2O CLUSTER INFORMATION

h2o.clusterInfo: Display the name, version, uptime, total nodes, total memory, total cores and health of a cluster running H2O.

h2o.clusterStatus: Retrieve information on the status of the cluster running H2O.

H2O LOGGING

h2o.clearLog: Clear all H2O R command and error response logs from the local disk.

h2o.downloadAllLogs: Download all H2O log files to the local disk.

h2o.logAndEcho: Write a message to the H2O Java log file and echo it back.

h2o.openLog: Open existing logs of H2O R POST commands and error responses on disk.

h2o.getLogPath: Get the file path for the H2O R command and error response logs.

h2o.startLogging: Begin logging H2O R POST commands and error responses.

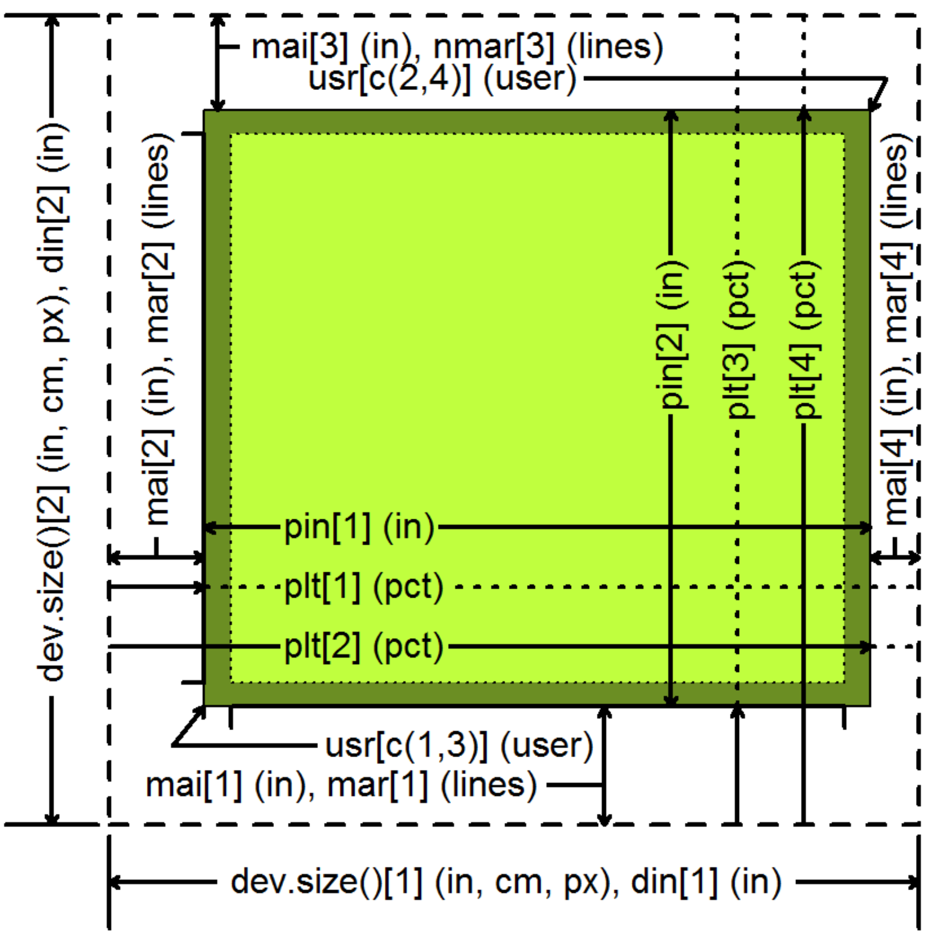
h2o.stopLogging: Stop logging H2O R POST commands and error responses.

How Big is Your Graph?

An R Cheat Sheet

Introduction

All functions that open a device for graphics will have **height** and **width** arguments to control the size of the graph and a **pointsize** argument to control the relative font size. In **knitr**, you control the size of the graph with the chunk options, **fig.width** and **fig.height**. This sheet will help you with calculating the size of the graph and various parts of the graph within R.



Your graphics device

dev.size() (width, height)
par("din") *(r.o.)* (width, height) in inches

Both the **dev.size** function and the **din** argument of **par** will tell you the size of the graphics device. The **dev.size** function will report the size in

1. inches (**units="in"**), the default
2. centimeters (**units="cm"**)
3. pixels (**units="px"**)

Like several other **par** arguments, **din** is read only *(r.o.)* meaning that you can ask its current value (**par("din")**) but you cannot change it (**par(din=c(5,7))** will fail).

Your plot margins

par("mai") (bottom, left, top, right) in inches
par("mar") (bottom, left, top, right) in lines

Margins provide you space for your axes, axis, labels, and titles.

A "line" is the amount of vertical space needed for a line of text.

If your graph has no axes or titles, you can remove the margins (and maximize the plotting region) with

par(mar=rep(0,4))

Your plotting region

par("pin") (width, height) in inches
par("plt") (left, right, bottom, top) in pct

The **pin** argument **par** gives you the size of the plotting region (the size of the device minus the size of the margins) in inches.

The **plt** argument gives you the percentage of the device from the left/bottom edge up to the left edge of the plotting region, the right edge, the bottom edge, and the top edge. The first and third values are equivalent to the percentage of space devoted to the left and bottom margins. Subtract the second and fourth values from 1 to get the percentage of space devoted to the right and top margins.

Your x-y coordinates

par("usr") (xmin, ymin, xmax, ymax)

Your x-y coordinates are the values you use when plotting your data. This normally is not the same as the values you specified with the xlim and ylim arguments in plot. By default, R adds an extra 4% to the plotting range (see the dark green region on the figure) so that points right up on the edges of your plot do not get partially clipped. You can override this by setting xaxs="i" and/or the yaxs="i" in par.

Run par("usr") to find the minimum X value, the maximum X value, the minimum Y value, and the maximum Y value. If you assign new values to usr, you will update the x-y coordinates to the new values.

Getting a square graph

par("pty")

You can produce a square graph manually by setting the width and height to the same value and setting the margins so that the sum of the top and bottom margins equal the sum of the left and right margins. But a much easier way is to specify **pty="s"**, which adjusts the margins so that the size of the plotting region is always square, even if you resize the graphics window.

Converting units

For many applications, you need to be able to translate user coordinates to pixels or inches. There are some cryptic shortcuts, but the simplest way is to get the range in user coordinates and measure the proportion of the graphics device devoted to the plotting region.

```
user.range <- par("usr")[c(2,4)] -
  par("usr")[c(1,3)]

region.pct <- par("plt")[c(2,4)] -
  par("plt")[c(1,3)]

region.px <-
  dev.size(units="px") * region.pct

px.per.xy <- region.px / user.range
```

To convert a horizontal or distance from the x-coordinate value to pixels, multiply by **px.per.xy[1]**. To convert a vertical distance, multiply by **region.px.per.xy[2]**. To convert a diagonal distance, you need to invoke Pyhthagoras.

```
a.px <- x.dist*px.per.xy[1]
b.px <- y.dist*px.per.xy[2]
c.px <- sqrt(a.px^2+b.px^2)
```

To rotate a string to match the slope of a line segment, you need to convert the distances to pixels, calculate the arctangent, and convert from radians to degrees.

```
segments(x0, y0, x1, y1)
delta.x <- (x1 – x0) * px.per.xy[1]
delta.y <- (y1 – y0) * px.per.xy[y]
angle.radians <- atan2(delta.y, delta.x)
angle.degrees <- angle.radians * 180 / pi
text(x1, y1, "TEXT", srt=angle.degrees)
```

Panels

par("fig") (width, height) in pct
par("fin") (width, height) in inches

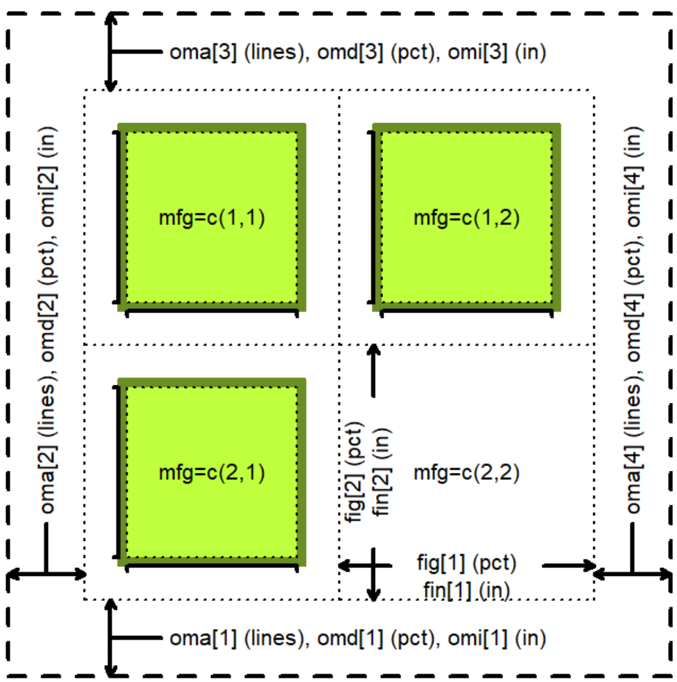
If you display multiple plots within a single graphics window (e.g., with the **mfrow** or **mfcol** arguments of **par** or with the **layout** function), then the **fig** and **fin** arguments will tell you the size of the current subplot window in percent or inches, respectively.

par("oma") (bottom, left, top, right) in lines
par("omd") (bottom, left, top, right) in pct
par("omi") (bottom, left, top, right) in inches

Each subplot will have margins specified by **mai** or **mar**, but no outer margin around the entire set of plots, unless you specify them using **oma**, **omd**, or **omi**. You can place text in the outer margins using the **mtext** function with the argument **outer=TRUE**.

par("mfg") (r, c) or (r, c, maxr, maxc)

The **mfg** argument of **par** will allow you to jump to a subplot in a particular row and column. If you query with **par("mfg")**, you will get the current row and column followed by the maximum row and column.



Character and string sizes

strheight()

The **strheight** functions will tell you the height of a specified string in inches (**units="inches"**), x-y user coordinates (**units="user"**) or as a percentage of the graphics device (**units="figure"**).

For a single line of text, **strheight** will give you the height of the letter "M". If you have a string with one of more linebreaks ("\n"), the **strheight** function will measure the height of the letter "M" plus the height of one or more additional lines. The height of a line is dependent on the line spacing, set by the **lheight** argument of **par**. The default line height (**lheight=1**), corresponding to single spaced lines, produces a line height roughly 1.5 times the height of "M".

strwidth()

The **strwidth** function will produce different widths to individual characters, representing the proportional spacing used by most fonts (a "W" using much more space than an "i"). For the width of a string, the **strwidth** function will sum up the lengths of the individual characters in the string.

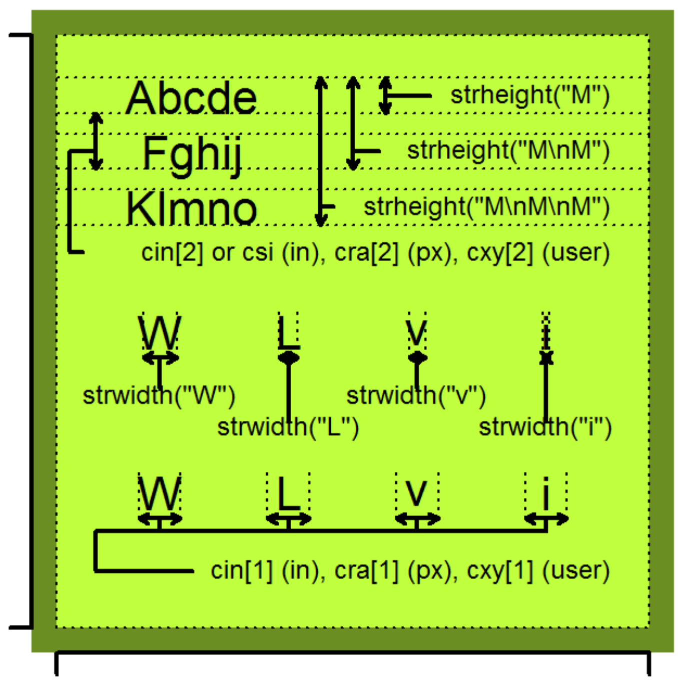
par("cin") *(r.o.)* (width, height) in inches
par("csi") *(r.o.)* height in inches
par("cra") *(r.o.)* (width, height) in pixels
par("cxy") *(r.o.)* (width, height) in xy coordinates

The single value returned by the **csi** argument of **par** gives you the height of a line of text in inches. The second of the two values returned by **cin**, **cra**, and **cxy** gives you the height of a line, in inches, pixels, or xy (user) coordinates.

The first of the two values returned by the **cin**, **cra**, and **cxy** arguments to **par** gives you the approximate width of a single character, in inches, pixels, or xy (user) coordinates. The width, very slightly smaller than the actual width of the letter "W", is a rough estimate at best and ignores the variable with of individual letters.

These values are useful, however, in providing fast ratios of the relative sizes of the differing units of measure

px.per.in <- par("cra") / par("cin")
px.per.xy <- par("cra") / par("cxy")
xy.per.in <- par("cxy") / par("cin")



If your fonts are too big or too small

Fixing this takes a bit of trial and error.

1. Specify a larger/smaller value for the **pointsize** argument when you open your graphics device.

2. Trying opening your graphics device with different values for **height** and **width**. Fonts that look too big might be better proportioned in a larger graphics window.

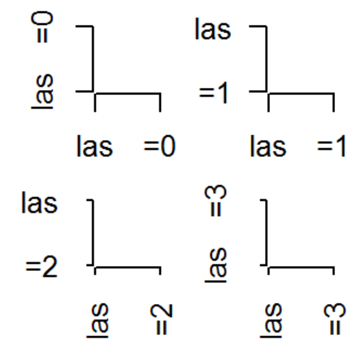
3. Use the **cex** argument to increase or decrease the relative size of your fonts.

If your axes don't fit

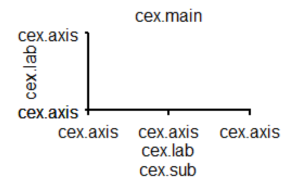
There are several possible solutions.

1. You can assign wider margins using the **mar** or **mai** argument in **par**.

2. You can change the orientation of the axis labels with **las**. Choose among
   a. **las=0** both axis labels parallel
   b. **las=1** both axis labels horizontal
   c. **las=2** both axis labels perpendicular
   d. **las=3** both axis labels vertical.



3. change the relative size of the font
   a. **cex.axis** for the tick mark labels.
   b. **cex.lab** for **xlab** and **ylab**.
   c. **cex.main** for the main title
   d. **cex.sub** for the subtitle.



Time Series Imputation with imputeTS: : CHEAT SHEET

Mission

Missing Data is nearly everywhere. Also in time series, especially in sensor recordings missing data is common.

imputeTS helps you with your missing data problems.

Features

The package provides easy to use functions in these areas:

1. Imputation Functions
   Several algorithms for replacing NAs with reasonable values (imputation).
2. Missing Data Visualizations
   Plots for analysis of the distribution of NAs, patterns and imputation performance.
3. Stats and Datasets
   Functions for printing missing data stats and benchmarking datasets.

Scope

imputeTS specializes on univariate time series that are:

- numeric
- equally-spaced

Visualizations

There are multiple plots provided for analysing the missing data before and after imputation. All plotting functions start with ggplot_na_plotname.

Function	Description
ggplot_na_distribution	Getting a first overview of NAs
ggplot_na_intervals	Insights about NAs in specific periods
ggplot_na_gapsize	Insights about occurring NA gapsizes
ggplot_na_imputations	Evaluating imputation quality

Imputation

The package offers multiple missing data replacement (imputation) functions, which are really easy to use.

```
na_interpolation(x, option = “spline“)
```

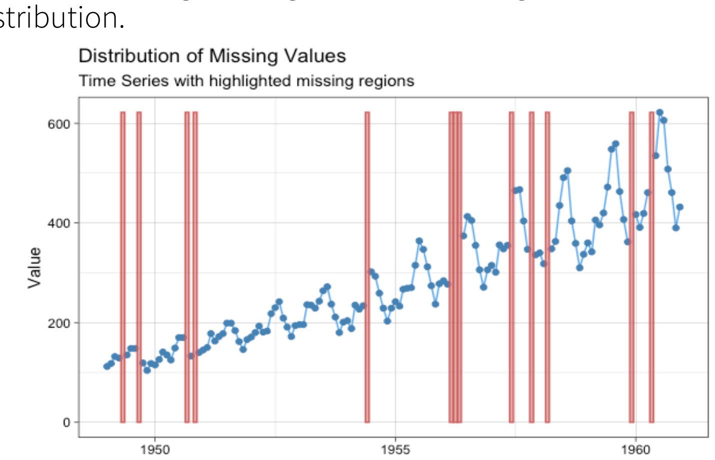
Imputation Function · Your input time series · Additional Parameters

List of available Algorithms

Function	Description
na_interpolation	Imputation by Interpolation
na_kalman	Imputation by Kalman Smoothing
na_locf	Last Observation Carried Forward
na_ma	Imputation by Moving Average
na_mean	Imputation by Mean Value
na_random	Imputation by Random Sample
na_remove	Remove Missing Values
na_replace	Replace Missing Values by a Defined Value
na_seadec	Seasonally Decomposed Imputation
na_seasplit	Seasonally Splitted Imputation

Missing Data Overview Plots

The ‘distribution’, ‘intervals’ and ‘gapsize’ plots can be used on new datasets to gain insights about missing data patterns and distribution.

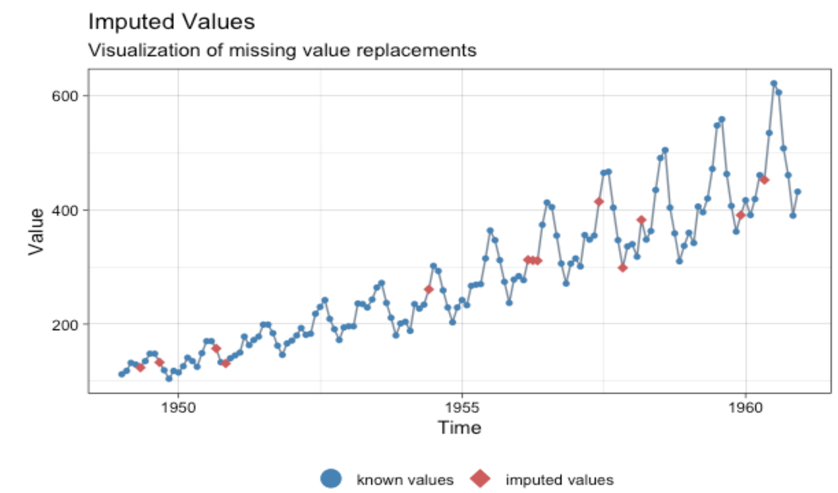



```
ggplot_na_distribution(tsAirgap)
```

example data with NAs

Imputation Analysis Plots

Imputation results can be visualized with the ‘imputations’ plot. Here first na_kalman is performed and then the results are plotted.




```
imp <- na_kalman(tsAirgap)
ggplot_na_imputations(tsAirgap, imp)
```

imputation · visualization

Workflows

The functions also work well in tidy style pipe workflows. Here an example of first using imputation and later forecasting and plotting.

```
library(“forecast”)
tsAirgap %>% na_interpolation() %>%
ets() %>% forecast(h=36) %>%
autoplot()
```

can be put in pipe workflows · a 36 step forecast is created and plotted

Datasets

The package includes three datasets for imputation experiments.

Function	Description
tsAirgap	Monthly totals of international airline passengers. 144 Observations / 13 NAs
tsNH4	NH4 concentration in a wastewater system. 3552 observations / 883 NAs
tsHeating	A heating systems supply temperature. 606837 observations / 57391 NAs

CITATION

You can cite imputeTS the following:

Moritz, Steffen and Bartz-Beielstein, Thomas. "imputeTS: Time Series Missing Value Imputation in R." R Journal 9.1 (2017). doi: 10.32614/RJ-2017-009.

 • Steffen Moritz • steffen.moritz@gmail.com • https://github.com/SteffenMoritz/imputeTS

package version 3.1 • Updated: July 2020

Audit sampling with jfa: : **CHEAT SHEET**

Basics

jfa is an R package that facilitates statistical planning, selection, and evaluation of audit samples.

The package provides five functions that allow users to easily apply Bayesian or classical probability theory in the standard audit sampling workflow.

Installation

Installing the package can be done via:
`install.packages('jfa')`

Loading the package can be done via:
`library(jfa)`

Example

The blue code blocks next to the function descriptions provide a working example of the intended workflow.

The data for this example can be loaded via:
`data('BuildIt')`

Construct a prior probability distribution (optional)

`jfa::auditPrior()`

This function creates a prior distribution for the misstatement in the population based on audit evidence specified via the `method` argument. The prior distribution can be used as input for the `prior` argument in other functions to perform Bayesian inference.

- `likelihood`: Specifies the family of the prior probability distribution.

```
auditPrior(method = 'default',
           likelihood = 'poisson', ...)
```

Calculate the minimum sample size

`jfa::planning()`

Given a performance materiality or a minimum precision, this function calculates the minimum sample size to achieve these objectives based on the binomial, Poisson, or hypergeometric `likelihood`. A `prior` can be specified to perform Bayesian planning.

- `expected`: A fraction or an integer specifying the expected errors in the sample.

```
planning(materiality = 0.05,
         expected = 0.01,
         likelihood = 'poisson',
         conf.level = 0.95,
         prior = FALSE, ...)
```

Select the required items from the population

`jfa::selection()`

This function takes a data frame and performs sampling according to one of three popular `method`'s: random sampling, cell sampling, or fixed interval sampling. Sampling is done in combination with one of two sampling `units`: items (rows) or monetary units.

```
selection(data = BuildIt,
          size = 93,
          units = 'items',
          method = 'interval', ...)
```

Evaluate the misstatement in the population

`jfa::evaluation()`

This function takes a data sample (using `data`, `values`, and `values.audit`) or summary statistics from a sample (using `x` and `n`) and performs statistical evaluation on the misstatement in the population according to the specified `method`. A `prior` can be specified to perform Bayesian evaluation.

- `prior`: An object returned by `auditPrior()` that specifies the prior distribution.

```
evaluation(materiality = 0.05,
           method = 'poisson',
           alternative = 'less',
           conf.level = 0.95,
           x = 0,
           n = 93,
           prior = FALSE, ...)
```

Create a report of the statistical results

`jfa::report()`

This function takes an object of class `jfaEvaluation` as returned by `evaluation()` and automatically generates a report containing the statistical results and their interpretation.

```
report(object = evaluationResult,
       file = 'report.html', ...)
```

Deep Learning with Keras : : CHEAT SHEET

Keras TensorFlow

Intro

Keras is a high-level neural networks API developed with a focus on enabling fast experimentation. It supports multiple back-ends, including TensorFlow, CNTK and Theano.

TensorFlow is a lower level mathematical library for building deep neural network architectures. The `keras` R package makes it easy to use Keras and TensorFlow in R.

Define
- Model
- Sequential model
- Multi-GPU model

→ **Compile**
- Optimiser
- Loss
- Metrics

→ **Fit**
- Batch size
- Epochs
- Validation split

→ **Evaluate**
- Evaluate
- Plot

→ **Predict**
- classes
- probability

https://keras.rstudio.com

https://www.manning.com/books/deep-learning-with-r

The "Hello, World!" of deep learning

INSTALLATION

The `keras` R package uses the Python keras library. You can install all the prerequisites directly from R.

https://keras.rstudio.com/reference/install_keras.html

```
library(keras)
install_keras()
```

See ?install_keras for GPU instructions

This installs the required libraries in an Anaconda environment or virtual environment **'r-tensorflow'**.

Working with keras models

DEFINE A MODEL

keras_model() Keras Model

keras_model_sequential() Keras Model composed of a linear stack of layers

multi_gpu_model() Replicates a model on different GPUs

COMPILE A MODEL

compile(object, optimizer, loss, metrics = NULL**)**
Configure a Keras model for training

FIT A MODEL

fit(object, x = NULL, y = NULL, batch_size = NULL, epochs = 10, verbose = 1, callbacks = NULL, …**)**
Train a Keras model for a fixed number of epochs (iterations)

fit_generator() Fits the model on data yielded batch-by-batch by a generator

train_on_batch() test_on_batch() Single gradient update or model evaluation over one batch of samples

EVALUATE A MODEL

evaluate(object, x = NULL, y = NULL, batch_size = NULL**)** Evaluate a Keras model

evaluate_generator() Evaluates the model on a data generator

PREDICT

predict() Generate predictions from a Keras model

predict_proba() and **predict_classes()**
Generates probability or class probability predictions for the input samples

predict_on_batch() Returns predictions for a single batch of samples

predict_generator() Generates predictions for the input samples from a data generator

OTHER MODEL OPERATIONS

summary() Print a summary of a Keras model

export_savedmodel() Export a saved model

get_layer() Retrieves a layer based on either its name (unique) or index

pop_layer() Remove the last layer in a model

save_model_hdf5(); load_model_hdf5() Save/Load models using HDF5 files

serialize_model(); unserialize_model()
Serialize a model to an R object

clone_model() Clone a model instance

freeze_weights(); unfreeze_weights()
Freeze and unfreeze weights

CORE LAYERS

layer_input() Input layer

layer_dense() Add a densely-connected NN layer to an output

layer_activation() Apply an activation function to an output

layer_dropout() Applies Dropout to the input

layer_reshape() Reshapes an output to a certain shape

layer_permute() Permute the dimensions of an input according to a given pattern

n

layer_repeat_vector() Repeats the input n times

x f(x)

layer_lambda(object, f) Wraps arbitrary expression as a layer

L1 L2

layer_activity_regularization() Layer that applies an update to the cost function based input activity

layer_masking() Masks a sequence by using a mask value to skip timesteps

layer_flatten() Flattens an input

TRAINING AN IMAGE RECOGNIZER ON MNIST DATA

```
# input layer: use MNIST images
mnist <- dataset_mnist()
x_train <- mnist$train$x;  y_train <- mnist$train$y
x_test <- mnist$test$x;  y_test <- mnist$test$y

# reshape and rescale
x_train <- array_reshape(x_train, c(nrow(x_train), 784))
x_test <- array_reshape(x_test, c(nrow(x_test), 784))
x_train <- x_train / 255;  x_test <- x_test / 255

y_train <- to_categorical(y_train, 10)
y_test <- to_categorical(y_test, 10)

# defining the model and layers
model <- keras_model_sequential()
model %>%
 layer_dense(units = 256, activation = 'relu',
             input_shape = c(784)) %>%
 layer_dropout(rate = 0.4) %>%
 layer_dense(units = 128, activation = 'relu') %>%
 layer_dense(units = 10, activation = 'softmax')

# compile (define loss and optimizer)
model %>% compile(
 loss = 'categorical_crossentropy',
 optimizer = optimizer_rmsprop(),
 metrics = c('accuracy')
)

# train (fit)
model %>% fit(
 x_train, y_train,
 epochs = 30, batch_size = 128,
 validation_split = 0.2
)
model %>% evaluate(x_test, y_test)
model %>% predict_classes(x_test)
```

RStudio

More layers

CONVOLUTIONAL LAYERS

layer_conv_1d() 1D, e.g. temporal convolution

layer_conv_2d_transpose() Transposed 2D (deconvolution)

layer_conv_2d() 2D, e.g. spatial convolution over images

layer_conv_3d_transpose() Transposed 3D (deconvolution)
layer_conv_3d() 3D, e.g. spatial convolution over volumes

layer_conv_lstm_2d() Convolutional LSTM

layer_separable_conv_2d() Depthwise separable 2D

layer_upsampling_1d()
layer_upsampling_2d()
layer_upsampling_3d()
Upsampling layer

layer_zero_padding_1d()
layer_zero_padding_2d()
layer_zero_padding_3d()
Zero-padding layer

layer_cropping_1d()
layer_cropping_2d()
layer_cropping_3d()
Cropping layer

POOLING LAYERS

layer_max_pooling_1d()
layer_max_pooling_2d()
layer_max_pooling_3d()
Maximum pooling for 1D to 3D

layer_average_pooling_1d()
layer_average_pooling_2d()
layer_average_pooling_3d()
Average pooling for 1D to 3D

layer_global_max_pooling_1d()
layer_global_max_pooling_2d()
layer_global_max_pooling_3d()
Global maximum pooling

layer_global_average_pooling_1d()
layer_global_average_pooling_2d()
layer_global_average_pooling_3d()
Global average pooling

ACTIVATION LAYERS

layer_activation(object, activation**)** Apply an activation function to an output

layer_activation_leaky_relu() Leaky version of a rectified linear unit

layer_activation_parametric_relu() Parametric rectified linear unit

layer_activation_thresholded_relu() Thresholded rectified linear unit

layer_activation_elu() Exponential linear unit

DROPOUT LAYERS

layer_dropout() Applies dropout to the input

layer_spatial_dropout_1d()
layer_spatial_dropout_2d()
layer_spatial_dropout_3d()
Spatial 1D to 3D version of dropout

RECURRENT LAYERS

layer_simple_rnn() Fully-connected RNN where the output is to be fed back to input

layer_gru() Gated recurrent unit - Cho et al

layer_cudnn_gru() Fast GRU implementation backed by CuDNN

layer_lstm() Long-Short Term Memory unit - Hochreiter 1997

layer_cudnn_lstm() Fast LSTM implementation backed by CuDNN

LOCALLY CONNECTED LAYERS

layer_locally_connected_1d()
layer_locally_connected_2d()
Similar to convolution, but weights are not shared, i.e. different filters for each patch

Preprocessing

SEQUENCE PREPROCESSING

pad_sequences() Pads each sequence to the same length (length of the longest sequence)

skipgrams() Generates skipgram word pairs

make_sampling_table() Generates word rank-based probabilistic sampling table

TEXT PREPROCESSING

text_tokenizer() Text tokenization utility

fit_text_tokenizer() Update tokenizer internal vocabulary

save_text_tokenizer(); load_text_tokenizer() Save a text tokenizer to an external file

texts_to_sequences();
texts_to_sequences_generator()
Transforms each text in texts to sequence of integers

texts_to_matrix(); sequences_to_matrix() Convert a list of sequences into a matrix

text_one_hot() One-hot encode text to word indices

text_hashing_trick() Converts a text to a sequence of indexes in a fixed-size hashing space

text_to_word_sequence() Convert text to a sequence of words (or tokens)

IMAGE PREPROCESSING

image_load() Loads an image into PIL format.

flow_images_from_data()
flow_images_from_directory()
Generates batches of augmented/normalized data from images and labels, or a directory

image_data_generator() Generate minibatches of image data with real-time data augmentation.

fit_image_data_generator() Fit image data generator internal statistics to some sample data

generator_next() Retrieve the next item

image_to_array(); image_array_resize()
image_array_save() 3D array representation

Keras TensorFlow

Pre-trained models

Keras applications are deep learning models that are made available alongside pre-trained weights. These models can be used for prediction, feature extraction, and fine-tuning.

application_xception()
xception_preprocess_input()
Xception v1 model

application_inception_v3()
inception_v3_preprocess_input()
Inception v3 model, with weights pre-trained on ImageNet

application_inception_resnet_v2()
inception_resnet_v2_preprocess_input()
Inception-ResNet v2 model, with weights trained on ImageNet

application_vgg16(); application_vgg19() VGG16 and VGG19 models

application_resnet50() ResNet50 model

application_mobilenet()
mobilenet_preprocess_input()
mobilenet_decode_predictions()
mobilenet_load_model_hdf5()
MobileNet model architecture

IMAGENET

ImageNet is a large database of images with labels, extensively used for deep learning

imagenet_preprocess_input()
imagenet_decode_predictions()
Preprocesses a tensor encoding a batch of images for ImageNet, and decodes predictions

Callbacks

A callback is a set of functions to be applied at given stages of the training procedure. You can use callbacks to get a view on internal states and statistics of the model during training.

callback_early_stopping() Stop training when a monitored quantity has stopped improving
callback_learning_rate_scheduler() Learning rate scheduler
callback_tensorboard() TensorBoard basic visualizations

Labelled data with labelled : : CHEAT SHEET

The **labelled** package provides a set of functions and methods to handle and to manipulate labelled data, as imported with **haven** package.

Basics

Labelled data is a common data structure in other statistical environment such as Stata, SAS or SPSS.
It consists of a set of additional attributes for numeric and character vectors (including columns of a data frame).

There are 3 types of attributes:

1. **Variable labels** (a short description of a variable)
2. **Value labels** (labels associated to specific values)
3. **Missing values**:
   - User-defined missing values (SPSS style)
   - Tagged NA (Stata and SAS style)

Variable labels

MANIPULATING A VECTOR

var_label(x) *or* **var_label**(df$v1)
Get the variable label associated to a vector x

var_label(x) <- "variable description"
Add/modify a variable label to x

var_label(x) <- NULL
Remove the variable label associated to x

MANIPULATING A DATA.FRAME

var_label(df)
List all variable labels associated with columns of df

var_label(df) <- list(v1 = "variable 1", v2 = "variable 2")
Update variable labels of some columns of df

df %>% **set_variable_labels**(v1 = "variable 1", v2 = "variable 2", v3 = NULL)
Update variable labels using dplyr syntax

df %>% **look_for**()
Return a data frame with all variable names and labels

df %>% **look_for**("s")
Search variables containing "s" in their name or label

df %>% **look_for**(details = TRUE)
Return additional details on each variable

Value labels

When value labels are attached to a numeric or character vector, the vector's class becomes **haven_labelled**. A major difference with a factor is that values of the vector are not changed and it is not mandatory to attach a label to each value.

MANIPULATING A VECTOR

val_label(x, value) *or* **val_label**(df$v1, value)
Get the label attached to a specific value of a vector

val_label(x, value) <- "label"
Set/Update the label attached to a specific value

val_label(x, value) <- NULL
Remove the label attached to a specific value

val_labels(x)
Get all value labels attached to a vector

val_labels(x) <- c(no = 0, yes = 1, maybe = 9)
Set/Update all value labels attached to a vector

val_labels(x) <- NULL
Remove all value labels attached to a vector

labelled(c("F", "F", "M"), c(Female = "F", Male = "M"))
Create a labelled vector

sort_val_labels(x, according_to = "values")
Sort value labels according to values (or labels)

drop_unused_value_labels(x)
Remove value labels not observed in the data

MANIPULATING A DATA.FRAME

df %>% **set_value_labels**(v1 = c(Yes = 1, No = 2), v2 = c(Male = "M", Female = "F"))
Define value labels of several variables

df %>% **add_value_labels**(v1 = c(Unknown = 9))
Add specific value labels to a variable (other already defined value labels remains unchanged)

df %>% **remove_value_labels**(v1 = 9)
Remove specific value labels to a variable

df %>% **set_value_labels**(v1 = NULL)
Remove all value labels attached to a variable

df %>% **drop_unused_value_labels**()
Remove value labels not observed in the data

Missing values

USER-DEFINED MISSING VALUES (SPSS STYLE)

Used to indicate that some values should be considered as missing. However, they will not be treated as NA as long as they are not converted to proper NA.
When missing values are attached to a numeric or character vector, the vector's class becomes **haven_labelled_spss**.
When importing a SPSS file, use the option *user_na = TRUE* to keep defined missing values (otherwise, they will be converted to NA).

na_values(x)
Get individual missing values attached to a vector

na_values(x) <- c(8, 9, 10)
df %>% **set_na_values**(v1 = c(8, 9, 10))
Set/Update individual missing values (NULL to remove)

na_range(x)
Get a range of missing values attached to a vector

na_range(x) <- c(8, 10)
df %>% **set_na_range**(v1 = c(8, 10))
Set/Update a range of missing values (NULL to remove)

user_na_to_na(x) *or* df %>% **user_na_to_na**()
Convert user-defined missing values to NA

is_na(x)
TRUE if NA or if a user-defined missing value

TAGGED NAs (STATA & SAS STYLE)

"Tagged" missing values work exactly like regular R missing values except that they store one additional byte of information: a tag, which is usually a letter ("a" to "z").

x <- c(1:5, tagged_na("a"), tagged_na("z"), NA)
tagged_na("a") generates a NA with a tag

is.na(x)
Tagged NAs work identically to regular NAs

is_tagged_na(x)
Test if it is a tagged NA

na_tag(x)
Display the tags associated to tagged NAs

format_tagged_na(x)
Convert x to a character vector showing the tagged NAs

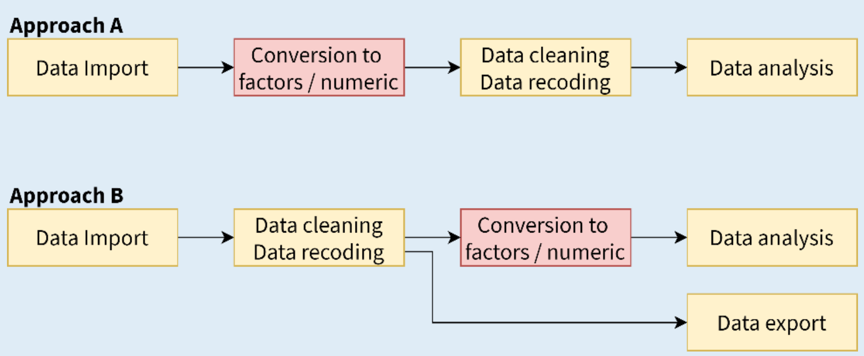
When using labelled data?

haven_labelled and *haven_labelled_spss* classes introduced in **haven** package allow to add metadata (variable labels, value labels and SPSS-style missing values) to vectors / data frame columns and to properly import these metadata from SAS, Stata or SPSS.

Functions and methods provided by **labelled** package are designed for easy manipulation of such labelled data.

It should be noted that **value labels** doesn't imply that your vectors should be considered as categorical or continuous. Therefore, value labels are not intended to be use for data analysis. For example, before performing modeling or plotting, you should convert vectors with value labels into factors or into classic numeric/character vectors.

Two main approaches could be considered:



In **approach A**, labelled vectors are converted into factors or into numeric/character vectors just after data import, using **unlabelled**(), **to_factor**() or **unclass**(). Then, data cleaning, data recoding and analysis are performed using classic **R** vector types.

In **approach B**, labelled vectors are kept for data cleaning and recoding, allowing to preserve original coding, in particular if data should be reexported after that step. Functions provided by **labelled** will be useful for managing value labels.

However, as in approach A, labelled vectors will have to be converted into classic factors or numeric vectors before data analysis as this is the way categorical and continuous variables should be coded for analysis.

Conversion

OF LABELLED VECTORS

If all value labels and user-defined missing values are removed from a labelled vector, the *haven_labelled* class will be removed and the vector will be transformed into a basic numeric or character vector. **Values of the vector will remain unchanged.**

remove_val_labels(x)
Remove value labels attached to a vector.

remove_user_na(x)
Remove user-defined (*na_values* and *na_range*) from a vector

unclass(x)
Remove the *haven_labelled* class. Therefore, the vector will be considered as a classical numeric or character vector. Value labels and user-defined missing values will still be visible as attributes attached to the vector.

When converting a labelled vector into a factor or a character vector of the value labels, be aware that **original values of the vector will be converted.**

to_character(x)
Convert into a character vector replacing values by their corresponding value label

to_factor(x)
Convert into a character vector replacing values by their corresponding value label

to_factor(x, levels = "prefixed")
Value labels will be prefixed with their original value

to_factor(x, strict = TRUE)
Convert into a factor only if all observed values have a value label

df %>% **to_factor**()
Convert all labelled vectors and only labelled vectors into factors

df %>% **to_factor**(labelled_only = FALSE)
Convert all columns (including non labelled vectors) into factors

unlabelled(x)
df %%>% **unlabelled**()
Labelled vectors will be converted into factors only if all observed values have a value label. Otherwise, they will be unclassed. Similar to df %>% to_factor(labelled_only = T, strict = T, unclass = T)

to_factor(x, drop_unused_labels = TRUE)
df %>% **unlabelled**(drop_unused_labels = TRUE)
Unused value labels will be dropped before conversion into factors

INTO LABELLED VECTORS

to_labelled(f)
Convert a factor into a numeric labelled vector.
Note that to_labelled(to_factor(x)) *and* x *will not be identitical (original coding will be lost).*

to_labelled(df)
If df was imported with the **foreign** package or if it is a data set created with **memisc** package, meta data (variable labels, value labels and user-defined missing values) will be converted into **labelled** format.

If any value label or user-defined missing value is added to a numeric or a character vector,
it will be automatically converted into a labelled vector.
Values of the vector will remain unchanged.

Miscellaneous

nolabel_to_na(x) *or* df %>% **nolabel_to_na**()
For labelled vectors, values <u>without</u> a value label will be converted into NA

val_labels_to_na(x) *or* df %>% **val_labels_to_na**()
For labelled vectors, values <u>with</u> a value label will be converted into NA

df2 %>% **copy_labels_from**(df1)
Copy variable labels, values labels and user-defined missing values from df1 to df2 based on shared columns names. Useful when attributes are lost after some data manipulation.

recode(x, `2` = 1, `3` =2)
Apply dplyr::recode() to a labelled vector.
Attached value labels will remain unchanged.

recode(x, `2` = 1, .combine_value_labels = TRUE)
This option will combine value labels of original values merged together to produce new value labels.
It is recommended to check that the result is appropriate.

update_labelled(x) *or* df %>% **update_labelled**()
If x/df was imported/created using an older version of **haven** or **labelled**, you may encounter some unexpected results. update_labelled() will update all labelled vectors to be consistent with the current implementation.

Leaflet Cheat Sheet

Leaflet for R

an open-source JavaScript library for mobile-friendly interactive maps

Quick Start

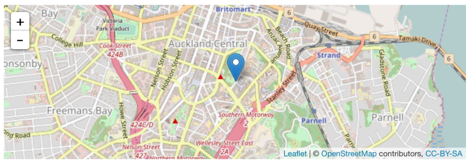
Installation

Use **install.packages("leaflet")** to installize the package or directly from Github *devtools::install_github("rstudio/leaflet").*

First Map

m <- leaflet() %>% *# leaflet works with the pipe operator*
addTiles() %>% *# setup the default OpenStreetMap map tiles*
addMarkers(lng = 174.768, lat = -36.852, popup = "The birthplace of R")
 # add a single point layer

m



Map Widget

Initialization

m <- leaflet(options = leafletOptions(...**))**

center	Initial geographic center of the map
zoom	Initial map zoom level
minZoom	Minimum zoom level of the map
maxZoom	Maximum zoom level of the map

Map Methods

m %>% setView(lng, lat, zoom, options = list()**)**
Set the view of the map (center and zoom level)
m %>% fitBounds(lng1, lat1, lng2, lat2**)**
Fit the view into the rectangle [lng1, lat1] - [lng2, lat2]
m %>% clearBounds()
Clear the bound, automatically determine from the map elements

Data Object

Both **leaflet()** and the **map** layers have an optional data parameter that is designed to receive spatial data with the following formats:

Base R — *The arguments of all layers take normal R objects:*
df <- data.frame(lat = ..., lng = ...)
leaflet(df) %>% addTiles() %>% addCircles()

sp *package* — library(sp) *Useful functions:*
SpatialPoints, SpatialLines, SpatialPolygons, ...

maps *package* — library(maps) *Build a map of states with colors:*
mapStates <- map("state", fill = TRUE, plot = FALSE)
leaflet(mapStates) %>% addTiles() %>%
addPolygons(fillColor = topo.colors(10, alpha = NULL), stroke = FALSE)

Markers

Use markers to call out points, express locations with latitude/longitude coordinates, appear as icons or as circles.
Data come from vectors or assigned data frame, or **sp** package objects.

Icon Markers

Regular Icons: default and simple
addMarkers(lng, lat, popup, label**)** *add basic icon markers*
makeIcon/icons (iconUrl, iconWidth, iconHeight, iconAnchorX, iconAnchorY, shadowUrl, shadowWidth, shadowHeight, ... **)** *customize marker icons*
iconList() *create a list of icons*
Awesome Icons: customizable with colors and icons
addAwesomeMarkers, makeAwesomeIcon, awesomeIcons, awesomeIconList
Marker Clusters: option of addMarters()
clusterOptions = markerClusterOptions()
freezeAtZoom Freeze the cluster at assigned zoom level

Circle Markers

addCircleMarkers(color, radius, stroke, opacity, ... **)**
Customize their color, radius, stroke, opacity

Popups and Labels

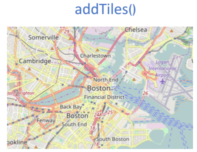
addPopups(lng, lat, ...content..., options) *Add standalone popups*
options = popupOptions(closeButton=FALSE)
addMarkers(..., popup, ...) *Show popups with markers or shapes*
addMarkers(..., label, labelOptions...) *Show labels with markers or shapes*
labelOptions = labelOptions(noHide, textOnly, textsize, direction, style)
addLabelOnlyMarkers() *Add labels without markers*

Lines and Shapes

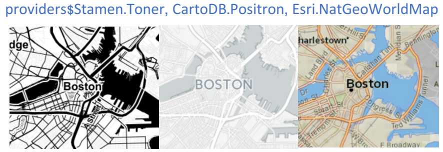
Polygons and Polylines
addPolygons(color, weight=1, smoothFactor=0.5, opacity=1.0, fillOpacity=0.5, fillColor= ~colorQuantile("YlOrRd", ALAND)(ALAND), highlightOptions, ... **)**
highlightOptions(color, weight=2, bringToFront=TRUE**)** *highlight shapes*
Use **rmapshaper::ms_simplify** to simplify complex shapes
Circles **addCircles(**lng, lat, weight=1, radius, ... **)**
Rectangles **addRectangles(**lng1, lat1, lng2, lat2, fillColor="transparent", ... **)**

Basemaps

addTiles() — providers$Stamen.Toner, CartoDB.Positron, Esri.NatGeoWorldMap



Default Tiles



Third-Party Tiles **addProviderTiles()**

Use **addTiles()** to add a custom map tile URL template, use **addWMSTiles()** to add WMS (Web Map Service) tiles

GeoJSON and TopoJSON

There are two options to use the GeoJSON/TopoJSON data.
* To read into **sp** objects with the **geojsonio** or **rgdal** package:
geojsonio::geojson_read(...,what="sp") rgdal::readOGR(...,"OGRGeoJSON")
* Or to use the **addGeoJSON()** and **addTopoJSON()** functions:
addTopoJSON/addGeoJSON(... weight, color, fill, opacity, fillOpacity...)
Styles can also be tuned separately with a *style: {...}* object.

Other packages including **RJSONIO** and **jsonlite** can help fast parse or generate the data needed.

Shiny Integration

To integrate a Leaflet map into an app:
* In the UI, call **leafletOutput(**"name"**)**
* On the server side, assign a **renderLeaflet(...)** call to the output
* Inside the **renderLeaflet** expression, return a Leaflet map object

Modification

To modify an existing map or add incremental changes to the map, you can use **leafletProxy()**. This should be performed in an observer on the server side.

Other useful functions to edit your map:
fitBounds(0, 0, 11, 11**)** *similar to setView*
fit the view to within these bounds
addCircles(1:10, 1:10, layerId = LETTERS[1:10]**)**
create circles with layerIds of "A", "B", "C"...
removeShape(c("B", "F")**)** *remove some of the circles*
clearShapes() *clear all circles (and other shapes)*

Inputs/Events

Object Events
Object event names generally use this pattern:
input$*MAPID_OBJCATEGORY_EVENTNAME*.
Triger an event changes the value of the Shiny input at this variable.
Valid values for *OBJCATEGORY* are *marker*, *shape*, *geojson* and *topojson*.
Valid values for *EVENTNAME* are *click*, *mouseover* and *mouseout*.

All of these events are set to either *NULL* if the event has never happened, or a *list()* that includes:
* lat The latitude of the object, if available; otherwise, the mouse cursor
* lng The longitude of the object, if available; otherwise, the mouse cursor
* id The layerId, if any

GeoJSON events also include additional properties:
* featureId The feature ID, if any
* properties The feature properties

Map Events
input$*MAPID*_click *when the map background or basemap is clicked value -- a list with lat and lng*
input$*MAPID*_bounds *provide the lat/lng bounds of the visible map area value -- a list with north, east, south and west*
input$*MAPID*_zoom *an integer indicates the zoom level*

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Adapted from Rstudio materials https://rstudio.github.io/leaflet/ 2017/05/01

Dates and times with lubridate : : CHEAT SHEET

Date-times

2017-11-28 12:00:00

2017-11-28 12:00:00
A **date-time** is a point on the timeline, stored as the number of seconds since 1970-01-01 00:00:00 UTC

*dt <- **as_datetime**(1511870400)*
"2017-11-28 12:00:00 UTC"

2017-11-28
A **date** is a day stored as the number of days since 1970-01-01

*d <- **as_date**(17498)*
"2017-11-28"

12:00:00
An hms is a **time** stored as the number of seconds since 00:00:00

*t <- hms::**as_hms**(85)*
00:01:25

PARSE DATE-TIMES (Convert strings or numbers to date-times)

1. Identify the order of the year (**y**), month (**m**), day (**d**), hour (**h**), minute (**m**) and second (**s**) elements in your data.
2. Use the function below whose name replicates the order. Each accepts a tz argument to set the time zone, e.g. ymd(x, tz = "UTC").

2017-11-28T14:02:00 — **ymd_hms(), ymd_hm(), ymd_h().** ymd_hms("2017-11-28T14:02:00")

2017-22-12 10:00:00 — **ydm_hms(), ydm_hm(), ydm_h().** ydm_hms("2017-22-12 10:00:00")

11/28/2017 1:02:03 — **mdy_hms(), mdy_hm(), mdy_h().** mdy_hms("11/28/2017 1:02:03")

1 Jan 2017 23:59:59 — **dmy_hms(), dmy_hm(), dmy_h().** dmy_hms("1 Jan 2017 23:59:59")

20170131 — **ymd(), ydm().** ymd(20170131)

July 4th, 2000 — **mdy(), myd().** mdy("July 4th, 2000")

4th of July '99 — **dmy(), dym().** dmy("4th of July '99")

2001: Q3 — **yq()** Q for quarter. yq("2001: Q3")

07-2020 — **my(), ym().** my("07-2020")

2:01 — hms::**hms()** Also lubridate::**hms()**, **hm()** and **ms()**, which return periods.* hms::hms(sec = 0, min= 1, hours = 2, roll = FALSE)

2017.5 — **date_decimal(**decimal, tz = "UTC"**)** date_decimal(2017.5)

now(tzone = ""**)** Current time in tz (defaults to system tz). now()

January

today(tzone = ""**)** Current date in a tz (defaults to system tz). today()

fast_strptime() Faster strptime. fast_strptime('9/1/01', '%y/%m/%d')

parse_date_time() Easier strptime. parse_date_time("9/1/01", "ymd")

GET AND SET COMPONENTS

Use an accessor function to get a component.

d ## "2017-11-28"
day(d) ## 28

Assign into an accessor function to change a component in place.

day(d) <- 1
d ## "2017-11-01"

2018-01-31 11:59:59 — **date(**x**)** Date component. date(dt)

2018-01-31 11:59:59 — **year(**x**)** Year. year(dt)
isoyear(x**)** The ISO 8601 year.
epiyear(x**)** Epidemiological year.

2018-**01**-31 11:59:59 — **month(**x, label, abbr**)** Month. month(dt)

2018-01-**31** 11:59:59 — **day(**x**)** Day of month. day(dt)
wday(x, label, abbr**)** Day of week.
qday(x**)** Day of quarter.

2018-01-31 **11**:59:59 — **hour(**x**)** Hour. hour(dt)

2018-01-31 11:**59**:59 — **minute(**x**)** Minutes. minute(dt)

2018-01-31 11:59:**59** — **second(**x**)** Seconds. second(dt)

2018-01-31 11:59:59 **UTC** — **tz(**x**)** Time zone. tz(dt)

week(x**)** Week of the year. week(dt)
isoweek() ISO 8601 week.
epiweek() Epidemiological week.

quarter(x**)** Quarter. quarter(dt)

semester(x, with_year = FALSE**)** Semester. semester(dt)

am(x**)** Is it in the am? am(dt)
pm(x**)** Is it in the pm? pm(dt)

dst(x**)** Is it daylight savings? dst(d)

leap_year(x**)** Is it a leap year? leap_year(d)

update(object, ..., simple = FALSE**)** update(dt, mday = 2, hour = 1)

Round Date-times

floor_date(x, unit = "second"**)** Round down to nearest unit. floor_date(dt, unit = "month")

round_date(x, unit = "second"**)** Round to nearest unit. round_date(dt, unit = "month")

ceiling_date(x, unit = "second", change_on_boundary = NULL**)** Round up to nearest unit. ceiling_date(dt, unit = "month")

Valid units are second, minute, hour, day, week, month, bimonth, quarter, season, halfyear and year.

rollback(dates, roll_to_first = FALSE, preserve_hms = TRUE**)** Roll back to last day of previous month. Also **rollforward()**. rollback(dt)

Stamp Date-times

stamp() Derive a template from an example string and return a new function that will apply the template to date-times. Also **stamp_date()** and **stamp_time()**.

1. Derive a template, create a function
   sf <- stamp("Created Sunday, Jan 17, 1999 3:34")
2. Apply the template to dates
   sf(ymd("2010-04-05"))
   ## [1] "Created Monday, Apr 05, 2010 00:00"

Tip: use a date with day > 12

Time Zones

R recognizes ~600 time zones. Each encodes the time zone, Daylight Savings Time, and historical calendar variations for an area. R assigns *one* time zone per vector.

Use the **UTC** time zone to avoid Daylight Savings.

OlsonNames() Returns a list of valid time zone names. OlsonNames()

Sys.timezone() Gets current time zone.

4:00 Pacific — 5:00 Mountain — 6:00 Central — 7:00 Eastern

with_tz(time, tzone = ""**)** Get the **same date-time** in a new time zone (a new clock time). Also **local_time(**dt, tz, units**)**. with_tz(dt, "US/Pacific")

PT MT CT ET

7:00 Pacific — 7:00 Mountain — 7:00 Central — 7:00 Eastern

force_tz(time, tzone = ""**)** Get the **same clock time** in a new time zone (a new date-time). Also **force_tzs()**. force_tz(dt, "US/Pacific")

Math with Date-times — Lubridate provides three classes of timespans to facilitate math with dates and date-times.

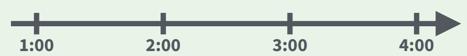
Math with date-times relies on the **timeline**, which behaves inconsistently. Consider how the timeline behaves during:

Periods track changes in clock times, which ignore time line irregularities.

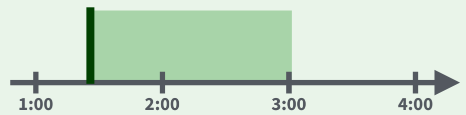
Durations track the passage of physical time, which deviates from clock time when irregularities occur.

Intervals represent specific intervals of the timeline, bounded by start and end date-times.

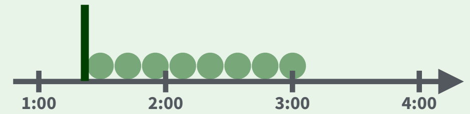
A normal day
nor <- ymd_hms("2018-01-01 01:30:00",tz="US/Eastern")



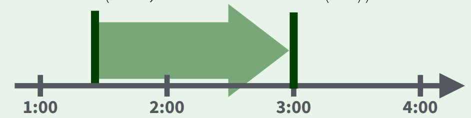
nor + minutes(90)



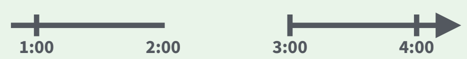
nor + dminutes(90)



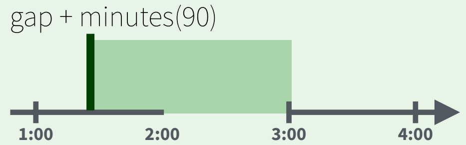
interval(nor, nor + minutes(90))



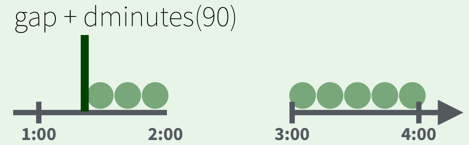
The start of daylight savings (spring forward)
gap <- ymd_hms("2018-03-11 01:30:00",tz="US/Eastern")



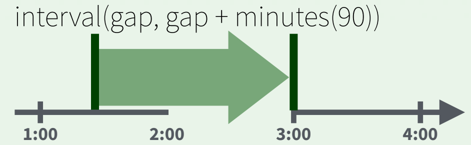
gap + minutes(90)



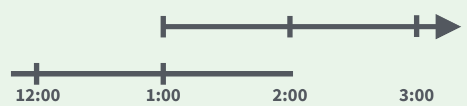
gap + dminutes(90)



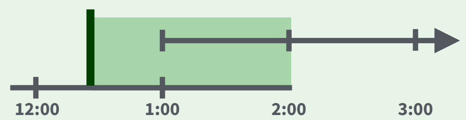
interval(gap, gap + minutes(90))



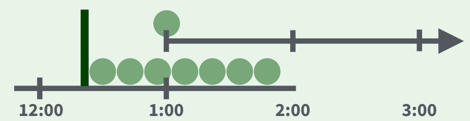
The end of daylight savings (fall back)
lap <- ymd_hms("2018-11-04 00:30:00",tz="US/Eastern")



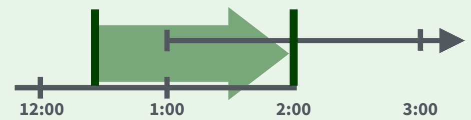
lap + minutes(90)



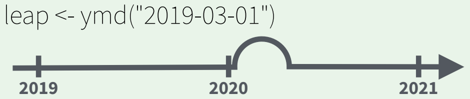
lap + dminutes(90)



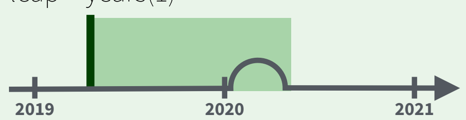
interval(lap, lap + minutes(90))



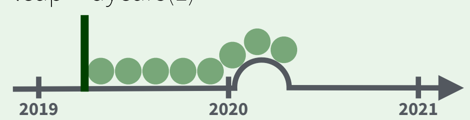
Leap years and leap seconds
leap <- ymd("2019-03-01")



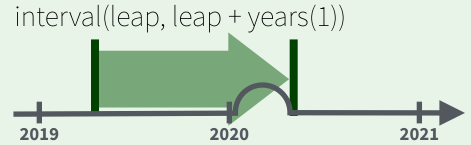
leap + years(1)



leap + dyears(1)



interval(leap, leap + years(1))



Not all years are 365 days due to **leap days**.

Not all minutes are 60 seconds due to **leap seconds**.

It is possible to create an imaginary date by adding **months**, e.g. February 31st

```
jan31 <- ymd(20180131)
jan31 + months(1)
## NA
```

%m+% and **%m-%** will roll imaginary dates to the last day of the previous month.

```
jan31 %m+% months(1)
## "2018-02-28"
```

add_with_rollback(e1, e2, roll_to_first = TRUE) will roll imaginary dates to the first day of the new month.

```
add_with_rollback(jan31, months(1),
roll_to_first = TRUE)
## "2018-03-01"
```

PERIODS

Add or subtract periods to model events that happen at specific clock times, like the NYSE opening bell.

Make a period with the name of a time unit ***pluralized***, e.g.

```
p <- months(3) + days(12)
p
"3m 12d 0H 0M 0S"
```

Number of months | Number of days | etc.

years(x = 1) x years.
months(x) x months.
weeks(x = 1) x weeks.
days(x = 1) x days.
hours(x = 1) x hours.
minutes(x = 1) x minutes.
seconds(x = 1) x seconds.
milliseconds(x = 1) x milliseconds.
microseconds(x = 1) x microseconds
nanoseconds(x = 1) x nanoseconds.
picoseconds(x = 1) x picoseconds.

period(num = NULL, units = "second", ...) An automation friendly period constructor. period(5, unit = "years")

as.period(x, unit) Coerce a timespan to a period, optionally in the specified units. Also **is.period()**. as.period(i)

period_to_seconds(x) Convert a period to the "standard" number of seconds implied by the period. Also **seconds_to_period()**. period_to_seconds(p)

DURATIONS

Add or subtract durations to model physical processes, like battery life. Durations are stored as seconds, the only time unit with a consistent length. **Difftimes** are a class of durations found in base R.

Make a duration with the name of a period prefixed with a ***d***, e.g.

```
dd <- ddays(14)
dd
"1209600s (~2 weeks)"
```

Exact length in seconds | Equivalent in common units

dyears(x = 1) 31536000x seconds.
dmonths(x = 1) 2629800x seconds.
dweeks(x = 1) 604800x seconds.
ddays(x = 1) 86400x seconds.
dhours(x = 1) 3600x seconds.
dminutes(x = 1) 60x seconds.
dseconds(x = 1) x seconds.
dmilliseconds(x = 1) x $\times$ 10^{-3} seconds.
dmicroseconds(x = 1) x $\times$ 10^{-6} seconds.
dnanoseconds(x = 1) x $\times$ 10^{-9} seconds.
dpicoseconds(x = 1) x $\times$ 10^{-12} seconds.

duration(num = NULL, units = "second", …) An automation friendly duration constructor. duration(5, unit = "years")

as.duration(x, …) Coerce a timespan to a duration. Also **is.duration()**, **is.difftime()**. as.duration(i)

make_difftime(x) Make difftime with the specified number of units. make_difftime(99999)

INTERVALS

Divide an interval by a duration to determine its physical length, divide an interval by a period to determine its implied length in clock time.

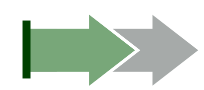
Make an interval with **interval()** or **%--%**, e.g.

Start Date | End Date

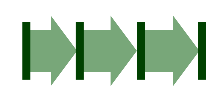
```
i <- interval(ymd("2017-01-01"), d)    ## 2017-01-01 UTC--2017-11-28 UTC
j <- d %--% ymd("2017-12-31")          ## 2017-11-28 UTC--2017-12-31 UTC
```

a **%within%** b Does interval or date-time *a* fall within interval *b*? now() %within% i

int_start(int) Access/set the start date-time of an interval. Also **int_end()**. int_start(i) <- now(); int_start(i)

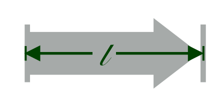


int_aligns(int1, int2) Do two intervals share a boundary? Also **int_overlaps()**. int_aligns(i, j)

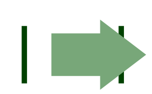


int_diff(times) Make the intervals that occur between the date-times in a vector. v <-c(dt, dt + 100, dt + 1000); int_diff(v)

int_flip(int) Reverse the direction of an interval. Also **int_standardize()**. int_flip(i)



int_length(int) Length in seconds. int_length(i)



int_shift(int, by) Shifts an interval up or down the timeline by a timespan. int_shift(i, days(-1))

as.interval(x, start, …) Coerce a timespan to an interval with the start date-time. Also **is.interval()**. as.interval(days(1), start = now())

Machine Learning with R

mlr

Introduction

***mlr* offers a unified interface for the basic building blocks of machine learning: tasks, learners, hyperparameters, etc.**

Tasks contain a description of a task (classification, regression, clustering, etc.) and a data set.

Learners specify a machine learning algorithm (GLM, SVM, xgboost, etc.) and its parameters.

Hyperparameters are learner settings that can be specified directly or tuned. A **parameter set** lists the possible hyperparameters for a given learner.

Wrapped Models are learners that have been trained on a task and can be used to make predictions.

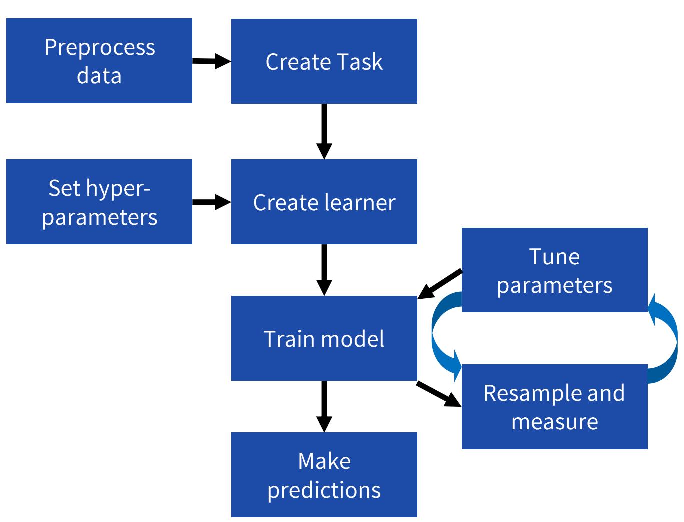
Predictions are the results of applying a model to either new data or the original training data.

Measures control how learner performance is evaluated, e.g. RMSE, LogLoss, AUC, etc.

Resampling estimates generalization performance by separating training data from test data. Common strategies include holdout and cross-validation.

Links: [Tutorial](#) | [CRAN](#) | [Github](#)

mlr workflow



Setup

Preprocessing data

`createDummyFeatures(obj=,target=,method=,cols=)`
Creates (0,1) flags for each non-numeric variable excluding `target`. Can be applied to entire dataset or only specific `cols`

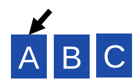
`normalizeFeatures(obj=,target=,method=,cols=, range=,on.constant=)`
Normalizes numerical features according to specified `method`:
- `"center"` (subtract mean)
- `"scale"` (divide by std. deviation)
- `"standardize"` (center and scale)
- `"range"` (linear scale to given range, default `range=c(0,1)`)

`mergeSmallFactorLevels(task=,cols=,min.perc=)`
Combine infrequent factor levels into a single merged level

`summarizeColumns(obj=)` where `obj` is a data.frame or task. Provides type, NA, and distributional data about each column

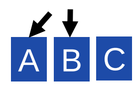
See also `capLargeValues dropFeatures removeConstantFeatures summarizeLevels`

Creating a task

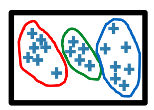


`makeClassifTask(data=,target=)`
Classification of a target variable, with optional positive class `positive`

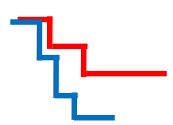
`makeRegrTask(data=,target=)`
Regression on a target variable



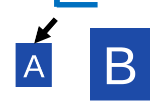
`makeMultilabelTask(data=,target=)`
Classification where the target can belong to more than one class per observation



`makeClusterTask(data=)`
Unsupervised clustering on a data set



`makeSurvTask(data=,target= c("time","event"))`
Survival analysis with a survival time column and an event column



`makeCostSensTask(data=,costs=)`
Cost-sensitive classification where each observation-cost pair has a specified cost

Other arguments that can be passed to a `task`:
- `weights=` Weighting vector to apply to observations
- `blocking=` Factor vector where each level indicates a block of observations that will not be split up in resampling

Making a learner

`makeLearner(cl=,predict.type=,...,par.vals=)`
Choose an algorithm class to perform the task and determine what that algorithm will predict
- `cl=`name of algorithm, e.g. `"classif.xgboost"` `"regr.randomForest"` `"cluster.kmeans"`
- `predict.type="response"` returns a prediction type that matches the source data; `"prob"` returns a predicted probability for classification problems only; `"se"` returns the a standard error of the prediction for regression problems only. Only certain learners can return `"prob"` and `"se"`
- `par.vals=` takes a list of hyperparameters and passes them to the learner; parameters can also be passed directly (`...`)

You can make multiple learners at once with `makeLearners()`

mlr has integrated over 170 different learning algorithms
- Full list: `View(listLearners())` shows all learners
- Available learners for a task: `View(listLearners(task))`
- Filtered list: `View(listLearners("classif", properties=c("prob", "factors")))` shows all classification learners `"classif"` which can predict probabilities `"prob"` and handle factor inputs `"factors"`
- See also `getLearnerProperties()`

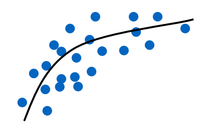
Training & Testing

Setting hyperparameters

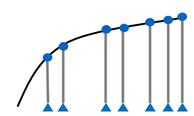
`setHyperPars(learner=,...)`
Set the hyperparameters (settings) for each learner, if you don't want to use the defaults. You can also specify hyperparameters in the `makeLearner()` call

`getParamSet(learner=)`
Show the possible universe of parameters for your learner; can take a learner directly, or a text string such as `"classif.qda"`

Train a model and predict



`train(learner=,task=)`
Train a model (`WrappedModel`) by applying a learner to a task. By default, the model will train on all observations. The underlying model can be extracted with `getLearnerModel()`



`predict(object=,task=,newdata=)`
Use a trained model to make predictions on a task or dataset. The resulting `pred` object can be viewed with `View(pred)` or accessed by `as.data.frame(pred)`

Measuring performance

`performance(pred=,measures=)`
Calculate performance of predictions according to one or more of several measures (use `listMeasures()` for full list):
- classif `acc auc bac ber brier[.scaled] f1 fdr fn fnr fp fpr gmean multiclass[.au1u .aunp .aunu .brier] npv ppv qsr ssr tn tnr tp tpr wkappa`
- regr `arsq expvar kendalltau mae mape medae medse mse msle rae rmse rmsle rrse rsq sae spearmanrho sse`
- cluster `db dunn G1 G2 silhouette`
- multilabel `multilabel[.f1 .subset01 .tpr .ppv .acc .hamloss]`
- costsens `mcp meancosts`
- surv `cindex`
- other `featperc timeboth timepredict timetrain`

For detailed performance data on classification tasks, use:
- `calculateConfusionMatrix(pred=)`
- `calculateROCMeasures(pred=)`

Resampling a learner

`makeResampleDesc(method=,...,stratify=)`
`method` must be one of the following:
- `"CV"` (cross-validation, for number of folds use `iters=`)
- `"LOO"` (leave-one-out cross-validation, for folds use `iters=`)
- `"RepCV"` (repeated cross-validation, for number of repetitions use `reps=`, for folds use `folds=`)
- `"Subsample"` (aka Monte-Carlo cross-validation, for iterations use `iters=`, for train % use `split=`)
- `"Bootstrap"` (out-of-bag bootstrap, uses `iters=`)
- `"Holdout"` (for train % use `split=`)

`stratify` keeps target proportions consistent across samples.

`makeResampleInstance(desc=,task=)` can reduce noise by ensuring the resampling is done identically every time.

`resample(learner=,task=,resampling=,measures=)`
Train and test model according to specified resampling strategy.

mlr includes several pre-specified resample descriptions: `cv2` (2-fold cross-validation), `cv3`, `cv5`, `cv10`, `hout` (holdout with split 2/3 for training, 1/3 for testing).
Convenience functions also exist to `resample()` with a specific strategy: `crossval()`, `repcv()`, `holdout()`, `subsample()`, `bootstrapOOB()`, `bootstrapB632()`, `bootstrapB632plus()`

Refining Performance

Tuning hyperparameters

Set search space using `makeParamSet(make<type>Param())`
- `makeNumericParam(id=,lower=,upper=,trafo=)`
- `makeIntegerParam(id=,lower=,upper=,trafo=)`
- `makeIntegerVectorParam(id=,len=,lower=,upper=, trafo=)`
- `makeDiscreteParam(id=,values=c(...))` (can also be used to test discrete values of numeric or integer parameters)

`trafo` transforms the parameter output using a specified function, e.g. `lower=-2,upper=2,trafo=function(x) 10^x` would test values between 0.01 and 100, scaled exponentially
Other acceptable parameter types include `Logical LogicalVector CharacterVector DiscreteVector`

Set a search algorithm with `makeTuneControl<type>()`
- `Grid(resolution=10L)` Grid of all possible points
- `Random(maxit=100)` Randomly sample search space
- `MBO(budget=)` Use Bayesian model-based optimization
- `Irace(n.instances=)` Iterated racing process
- Other types: `CMAES`, `Design`, `GenSA`

Tune using `tuneParams(learner=,task=,resampling=, measures=,par.set=,control=)`

Quickstart

Prepare data for training and testing

```
library(mlbench)
data(Soybean)
soy = createDummyFeatures(Soybean,target="Class")
tsk = makeClassifTask(data=soy,target="Class")
ho = makeResampleInstance("Holdout",tsk)
tsk.train = subsetTask(tsk,ho$train.inds[[1]])
tsk.test = subsetTask(tsk,ho$test.inds[[1]])
```

Convert the factor inputs in the Soybean dataset into (0,1) dummy features which can be used by the XGboost algorithm. Create a task to precict the "Class" column. Create a train set with 2/3 of data and a test set with the remaining 1/3 (default).

Create learner and evaluate performance

```
lrn = makeLearner("classif.xgboost",nrounds=10)
cv = makeResampleDesc("CV",iters=5)
res = resample(lrn,tsk.train,cv,acc)
```

Create an XGboost learner which will build 10 trees. Then test performance using 5-fold cross-validation. Accuracy should be between 0.90-0.92.

Tune hyperparameters and retrain model

```
ps = makeParamSet(makeNumericParam("eta",0,1),
  makeNumericParam("lambda",0,200),
  makeIntegerParam("max_depth",1,20))
tc = makeTuneControlMBO(budget=100)
tr = tuneParams(lrn,tsk.train,cv5,acc,ps,tc)
lrn = setHyperPars(lrn,par.vals=tr$x)
```

Tune hyperparameters `eta`, `lambda`, and `max_depth` by defining a search space and tuning using Model Based Optimization (MBO) to control the search. Then perform 100 rounds of 5-fold cross-validation, improving accuracy to ~0.93. Update the XGboost learner with the tuned hyperparameters.

```
mdl = train(lrn,tsk.train)
prd = predict(mdl,tsk.test)
calculateConfusionMatrix(prd)
mdl = train(lrn,tsk)
```

Train the model on the train set and make predictions on the test set. Show performance as a confusion matrix. Finally, re-train model on the full set to use on new data. You are now ready to go out into the real world and make 93% accurate predictions!

Legend for functions (not all parameters shown):
`function(required_parameters=,optional_parameters=)`

Configuration

mlr's default settings can be changed using `configureMlr()`:

- `show.info` Whether to show verbose output by default when training, tuning, resampling, etc. (`TRUE`)
- `on.learner.error` How to handle a learner error. `"stop"` halts execution, `"warn"` returns NAs and displays a warning, `"quiet"` returns NAs with no warning (`"stop"`)
- `on.learner.warning` How to handle a learner warning. `"warn"` displays a warning, `"quiet"` supresses it (`"warn"`)
- `on.par.without.desc` How to handle a parameter with no description. `"stop"`, `"warn"`, `"quiet"` (`"stop"`)
- `on.par.out.of.bounds` How to handle a parameter with an out-of-bounds value. `"stop"`, `"warn"`, `"quiet"` (`"stop"`)
- `on.measure.not.applicable` How to handle a measure not applicable to a learner. `"stop"`,`"warn"`,`"quiet"` (`"stop"`)
- `show.learner.output` Whether to show learner output to the console during training (`TRUE`)
- `on.error.dump` Whether to create an error dump for crashed learners if `on.learner.error` is not set to `"stop"` (`TRUE`)

Use `getMlrOptions()` to see current settings

Parallelization

mlr works with the `parallelMap` package to take advantage of multicore and cluster computing for faster operations. mlr automatically detects which operations are able to run in parallel.

To begin parallel operation use:
`parallelStart(mode=,cpus=,level=)`

- `mode` determines how the parallelization is performed:
  - `"local"` no parallelization applied, simply uses `mapply`
  - `"multicore"` multicore execution on a single machine, uses `parallel::mclapply`. Not available in Windows.
  - `"socket"` multicore execution in socket mode
  - `"mpi"` Snow MPI cluster on one or multiple machines using `parallel::makeCluster` and `parallel::clusterMap`
  - `"BatchJobs"` Batch queuing HPC clusters using `BatchJobs::batchMap`
- `cpus` determines how many logical cores will be used
- `level` controls parallelization: `"mlr.benchmark"` `"mlr.resample"` `"mlr.selectFeatures"` `"mlr.tuneParams"` `"mlr.ensemble"`

To end parallelization, use `parallelStop()`

Imputation

`impute(obj=,target=,cols=,dummy.cols=,dummy.type=)`
Applies specified logic to data frame or task containing NAs and returns an imputation description which can be used on new data

- `obj=`data frame or task on which to perform imputation
- `target=`specify target variable which will not be imputed
- `cols=`column names and logic for imputation*
- `dummy.cols=`column names to create a NA (T/F) column*
- `dummy.type=`set to `"numeric"` to use (0,1) instead of (T/F)

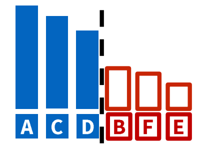
*Can also use `classes` and `dummy.classes` in place of `cols`

Imputation logic is passed to `cols` or `classes` via a list, e.g.: `cols=list(V1=imputeMean())` where `V1` is the column to which to apply the imputation, and `imputeMean()` is the imputation method. Available imputation methods include:
`imputeConst(const=)` `imputeMedian()` `imputeMode()` `imputeMin(multiplier=)` `imputeMax(multiplier=)` `imputeNormal(mean=,sd=)` `imputeHist(breaks=,use.mids=)` `imputeLearner(learner=,features=)`
`impute` returns a list containing the imputed dataset or task as well as an imputation description that can be used to reapply the same imputation to new data using `reimpute`

`reimpute(obj=,desc=)` Imputes missing values on a task or dataset (`obj`) using a description (`desc`) created by `impute`

Feature Extraction

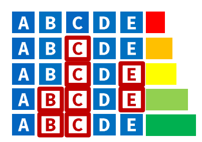
Feature filtering



`filterFeatures(task=,method=, perc=,abs=,threshold=)`
Uses a learner-agnostic feature evaluation method to rank feature importance, then includes only features in the top n percent (`perc=`), top n (`abs=`), or which meet a set performance threshold (`threshold=`).

Outputs a task with features that failed the test omitted. `method` defaults to `"randomForestSRC.rfsrc"`, but can be set to:
`"anova.test"` `"carscore"` `"cforest.importance"` `"chi.squared"` `"gain.ratio"` `"information.gain"` `"kruskal.test"` `"linear.correlation"` `"mrmr"` `"oneR"` `"permutation.importance"` `"randomForest.importance"` `"randomForestSRC.rfsrc"` `"randomForestSRC.var.select"` `"rank.correlation"` `"relief"` `"symmetrical.uncertainty"` `"univariate.model.score"` `"variance"`

Feature selection



`selectFeatures(learner=,task=, resampling=,measures=,control=)`
Uses a feature selection algorithm (`control`) to resample and build a model repeatedly using different feature sets each time in order to find the best set.

Available controls include:

- `makeFeatSelControlExhaustive(max.features=)` Try every combination of features up to optional `max.features`
- `makeFeatSelControlRandom(maxit=,prob=, max.features=)` Randomly sample features with probability `prob` (default 0.5) until `maxit` (default 100) iterations; return the best one found
- `makeFeatSelControlSequential(method=,maxit=, max.features=,alpha=,beta=)` Perform an iterative search using a `method` from the following: `"sfs"` forward search, `"sbs"` backward search, `"sffs"` floating forward search, `"sfbs"` floating backward search. `alpha` indicates minimum improvement required to add a feature; `beta` indicates minimum required to remove a feature
- `makeFeatSelControlGA(maxit=,max.features=,mu=, lambda=,crossover.rate=,mutation.rate=)` Genetic algorithm trains on random feature vectors, then uses crossover on the best performers to produce 'offspring', repeated over generations. `mu` is size of parent population, `lambda` is size of children population, `crossover.rate` is probability of choosing a bit from first parent, `mutation.rate` is probability of flipping a bit (on or off)

`selectFeatures` returns a `FeatSelResult` object which contains optimal features and an optimization path. To apply feature selection result (`fsr`) to your task (`tsk`), use:
`tsk = subsetTask(tsk,features=fsr$x)`

Benchmarking

`benchmark(learners=,tasks=,resamplings=,measures=)`
Allows easy comparison of multiple learners on a single task, a single learner on multiple tasks, or multiple learners on multiple tasks. Returns a benchmark result object.

Benchmark results can be accessed with a variety of functions beginning with `getBMR<object>`: `AggrPerformance` `FeatSelResults` `FilteredFeatures` `LearnerIds` `LeanerShortNames` `Learners` `MeasureIds` `Measures` `Models` `Performances` `Predictions` `TaskDescs` `TaskIds` `TuneResults`

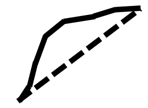
mlr contains several toy tasks which are useful for benchmarking:
`agri.task` `bc.task` `bh.task` `costiris.task` `iris.task` `lung.task` `mtcars.task` `pid.task` `sonar.task` `wpbc.task` `yeast.task`

Visualization

Performance

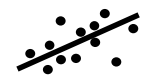
`generateThreshVsPerfData(obj=,measures=)` Measure performance at different probability cutoffs to determine optimal decision threshold for binary classification problems

- `plotThreshVsPerf(obj)` Plot visual representation of threshold curve(s) from `ThreshVsPerfData`



- `plotROCCurves(obj)` Plot receiver operating characteristic (ROC) curve from `ThreshVsPerfData`. Must set `measures=list(fpr,tpr)`

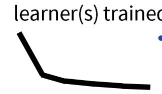
Residuals



- `plotResiduals(obj=)` Plots residuals for `Prediction` or `BenchmarkResult`

Learning curve

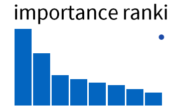
`generateLearningCurveData(learners=,task=, resampling=,percs=,measures=)` Measure performance of learner(s) trained on different percentages of task data



- `plotLearningCurve(obj=)` Plot curve showing learner performance vs. proportion of data used, uses `LearningCurveData`

Feature importance

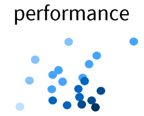
`generateFilterValuesData(task=,method=)` Get feature importance rankings using specified filter method



- `plotFilterValues(obj=)` Plot bar chart of feature importance based on filter method using `FilterValuesData`

Hyperparameter tuning

`generateHyperParsEffectData(tune.result=)` Get the impact of different hyperparameter settings on model performance



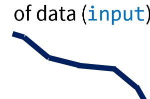
- `plotHyperParsEffect(hyperpars.effect.data=,x=,y=,z=)` Create a plot showing hyperparameter impact on performance using `HyperParsEffectData`

See also:

- `plotOptPath(op=)` Display details of optimization process. Takes `<obj>$opt.path`, where `<obj>` is an object of class `tuneResult` or `featSelResult`
- `plotTuneMultiCritResult(res=)` Show pareto front for results of tuning to multiple performance measures

Partial dependence

`generatePartialDependenceData(obj=,input=)` Get partial dependence of model (`obj`) prediction over each feature of data (`input`)

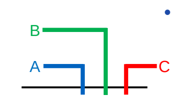


- `plotPartialDependence(obj=)` Plots partial dependence of model using `PartialDependenceData`

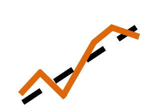
Benchmarking

- `plotBMRBoxplots(bmr=)` Distribution of performances
- `plotBMRSummary(bmr=)` Scatterplot of avg. performances
- `plotBMRRanksAsBarChart(bmr=)` Rank learners in bar plot

Other

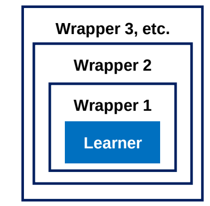


- `generateCritDifferencesData(bmr=, measure=,p.value=,test=)` Perform critical-differences test using either the Bonferroni-Dunn (`"bd"`) or `"Nemenyi"` test
- `plotCritDifferences(obj=)`



- `generateCalibrationData(obj=)` Evaluate calibration of probability predictions vs. true incidence
- `plotCalibration(obj=)`

Wrappers



Wrappers fuse a learner with additional functionality. mlr treats a learner with wrappers as a single learner, and hyperparameters of wrappers can be tuned jointly with underlying model parameters. Models trained with wrappers will apply them to new data.

Preprocessing and imputation

`makeDummyFeaturesWrapper(learner=)`
`makeImputeWrapper(learner=,classes=,cols=)`
`makePreprocWrapper(learner=,train=,predict=)`
`makePreprocWrapperCaret(learner=,...)`
`makeRemoveConstantFeaturesWrapper(learner=)`

Class imbalance

`makeOverBaggingWrapper(learner=)`
`makeSMOTEWrapper(learner=)`
`makeUndersampleWrapper(learner=)`
`makeWeightedClassesWrapper(learner=)`

Cost-sensitive learning

`makeCostSensClassifWrapper(learner=)`
`makeCostSensRegrWrapper(learner=)`
`makeCostSensWeightedPairsWrapper(learner=)`

Multilabel classification

`makeMultilabelBinaryRelevanceWrapper(learner=)`
`makeMultilabelClassifierChainsWrapper(learner=)`
`makeMultilabelDBRWrapper(learner=)`
`makeMultilabelNestedStackingWrapper(learner=)`
`makeMultilabelStackingWrapper(learner=)`

Other

`makeBaggingWrapper(learner=)`
`makeConstantClassWrapper(learner=)`
`makeDownsampleWrapper(learner=,dw.perc=)`
`makeFeatSelWrapper(learner=,resampling=,control=)`
`makeFilterWrapper(learner=,fw.perc=,fw.abs=, fw.threshold=)`
`makeMultiClassWrapper(learner=)`
`makeTuneWrapper(learner=,resampling=,par.set=, control=)`

Nested Resampling

mlr supports **nested resampling** for complex operations such as tuning and feature selection through wrappers. In order to get a good estimate of generalization performance and avoid data leakage, both an outer (for tuning/feature selection) and an inner (for the base model) resampling process are advised.

- Outer resampling can be specified in `resample` or `benchmark`
- Inner resampling can be specified in `makeTuneWrapper`, `makeFeatSelWrapper`, etc.

Ensembles

`makeStackedLearner(base.learners=,super.learner=, method=)` Combines multiple learners to create an ensemble

- `base.learners=`learners to use for initial predictions
- `super.learner=`learner to use for final prediction
- `method=`how to combine base learner predictions:
  - `"average"` simple average of all base learners
  - `"stack.nocv"`,`"stack.cv"` train super learner on results of base learners, with or without cross-validation
  - `"hill.climb"` search for optimal weighted average
  - `"compress"` with a neural network for faster performance

Intro stats with mosaic

(lattice version)

Essential R syntax

Names in R are *case sensitive*

Function and arguments

```
rflip(10)
```

Optional arguments

```
rflip(10, prob = 0.8)
```

Assignment

```
x <- rflip(10, prob = 0.8)
```

Getting help on any function

```
help(mean)
```

Loading packages

```
library(mosaic)
```

Arithmetic operations

`+ - * /`	basic operations
`^`	exponentiation
`( )`	grouping
`sqrt(x)`	square root
`abs(x)`	absolute value
`log10(x)`	logarithm, base 10
`log(x)`	natural logarithm, base e
`exp(x)`	exponential function e^x
`factorial(k)`	$k! = k(k-1)\ ...1$

Logical operators

`==`	is equal to (note double equal sign)
`!=`	is not equal to
`<`	is less than
`<=`	is less than or equal to
`>`	is greater than
`>=`	is greater than or equal to
`&`	**A & B** is **TRUE** if both **A** and **B** are **TRUE**
`|`	**A | B** is **TRUE** if one or both of **A** and **B** are **TRUE**
`%in%`	includes; for example `"C" %in% c("A", "B")` is **FALSE**

Formula interface

Use for graphics, statistics, inference, and modeling operations.

```
goal(y ~ x, data = mydata)
```

Read as "Calculate **goal** for **y** using **mydata** "broken down by" **x**, or "modeled by" **x**.

```
mean(age ~ sex, data = HELPrct)
```

For graphics:

```
goal(y ~ x | z, groups = w,
  data = mydata)
```

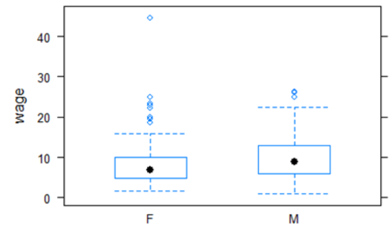
y : y-axis variable (*optional*)

x : x-axis variable (*required*)

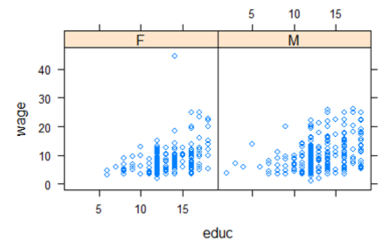
z : panel-by variable (*optional*)

w : color-by variable (*optional*)

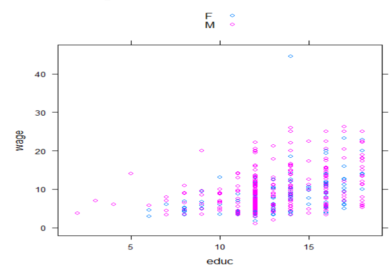
```
bwplot(wage ~ sex, data = CPS85)
```




```
xyplot(wage ~ educ | sex,
  data = CPS85)
```




```
xyplot(wage ~ educ,
  groups = sex, data = CPS85,
  auto.key = TRUE)
```



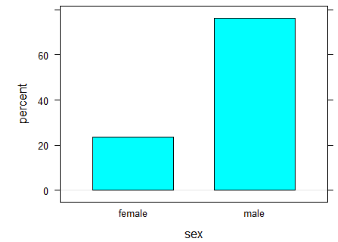
One categorical variable

Counts by category

```
tally(~ sex, data = HELPrct)
```

Percentages by category

```
tally(~ sex, format =
  "percent", data = HELPrct)
bargraph(~ sex, type =
  "percent", data = HELPrct)
```



Tests and confidence intervals

Exact test

```
result1 <-
  binom.test(~ (homeless ==
  "homeless"), data = HELPrct)
```

Approximate test (large samples)

```
result2 <-
  prop.test(~ (homeless ==
  "homeless"), data = HELPrct)
```

Extract confidence intervals and p-values

```
confint(result1)
pval(result2)
```

Examining data

Print short summary of all variables

```
inspect(HELPrct)
```

Number of rows and columns

```
dim(HELPrct)
nrow(HELPrct)
ncol(HELPrct)
```

Print first rows or last rows

```
head(KidsFeet)
tail(KidsFeet, 10)
```

Names of variables

```
names(HELPrct)
```

One quantitative variable

Make output more readable

```
options(digits = 3)
```

Compute summary statistics

```
mean(~ cesd, data = HELPrct)
```

Other summary statistics work similarly

```
median()  iqr()  max()  min()
fivenum()  sd()  var()  sum()
```

Table of summary statistics

```
favstats(~ cesd, data = HELPrct)
```

Summary statistics by group

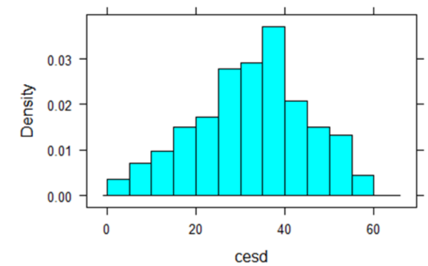
```
favstats(cesd ~ sex,
  data = HELPrct)
```

Quantiles

```
quantile(~ cesd, data = HELPrct,
  prob = c(0.25, 0.5, 0.8))
```

Histogram

```
histogram(~ cesd, width = 5,
  center = 2.5, data = HELPrct)
```



Normal probability plot

```
qqmath(~ cesd, dist = "qnorm",
  data = HELPrct)
```

Density plot

```
densityplot(~ cesd, data =
  HELPrct)
```

Dot plot

```
dotPlot(~ cesd, data = HELPrct)
```

One-sample t-test

```
result <- t.test(~ cesd, mu =
          34, data = HELPrct)
```

Extract confidence intervals and p-values

```
confint(result)
pval(result)
```


Adapted from *A Student's Guide to R* by NJ Horton, R Pruim & DT Kaplan • Updated: 02/18

Two categorical variables

Contingency table with margins

```
tally(~ substance + sex,
  margins = TRUE,
  data = HELPrct)
```

Percentages by column

```
tally(~ sex |substance,
  format = "percent",
  data = HELPrct)
```

Mosaic plot

```
mosaicplot(~ substance + sex,
  color = TRUE, data = HELPrct)
```

Chi-square test

```
xchisq.test(~ substance + sex,
  data = HELPrct,
  correct = FALSE)
```

Distributions

Normal distribution function

```
pnorm(13, mean = 10, sd = 2)
```

Normal distribution function with graph

```
xpnorm(1.645, mean = 0, sd = 1)
```

Normal distribution quantiles

```
qnorm(0.95) # mean = 0, sd = 1
```

Normal distribution quantiles with graph

```
xqnorm(0.85, mean = 10, sd = 2)
```

Binomial density function (“size” means n)

```
dbinom(5, size = 8, prob = 0.65)
```

Binomial distribution function

```
pbinom(5, size = 8, prob = 0.65)
```

Central portion of distribution

```
cdist("norm", 0.95)
cdist("t", c(0.90, 0.99), df = 5)
```

Plotting distributions

```
plotDist("binom", size = 8,
  prob = 0.65, xlim = c(-1, 9))
plotDist("norm", mean = 10,
  sd = 2)
```

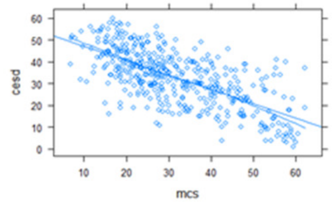
Two quantitative variables

Correlation coefficient

```
cor(cesd ~ mcs, data = HELPrct)
```

Scatterplot with regression line and smooth

```
xyplot(cesd ~ mcs,
  type = c("p", "r", "smooth"),
  data = HELPrct)
```



Simple linear regression

```
cesdmodel <- lm(cesd ~ mcs,
  data = HELPrct)
msummary(cesdmodel)
```

Prediction

```
lmfunction <- makeFun(cesdmodel)
lmfunction(mcs = 35)
```

Extract useful quantities

```
anova(cesdmodel)
coef(cesdmodel)
confint(cesdmodel)
rsquared(cesdmodel)
```

Diagnostics; plot residuals

```
histogram(~resid (cesdmodel),
  density = TRUE)
qqmath(~resid(cesdmodel))
```

Diagnostics; plot residuals vs. fitted

```
xyplot(resid(cesdmodel) ~
  fitted(cesdmodel),
  type = c("p", "smooth", "r"))
```

Categorical response, quantitative predictor

Logistic regression

```
logit_mod <-
  glm(homeless ~ age + female,
  family = binomial, data = HELPrct)
msummary(logitmod)
```

Odds ratios and confidence intervals

```
exp(coef(logit_mod))
exp(confint(logit_mod))
```

Data management

From `dplyr` package

Drop or reorder variables

```
select()
```

Create new variables from existing ones

```
mutate()
```

Retain specific rows from data

```
filter()
```

Sort data rows

```
arrange()
```

Compute summary statistics by group

```
group_by()
summarize()
```

Merge data tables

```
left_join()
inner_join()
```

Importing data

Import file from computer or URL

```
MustangPrice <-
  read.file("C:/MustangPrice.csv")
# NOTE: R uses forward slashes!
Dome <-
  read.file("http://www.mosaic-
web.org/go/datasets/Dome.csv")
```

Randomization and simulation

Fix random number sequence

```
set.seed(42)
```

Tossing coins

```
rflip(10) # default prob is 0.5
```

Do something repeatedly

```
do(5) * rflip(10, prob = 0.75)
```

Draw a simple random sample

```
sample(LETTERS, 10)
deal(Cards, 5) # poker hand
```

Resample with replacement

```
Small <- sample(KidsFeet, 10)
resample(Small)
```

Random permutation (shuffling)

```
shuffle(Cards)
```

Random values from distributions

```
rbinom(5, size = 10, prob = 0.7)
rnorm(5, mean = 10, sd = 2)
```

Quantitative response, categorical predictor

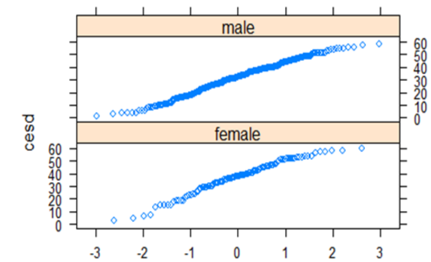
Two-level predictor: two-sample t test

Numeric summaries

```
favstats(~cesd | sex,
  data = HELPrct)
```

Comparative normal probability plot

```
qqmath(~cesd | sex, data = HELPrct,
  layout = c(1, 2)) # also bwplot
```



Dotplot for smaller samples

```
xyplot(sex ~ length, alpha = 0.6,
  cex = 1.4, data = KidsFeet)
```

Two-sample t-test and confidence interval

```
result <- t.test(cesd ~ sex,
  var.equal = FALSE, data = HELPrct)
confint(result)
```

More than two levels: Analysis of variance

Numeric summaries

```
favstats(cesd ~ substance,
  data = HELPrct)
```

Graphic summaries

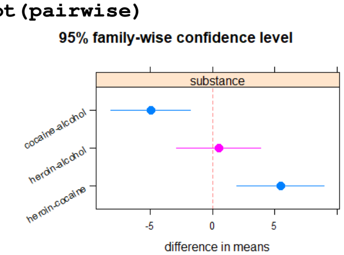
```
bwplot(cesd ~ substance, pch = "|",
  data = HELPrct)
```

Fitt and summarize model

```
modsubstance <- lm(cesd ~ substance,
  data = HELPrct)
anova(modsubstance)
```

Which differences are significant?

```
pairwise <- TukeyHSD(modsubstance)
mplot(pairwise)
```



nardl Package

An R package to estimate the nonlinear cointegrating autoregressive distributed lag model

Specifying the Model

Possible syntaxes for specifying the variables in the model:

- **nardl with fixed p and q lags**

nardl(fod~inf,p,q,data=fod,ic="aic",maxlags = FALSE,graph = FALSE,case=3)

- **Auto selected lags (maxlags=TRUE)**

nardl(food~inf,data=fod,ic="aic",maxlags = TRUE,graph = FALSE,case=3)

The formula:

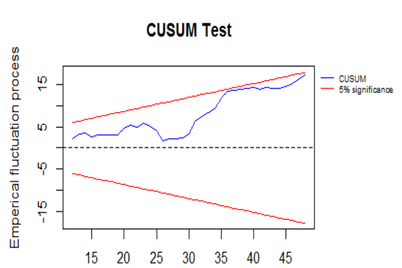
- y~x | z1+z2….
- y the dependent variable
- x the decomposed variable (this package version can't assume more than one decomposed variable)
- z1+z2+… independent variables

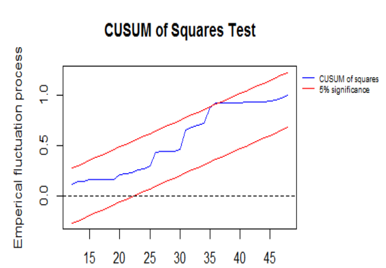
- Data is the dataframe
- p number of lags of the dependent variable
- q number of lags of the independent variables
- ic : c("aic","bic","ll","R2") criteria model selection
- maxlags if TRUE auto lags selection
- case case number 3 for (unrestricted intercert, no trend) and 5 (unrestricted intercept, unrestricted trend), 1 2 and 4 not supported

Cusum and CusumQ plot

Cusum and CusumQ plot (graph=TRUE)

nardl(food~inf,data=fod,ic="aic",maxlags = TRUE,graph = TRUE,case=3)





Cointegration bounds test

pssbounds(obs, fstat, tstat = NULL, case, k)

pssbounds specification include:

- Case case number 3 for (unrestricted intercert, no trend) and 5 (unrestricted intercept, unrestricted trend), 1 2 and 4 not supported
- fstat represent the value of the F-statistic
- obs represent the number of observation
- k number of regressors appearing in lag levels

Example:

reg<-nardl(food~inf,fod,ic="aic",maxlags = TRUE,graph = TRUE,case=3)

pssbounds(case=reg$case,fstat=reg$fstat,obs=reg$obs,k=reg$k)

LM test for serial correlation

LM test for serial correlation

bp2(object, nlags, fill = NULL, type = c("F", "Chi2"))

- **Methods and options are:**
- object fitted lm model
- nlags positive integer number of lags
- fill starting values for the lagged residuals in the auxiliary regression. By default 0.
- type Fisher or Chisquare statistics

Example :

reg<-nardl(food~inf,fod,ic="aic",maxlags = TRUE,graph = TRUE,case=3)

bp2(regfit,regnp,fill=0,type="F")

Lagrange multiplier test

Lagrange multiplier test for conditional heteroscedasticity of Engle (1982), as described by Tsay (2005, pp. 101-102)

ArchTest(x, lags = 12, demean = FALSE)

- **Methods and options are:**
- x numeric vector
- lags positive integer number of lags.
- demean logical: If TRUE, remove the mean before computing the test statistic.

Example :

reg<-nardl(food~inf,fod,ic="aic",maxlags = TRUE,graph = TRUE,case=3)
x<-reg$selresidu
nlag<-reg$np
ArchTest(x,lags=nlag)

Dynamic multipliers plot

Dynamic multiplier plot

plotmplier(model, np, k, h)

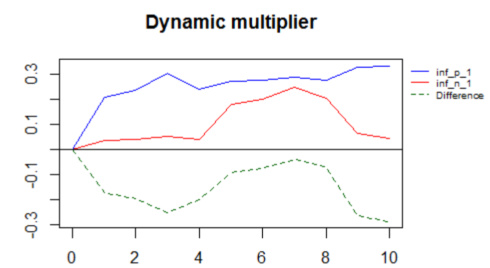
Methods and options are:

- model the fitted model
- np the selected number of lags
- k number of decomposed independent variables
- h is the horizon over which multipliers will be computed

Example

reg<-nardl(food~inf,p=4,q=4,fod,ic="aic",maxlags = FALSE,graph = TRUE,case=3)

plotmplier(reg,reg$np,1,10)



pssbounds

pssbound function display the necessary critical values to conduct the Pesaran, Shin and Smith 2001 bounds test for cointegration. See http://andyphilips.github.io/pssbounds/.

pssbounds(obs, fstat, tstat = NULL, case, k)

Methods and options are:

- obs number of observations
- fstat value of the F-statistic
- tstat value of the t-statistic
- case case number
- k number of regressors appearing in lag levels

Example

reg<-nardl(food~inf,fod,ic="aic",maxlags = TRUE,graph = TRUE,case=3)

pssbounds(case=reg$case,fstat=reg$fstat,obs=reg$obs,k=reg$k)

F-stat concludes I(1) and cointegrating, t-stat concludes I(0).

This is one page presents the nardl package. Taha Zaghdoudi package version 0.1.5 https://github.com/zedtaha/nardl

nimble models: : CHEAT SHEET

NIMBLE workflow

required arguments
optional arguments

Write model code

`nimbleCode()` NIMBLE lang
`readBUGSmodel()` read BUGS

Create model object

`nimbleModel()`

from **`nimbleCode()`**
constants of the model e.g. for-loop ranges, known index vectors
values to label as data nodes
starting values for the parameters

```
myModel <- nimbleModel(
code = modelCode,
constants = list(N = 8,
numGroups = 4, ...),
data = list(y = myData,
  X = myCovs),
inits = list(beta0 = 0,
   beta1 = 0, ...))
```

`constants` can't be changed after creating a model
`data & inits` can be changed

Configure an MCMC algorithm

`configureMCMC()` Advanced customization

Build an MCMC object

`buildMCMC()`

model object or **MCMC configuration**
variables names for MCMC output
thinning interval
a second set of variables with its own thinning

```
myMCMC <- buildMCMC(
conf = [myModel|myConf],
monitors = c("beta0",...),
thin = 10,
monitors2, thin2)
```

Run MCMC

`runMCMC()` using MCMC object
`nimbleMCMC()` one-line invocation

Compile in C++ for faster execution
MCMC from **`buildMCMC()`** compiled or uncompiled
number of MCMC iterations & burnin

```
compMCMC <- compileNimble(
myMCMC,project = myModel)

samples <- runMCMC(
mcmc = compMCMC,
iter=1000, nburnin=100)
```

from **`nimbleCode()`**
as in **`nimbleModel()`**
number of MCMC iterations & burnin

```
samples <- nimbleMCMC(
code = modelCode,
data, constants, inits,
niter, nburnin)
```

Writing model code

Split code over multiple lines to help people read it.

```
modelCode <- nimbleCode({
  beta0 ~ dnorm(0, sd = 1000)
  beta1 ~ dnorm(0, 1E-6)
  sdGroups ~ dunif(0, 100)
  fixed_effects[1:N] <- beta0 + beta1 * X[1:N]
  for(i in 1:N) {
    log(eta[i]) <- fixed_effects[i] +
                   alpha[groupID[i]]
     y[i] ~ dpois(eta[i])
  }
  for(iGroup in 1:numGroups) {
    alpha[iGroup] ~ dnorm(0, sd = sdGroups)
  }
})
```

Use named arguments for non-default parameterization e.g. `beta0` and `beta1` follow equivalent distributions (default is precision, `tau`).

Link functions can be declared on the left-hand side.

Order of declaration does not matter `alpha[iGroup]` can be declared after being used in other declarations.

Vectorized declarations create vector nodes. This means `fixed_effects[1:N]` will be a single node. One vector node vs. multiple scalar nodes give different model graphs, so use with care.

Provide explicit index ranges or use empty brackets (`[]`) and provide the `dimensions` argument to `nimbleModel()`.

Nested indexing is a good way to implement experimental groups or factor levels. If groups are known from the design, include them in `constants`.

Using models

● **Models can be compiled.**
`cModel <- compileNimble(myModel)`
In methods below, "**`model`**" can be `cModel` or `myModel`.

● **Models can access and change variables.**
```
model$beta0 <- 5
model[["beta0"]] <- 5
```

● **Models can simulate or calculate log-probabilities.**

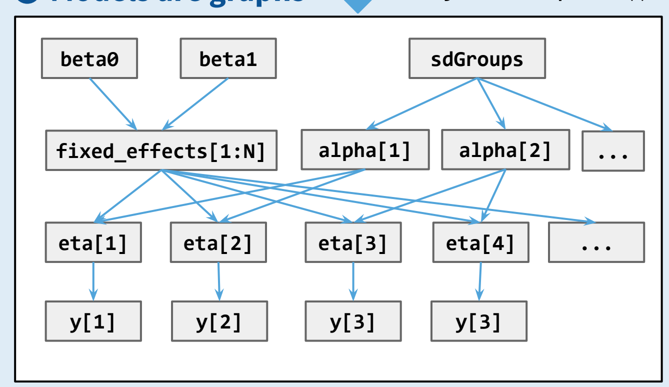
`model$calculate(nodes)`
returns sum of log probability densities.

`model$calculateDiff(nodes)`
returns difference in sum of log probability densities between current and previous node values.

`model$getLogProb(nodes)`
returns sum of most recently calculated log probability densities.

`model$simulate(nodes, includeData = FALSE)`
simulates into stochastic nodes.
`includeData = FALSE` protects data.

● **Models are graphs** `myModel$plot()`



● **Models know about nodes, variables and relationships.**

`model$getNodesNames()`
returns node names
e.g. `"eta[1]", "eta[2]",...`

`model$getVarNames()`
returns variable names
e.g. `"eta"`

`model$expandNodeNames(nodes)`
e.g. `"y"` is expanded to `"y[1]", "y[2]",...`

`model$getDependencies(nodes, ...)`
returns nodes that depend on input nodes.

● **Uncompiled models can be debugged, updated, and copied.**

Flag nodes as data and set inits
```
myModel$setData("y")
myModel$setInits(inits)
```
Debug model errors
`myModel$check()`
check for missing/invalid values.
`myModel$initializeInfo()`
which nodes are not fully initialized?
`myModel$checkBasics()`
check for size/dimension mismatches and `NA`.
Make a copy
`myModel$newModel(replicate = TRUE)`

● **Models know properties of nodes.**
```
model$getDimension(node)
model$getDistribution(nodes)
model$isDeterm(nodes)
model$isStoch(nodes)
model$isData(nodes)
model$isDiscrete(nodes)
model$isMultivariate(nodes)
model$isBinary(nodes)
model$isEndNode(nodes)
model$isTruncated(nodes)
```

NIMBLE

nimble distributions and functions: : CHEAT SHEET

Declarations

STOCHASTIC
`x ~ ddist(args)`

DETERMINISTIC
`z <- fn(args)`

TRUNCATED STOCHASTIC
`x ~ T(ddist(args), min, max)`

CENSORED STOCHASTIC
`seg ~ dinterval(t, c[1:nSegments])`
`t ~ ddist(args)`

CONSTRAINT
`one ~ dconstraint(condition)`

Deterministic Functions

SCALAR or COMPONENT-WISE

Logical: `|, &, !, >, >=, <, <=, !=, ==, equals, step`

Arithmetic: `+, -, *, /, ^, pow(x, y) %%, exp, log, sqrt, abs, cube`

Trigonometric: `sin, cos, tan, asin, acos, atan, asinh, acosh, atanh`

Links: `logit, probit, cloglog`
(links can also be used on left-hand side of a declaration)

Inverse links: `ilogit/expit, iprobit/phi, icloglog`

Rounding: `ceiling, floor, round, trunc`

Specials: `lgamma/loggam, besselK, log1p, lfactorial, logfact`

Distributions: `d, p, q, r` forms of available distributions can be used as deterministic functions.

VECTOR and/or MATRIX

Returning scalar: `inprod, logdet, sum, mean, sd, prod, min, max`

Returning vector: `pmin, pmax, eigen(x)$values, svd(x)$d`

Returning matrix: `inverse, chol, %*%, t, solve, forwardsolve, backsolve, eigen(x)$vectors, svd(x)$u, svd(x)$v`

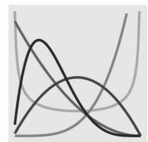
Write you own!

See Ch 12 of User Manual

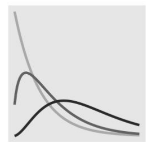
NIMBLE allows you to write **new distributions and functions** using `nimbleFunction()`.

Univariate Distributions

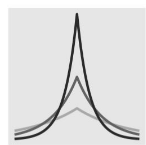
Continuous



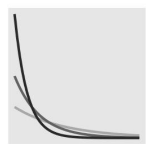
BETA
```
y ~ dbeta([shape1,shape2 |
           mean, sd])
shape1=mean^2*(1-mean)/sd^2-mean
shape2=mean*(1-mean)^2/sd^2+mean-1
```



CHI-SQUARE
`y ~ dchisq(df)`

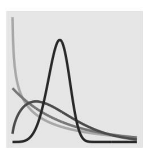


DOUBLE EXPONENTIAL (LAPLACE)
```
y ~ ddexp(location,
          [scale|rate|var])
scale = 1/rate
scale = sqrt(var/2)
```



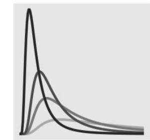
EXPONENTIAL
```
y ~ dexp([rate|scale])
rate = 1/scale
```


FLAT (improper)
`y ~ dflat()`

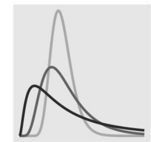


GAMMA
```
y ~ dgamma([shape,[rate|scale]]
           |[mean,sd])
scale = 1/rate
shape = mean^2/sd^2
scale = sd^2/mean
```

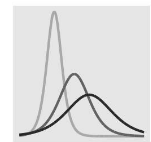

HALF FLAT (improper)
`y ~ dhalfflat()`



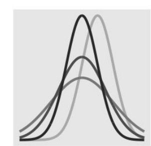
INVERSE GAMMA
```
y ~ dinvgamma(shape,
              [rate|scale])
rate = 1/scale
```



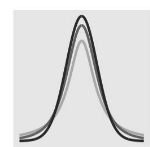
LOGISTIC
```
y ~ dlogis(location,
           [rate|scale])
scale = 1/rate
```



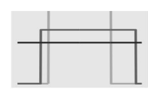
LOG-NORMAL
```
y ~ dlnorm(meanlog,
           [taulog|sdlog|varlog])
sdlog = 1/sqrt(taulog)
sdlog = sqrt(varlog)
```



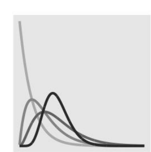
NORMAL
```
y ~ dnorm(mean,
          [tau|sd|var])
sd = 1/sqrt(tau)
sd = sqrt(var)
```



STUDENT T
```
y ~ dt(mu, [tau|sigma|sigma2], df)
sigma = 1/sqrt(tau)
sigma = sqrt(sigma2)
```



UNIFORM
`y ~ dunif(min, max)`

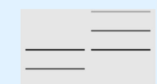


WEIBULL
```
y ~ dweib(shape,
          [lambda|scale|rate])
scale = lambda^(-1/shape)
scale = 1/rate
```

DISTRIBUTION NAME
```
y ~ ddist([default|alternative])
canonical = fn(provided)
```

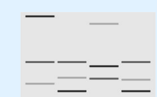
Lifted nodes are inserted when non-canonical parameters are used. Default parameters are not necessarily canonical.

Discrete

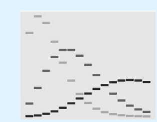


BERNOULLI
`y ~ dbern(prob)`

BINOMIAL
`y ~ dbinom(prob, size)`



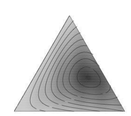
CATEGORICAL
`y ~ dcat(prob)`



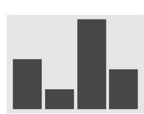
NEGATIVE BINOMIAL
`y ~ dnegbin(prob, size)`

POISSON
`y ~ dpois(lambda)`

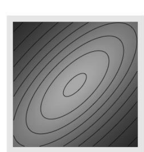
Multivariate distributions



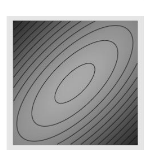
DIRICHLET
`y[] ~ ddirch(alpha[])`



MULTINOMIAL
`y[] ~ dmulti(prob[], size)`

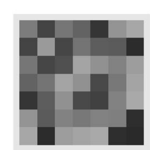


MULTIVARIATE NORMAL
```
y[] ~ dmnorm(mean[],
  [prec[,] | cov[,] | cholesky[,]],
  prec_param)
```



MULTIVARIATE STUDENT T
```
y[] ~ dmvt(mu[],
  [prec[,] | scale[,] | cholesky[,]],
  df, prec_param)
```

```
cholesky = chol(prec)  : prec_param=1
cholesky = chol(cov)   : prec_param=0 for dmnorm
cholesky = chol(scale): prec_param=0 for dmvt
cholesky is chol(prec) when prec_param=1,
chol(cov)|chol(scale) when prec_param=0
```

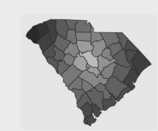


WISHART
```
y[,] ~ dwish(
    [R[,] | S[,] | cholesky[,]],
    df, scale_param)
```

INVERSE WISHART
```
y[,] ~ dinvwish([S[,] | R[,] | cholesky[,]],
        df,scale_param)
```

```
cholesky = chol(R): scale_param=0
cholesky = chol(S): scale_param=1
cholesky is chol(S) when scale_param=1,
            chol(R) when scale_param=0
```

Distributions for spatial models

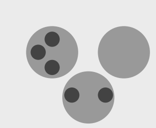


CONDITIONAL AUTOREGRESSIVE
intrinsic (improper)
```
y[] ~ dcar_normal(adj[],
        weights[], num[],
        tau, c, zero_mean)
```
proper
```
y[] ~ dcar_proper(mu[], C[],
        adj[], num[], M[],
        tau, gamma)
```

See Ch 9 of User Manual

Bayesian nonparametric distributions

See Ch 10 of User Manual



CHINESE RESTAURANT PROCESS
`y[] ~ dCRP(conc, size)`
conc= concentration parameter

STICK BREAKING PROCESS
`y[] ~ stick_breaking(z[])`
z = vector of breaking points

NIMBLE

oSCR : : CHEAT SHEET

The oSCR package, pronounced "Oscar", provides a set of functions for working with Spatial Capture Recapture (SCR) models.

Getting the package

Package hosted on GitHub

```
library (devtools)
install_github("jaroyle/oSCR")
library(oSCR)
```

Workflow

- Every model you run on oSCR has the following 4 basic steps.
- Modeled after unmarked workflow

1. Format the sampling data

One file for each one:

- Spatial encounter histories
- Detector information

2. Define and format the State Space

- Size and resolution of the *state space*
- Spatial covariates for density

3. Analyze the data – model fitting

- Likelihood based: use AIC to do model selection
- No need to use other packages, oSCR has helper functions to do the model selection.

4. Post processing model output for inference:

- This means that now that you have your parameters all you have to do is interpret your results!

Modelling framework

A. Single-session models

- Repeated sample occasions on a single population of individuals using a single array of traps.

B. Multi-session models

- Data grouped in strata or groups which are independent in space or time.

C. Explicit sex-structured models

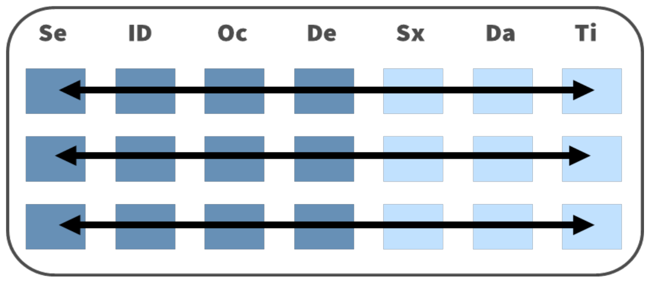
D. Multi-session sex-structured models

1. Format sampling data

Before starting to use oSCR you need to format the datafiles in a scrFrame which consists of two basic spreadsheets: **edf** and **tdf**.

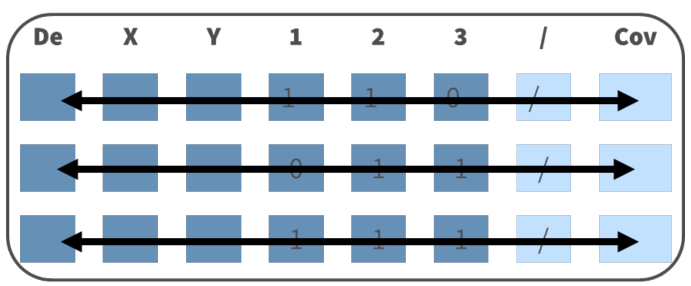
1.1 edf : encounter data file.

- Single **data frame**.
- Each row has individual detection events.
- Dark blue = required; light blue = optional.
- Columns contain capture information:
  - Session (Se)
  - Individual ID (ID)
  - Occasion (Oc)
  - Detector* (De)
  - Sex (Sx)
  - Date (Da)
  - Time (Ti)



1.2 tdf : trap deployment data file.

- A **list** with information for each session (tdf1, tdf2, …).
- Each row is a trap.
- Columns contain trap information
  - Detector* (De)
  - X (required, UTM)
  - Y (required, UTM)
  - Binary trap operation data for malfunctions, rotations (required if problems were found; 1, 2, 3, … n)
  - Separator (e.g., /)
  - Trap level covariates (different column per covariate)



*Notice that both edf and tdf have the same **Detector (De)** column that **MUST** match (same name, class, relational database).

1.3 data2oscr() : is a function that links **edf** and **tdf** files via the detector* names. Creates **scrFrame**.

```
data <- data2oscr(
edf,          # encounter data file
tdf,          # list containing trap deployment file
sess.col*,    # session col number or name in edf
id.col*,      # individual ID col # or name in edf
occ.col,      # occasion col number or name in edf
trap.col*,    # detector col number or name in edf
sex.col*,     # sex col number or name in edf
sex.nacode,   # character for unknown sex in edf
K,            # number of occasions
ntraps,       # number of traps
trapcov.names,# vector of un-numbered cov names
tdf.sep)      # separator (e.g., "/")
```

```
* which(colnames(edf) %in% "name of column in edf")
```

1.4 Summary functions for scrFrame :

- scrFrame contains information from the **edf** and **tdf** via detector names.

```
sf<-data$scrFrame
```

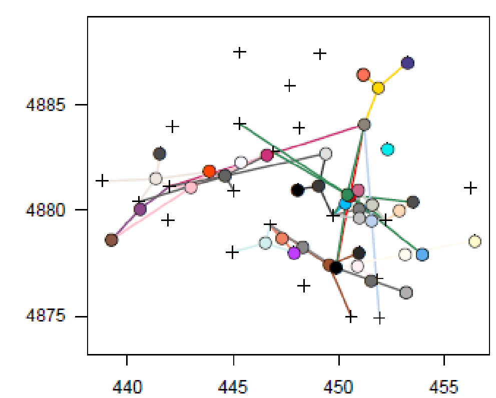
sf$caphist	Array of individual-by-trap-by-occasion (n x J x K). Binary or counts.
sf$traps	Data frame containing at least trap ID and coordinates of traps. Best with UTM.
sf$indcovs	Sex data (0 female, 1 male) or any bivariate covariate. NAs allowed.
sf$trapCovs	List of session specific trap covariates. Row per trap, and column per covariate.
sf$sigCovs	A data frame of covariates that affect space use (sigma, σ).
sf$trapOperation	A list of session specific information on trap operational data.
sf$occasions	A vector of number of occasions per session .
sf$mmdm	Mean maximum distance moved pooled across sessions. ½ mmdm ~ σ
sf$mdm	Maximum distance moved pooled across sessions.
$telemetry	Telemetry object for fitting resource selection models.

1.5 Summary of scrFrame

```
sf
                S1
n individuals  47
n traps        38
n occasions     8

                    S1
avg caps          3.21
avg spatial caps  2.02
mmdm              4.65
```

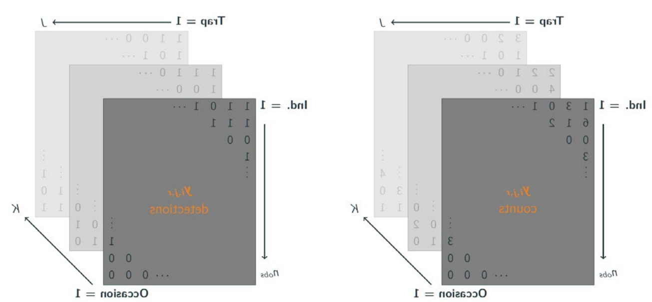
1.6 Spatial captures per session

```
plot(sf) #y and x are UTM
```



oSCR : : CHEAT SHEET

1.4.1 Navigating the scrFrame



Capture history

- Session 1, all individuals, all traps, occasion 3
 `sf$caphist[[1]][ , ,3]`
- Session 1, individual 4, all traps, all occasions
 `sf$caphist[[1]][4, , ]`

Traps

- Session 1 trap coordinates
 `sf$traps[[1]]`

Trap covariates

- Trap covariate df session 1 occasion 4
 `sf$trapCovs[[1]][[4]]`

Trap operation

- Session 1 trap trap operation matrix
 `sf$trapOperation [[1]]`

Covariates that affect sigma (σ)

- These covariates are NOT session specific. This is a sessions=rows dataframe

`sf$ sigCovs[[1]]`

Vectors and single numbers

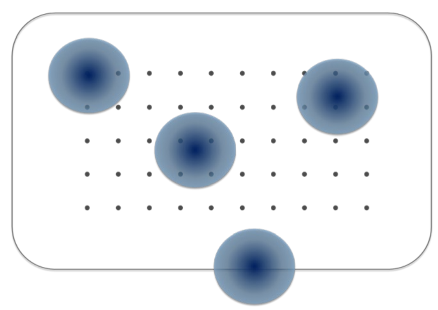
```
sf$ occasions
sf$mmdm
sf$mdm
```

Datasets available

> data(package = “oSCR”)
> data(ocelot)
> data(“beardata”)
> data(“nybears”)
> data(“peromyscus”)
> data(“mink”)

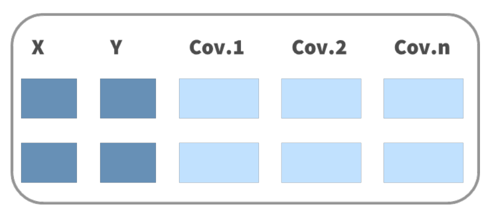
2. Create the State Space

The **State Space (S)** is the core element of SCR models. It defines where individuals can live and should represent activity centers of all sampled individuals.



ssDF: the State Space Data Frame

- List with spatially explicit information from each session.
- At least include the coordinates (X, Y) of the discrete state space (UTM).
- Can include spatial covariates for a continuous state space to study variation in Density.
- Non habitat can be removed by removing unwanted coordinates (e.g., parking lot).



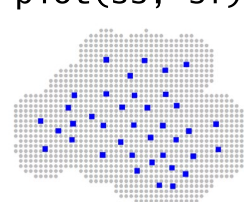
2.1. make.ssDF():

- Remember that ½ mmdm ~ σ
- Extracts covariates and removes non habitat

```
ss <- make.ssDF(scrFrame,
buffer, #~3 to 4σ around traps
res) # ≤ σ̂
```

2.2. Plot the state space

- Plot state space
 `plot(ss)`
- Plot state space & traps
 `plot(ss, sf)`

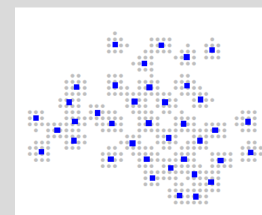


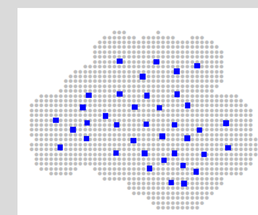
Vary the buffer and/or resolution

Varying buffer, fixed resolution

```
make.ssDF(sf,
buffer = 1,
res = 0.5)
```

```
make.ssDF(sf,
buffer = 3,
res = 0.5)
```

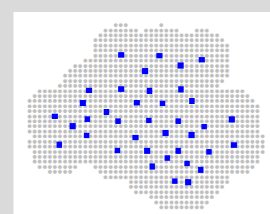


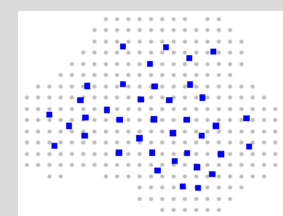


Fixed buffer, varying resolution

```
make.ssDF(sf,
buffer = 3,
res = 0.1)
```

```
make.ssDF(sf,
buffer = 3,
res = 0.5)
```





3. Fit the model

3.1. Single-session model: Fit the model with oSCR.fit():

```
sf <- data$scrFrame
mod <- oSCR.fit(model,
                scrFrame, #sf
                ssDF, …)
```

- See pg. 3 for null model and multi-session models.

model is a list with 3 basic formulations:
 `list(D ~ 1, p0 ~ 1, sig ~ 1)`

Variation in…	
D	pixel density
p0	baseline encounter prob/rate
sig	sigma (σ)

3.2. Backtransform to the real scale

```
get.real(model,
         newdata,
         d.factor,
         type)
```

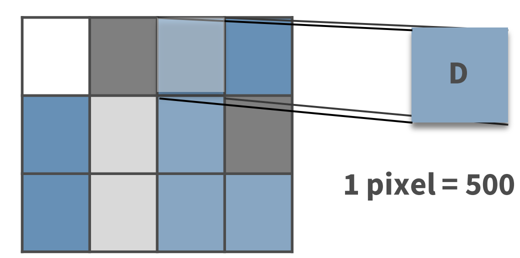
model	fitted model
newdata	Optional new data object for predictions
d.factor	optional scale the estimates to a different resolution
type	density (“dens”), detection probability (“det”), sigma(“sig”)

“dens”
Sex-specific estimates of density, and the density estimates are **per pixel.**

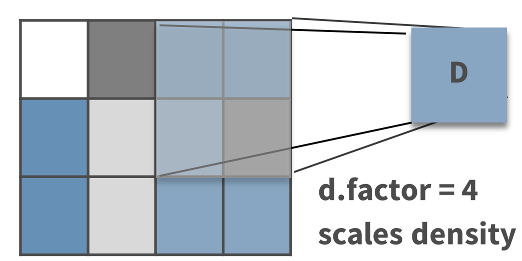
“det”
Estimate of detection at distance from activity center = 0.

“sig”
Estimates of the spatial scale of detection.

d.factor



1 pixel = 500 m x 500 m



d.factor = 4
scales density to 1 km²
When using the 500 m resolution

oSCR : : CHEAT SHEET

Page 3 describes the specific functions and workflow for the null model and multi-session model in the oSCR package.

Model specifics

Null model (SCR$_0$)

- The null model assumes homogeneous density which means all pixels have the same expected density.
- For additional arguments see `?oSCR.fit()`

```
mod1 <- oSCR.fit(list(D ~ 1,
p0 ~ 1, sig ~ 1),
scrFrame, #scrFrame object
ssDF, #ssDF object
… ) #other arguments
mod1 #summary
```

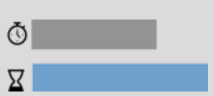
If you included sex as a covariate in the scrFrame:

- Sex ratio psi () will be included in the summary
- Can compare AIC with and without sex effects

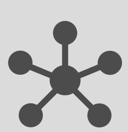
Multi-session model

Are your data organized in multi-sessions and you want to analyze all of them jointly?

Spatial sessions: different study areas (e.g., parks, trapping grids)



Temporal sessions: same areas different times (e.g. seasons, years)



Session specific **population size** N_g (g=group/session)

- Test for differences among sessions using AIC.
- Can share parameters among sessions or not.

- The **multi-session** model follows similar steps as the single session model.
- The **edf** files from multiple sessions may be merged into one data frame prior to data2oscr
  edf <- rbind(edf1, edf2, …)
- The **tdf** files must be separate files for each session.

1. data2oscr for multi-session scrFrame

```
data <- data2oscr(
 edf,   # include session column
 list(tdf1, tdf2, …),  # tdf files
 sess.col*,  # session col in edf
 id.col*,  # individual ID col in edf
 occ.col,  # occasion col in edf
 trap.col*,  # detector col in edf
 sex.col*,  # sex col in edf
 sex.nacode,  # unknown sex in edf
 K,  # vector with occasions per session
 ntraps)  # vector with traps per session
```

```
sf <- data$sf
sf # summary info per session (S1, S2..)
```

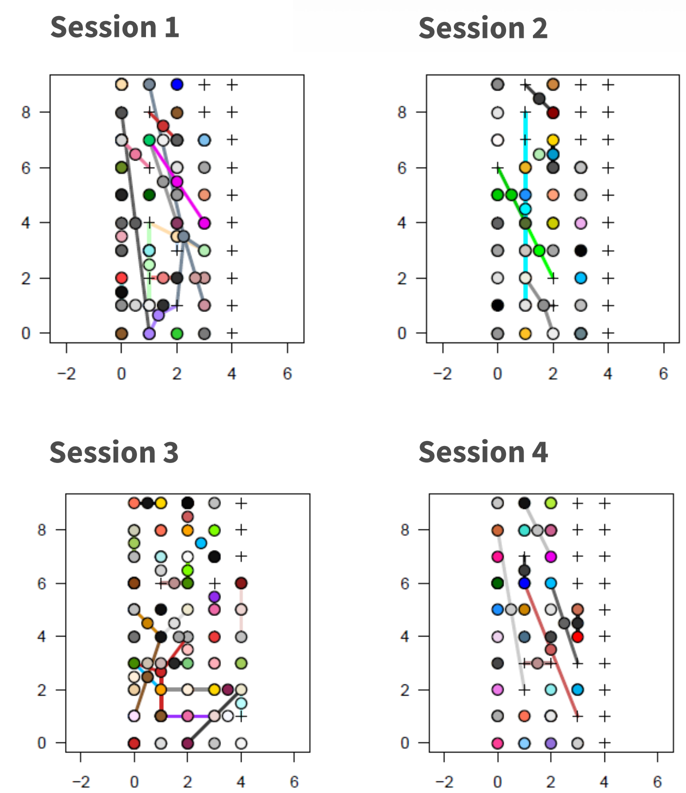
1.2. Summary of multi-session scrFrame

```
              S1 S2  S3 S4
n individuals 77 60 108 54
n traps       50 50  50 50
n occasions    7  5   6  4

                   S1   S2   S3   S4
avg caps         1.91 1.47 1.71 1.37
avg spatial caps 1.30 1.15 1.27 1.13
mmdm             2.57 2.32 1.76 2.84

Pooled MMDM:  2.21
```

1.3. Plot spatial captures in a multi-session scrFrame

- Use plot(sf) to plot a spatial capture per session

```
par(mfrow=c(1,n)) # n = sessions
plot(sf) # plot all sessions
```



2. Make the State Space Data Frame of a multi-session scrFrame

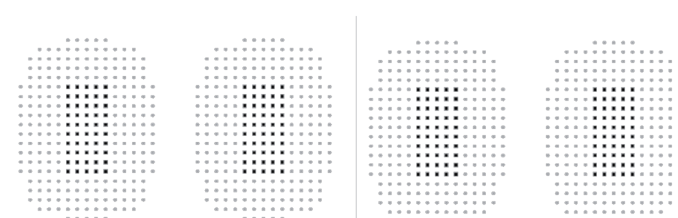
```
ss <- make.ssDF(
scrFrame, # multi-session
buffer, #buffer width
res) #state space resolution
```

- You can vary the buffer and resolution as in the single-session model.

```
?make.ssDF() # Look at the help file for other arguments
```

- Visualize the state space

```
par(mfrow=c(1,n)) # n = sessions
plot.ssDF(ss, # state space
          sf) # traps
```



3. Model fitting

- Specify models that consider or not variation among sessions.
  - fixed vs. session specific **D**
  - fixed vs. session specific **p0**
  - fixed vs. session specific **space use (σ)**

Model	Algebra	In oSCR.fit
Density	$log(D(s_i)) = \beta_0$	`D ~ 1`
Density	$log(D(s_i)) = \beta_0 + \beta_{1(g)} Session_g$	`D ~ session`
Detection	$logit(p_0) = \alpha_0$	`p0 ~ 1`
Detection	$logit(p_0) = \alpha_0 + \alpha_{1(g)} Session_g$	`p0 ~ session`
Space use	$log(\sigma) = \gamma_0$	`sig ~ 1`
Space use	$log(\sigma) = \gamma_0 + \gamma_{1(g)} Session_g$	`sig ~ session`

- Include all models into a list using fitList.oSCR():

```
f1 <- fitList.oSCR(
mods, # list of fitted models
rename) # if TRUE models are renamed with sensible names
```

- Compare multiple models

```
ms <- modSel.oSCR(f1)
```

- Generate an AIC table to compare multiple models

```
ms$aic
```

- Generate a coefficient table

```
ms$coef.tab
```

- Generate a model averaged coefficients

```
ma <- ma.coef(ms) # include a modSel.oSCR object
```

3.1. Back transform to the real scale

```
top.model <- m3

pred.df <- data.frame(session =
factor (c(1, 2, 3, 4, … )))

pred.det <- get.real(
model = top.model, type = "det",
newdata = pred.df)
```

Get an Overview with overviewR: : CHEAT SHEET

Generate Tables

overview_tab generates a data frame that collapses the time condition for each id by taking into account potential gaps in the time frame

id	time	Var1	Var2
A	1990		
A	1991		
A	1992		
B	1990		

id	time
A	1990 - 1992
B	1990

```
output_table <-
overview_tab(
  dat = toydata,
  id = ccode,
  time = year)
```

add data frame

define your time and scope variables

overview_crosstab generates a cross table that divides the data based on two conditions


```
output_crosstab <-
overview_crosstab(
    dat = toydata,
    cond1 = gdp,
    cond2 = population,
    threshold1 = 25000,
    threshold2 = 27000,
    id = ccode,
    time = year
  )
```

define your conditions with cond1 and cond2

set your thresholds

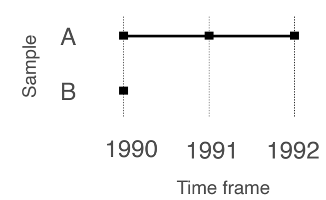
Note, if a data set is used that has multiple observations on the id-time unit, the function automatically aggregates the data set using the mean of condition 1 (**cond1**) and condition 2 (**cond2**).

If you store your results in an object, you can use **overview_print** to export them to a LaTeX output.

Generate Plots

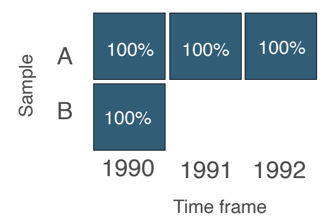
Sample overview

overview_plot illustrates the information that is generated in overview_table in a ggplot2 graphic




```
overview_plot(
     dat = toydata,
     id = ccode,
     time = year)
```

overview_heat is similar to overview_plot but presents the frequency of data points by id-time-unit in a heat map



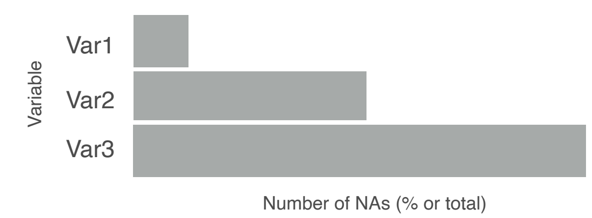

```
overview_heat(
     dat = toydata,
     id = ccode,
     time = year,
     perc = TRUE,
     exp_total = 12)
```

displays percentage

max observations by id-time unit

Missing values (NAs)

overview_na returns a horizontal ggplot2 bar plot that indicates the amount of missing data (NAs) for each variable




```
overview_na(toydata_with_na)
```

relative distribution

```
overview_na(toydata_with_na,
            perc = FALSE)
```

FALSE gives total number

Export Results

Tables

overview_print generates a LaTeX output (works with both overview_tab and overview_crosstab output)

```
overview_print(
     obj = output_table)
```

```
overview_print(
     obj = output_crosstab,
     crosstab = TRUE)
```

TRUE for cross tables

The table can be modified with the **title**, **id**, **time**, **cond1**, and **cond2** arguments to replace default names

It also allows to save your output in a .tex file

```
overview_print(
   obj = output_table,
   save_out = TRUE,
   path = “SET-YOUR-PATH",
   file = "output.tex")
```

define where your output should be stored

The outputs of **overview_tab** and **overview_crosstab** are also compatible with other packages and functions such as **xtable**, **flextable**, or **kable** from **knitr**.

To generate a table in Rmarkdown with **knitr::kable**:

```
knitr::kable(output_table)
```

Plots

As the plots are based on ggplot2, plots can be stored with **ggplot2::ggsave**

```
ggplot2::ggsave(
     output_plot,
     filename = “FILENAME.png”)
```

add plot object

add filename

Alternatively, storing the object also works this way:

```
png(“FILENAME.png”)

output_plot

dev.off()
```

Package Development: : CHEAT SHEET

Package Structure

A package is a convention for organizing files into directories.

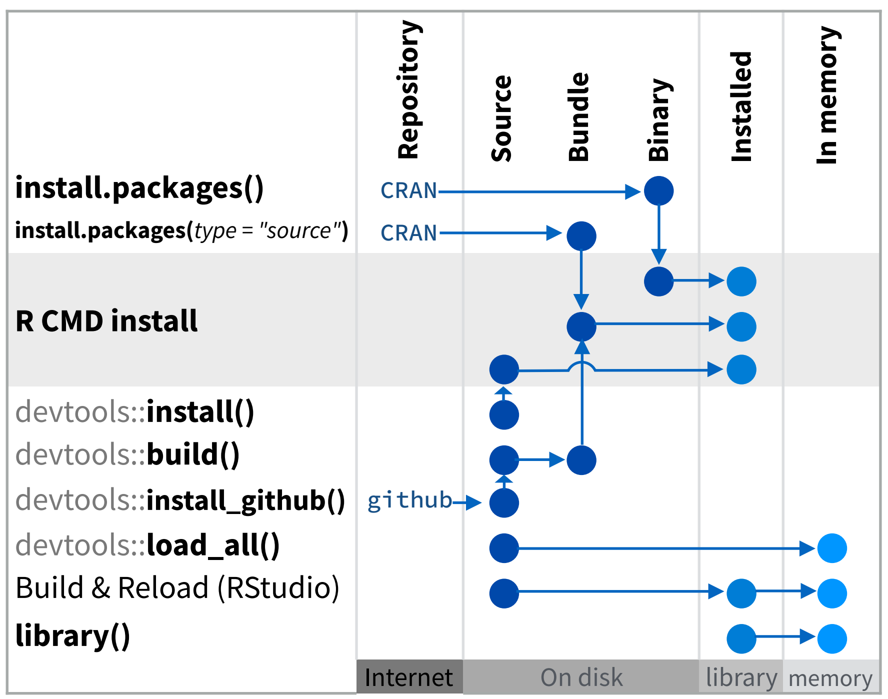
This sheet shows how to work with the 7 most common parts of an R package:

Package	
DESCRIPTION	SETUP
R/	WRITE CODE
tests/	TEST
man/	DOCUMENT
vignettes/	TEACH
data/	ADD DATA
NAMESPACE	ORGANIZE

The contents of a package can be stored on disk as a:

- **source** - a directory with sub-directories (as above)
- **bundle** - a single compressed file (*.tar.gz*)
- **binary** - a single compressed file optimized for a specific OS

Or installed into an R library (loaded into memory during an R session) or archived online in a repository. Use the functions below to move between these states.



devtools::**use_build_ignore**(*"file"*)
Adds file to .Rbuildignore, a list of files that will not be included when package is built.

Setup (DESCRIPTION)

The DESCRIPTION file describes your work, sets up how your package will work with other packages, and applies a copyright.

- ☑ You must have a DESCRIPTION file
- ☑ Add the packages that yours relies on with
  devtools::**use_package()**
  Adds a package to the Imports or Suggests field

CC0	MIT	GPL-2
No strings attached.	MIT license applies to your code if re-shared.	GPL-2 license applies to your code, *and all code anyone bundles with it*, if re-shared.

```
Package: mypackage
Title: Title of Package
Version: 0.1.0
Authors@R: person("Hadley", "Wickham", email =
    "hadley@me.com", role = c("aut", "cre"))
Description: What the package does (one paragraph)
Depends: R (>= 3.1.0)
License: GPL-2
LazyData: true
Imports:
    dplyr (>= 0.4.0),
    ggvis (>= 0.2)
Suggests:
    knitr (>= 0.1.0)
```

Import packages that your package *must have* to work. R will install them when it installs your package.

Suggest packages that are not very essential to yours. Users can install them manually, or not, as they like.

Write Code (R/)

All of the R code in your package goes in R/. A package with just an R/ directory is still a very useful package.

- ☑ Create a new package project with
  devtools::**create**("path/to/name")
  Create a template to develop into a package.
- ☑ Save your code in R/ as scripts (extension .R)

WORKFLOW

1. Edit your code.
2. Load your code with one of
   devtools::**load_all()**
   Re-loads all *saved* files in R/ into memory.
   Ctrl/Cmd + Shift + L (keyboard shortcut)
   Saves all open files then calls load_all().
3. Experiment in the console.
4. Repeat.

- Use consistent style with **r-pkgs.had.co.nz/r.html#style**
- Click on a function and press **F2** to open its definition
- Search for a function with **Ctrl + .**

Visit **r-pkgs.had.co.nz** to learn much more about writing and publishing packages for R

Test (tests/)

Use tests/ to store tests that will alert you if your code breaks.

- ☑ Add a **tests/** directory
- ☑ Import **testthat** with devtools::**use_testthat()**, which sets up package to use automated tests with testthat
- ☑ Write tests with **context()**, **test()**, and expect statements
- ☑ Save your tests as .R files in **tests/testthat/**

WORKFLOW

1. Modify your code or tests.
2. Test your code with one of
   devtools::**test()**
   Runs all tests in tests/
   Ctrl/Cmd + Shift + T
   (keyboard shortcut)
3. Repeat until all tests pass

Example Test

```
context("Arithmetic")

test_that("Math works", {
  expect_equal(1 + 1, 2)
  expect_equal(1 + 2, 3)
  expect_equal(1 + 3, 4)
})
```

Expect statement	Tests
expect_equal()	is equal within small numerical tolerance?
expect_identical()	is exactly equal?
expect_match()	matches specified string or regular
expect_output()	prints specified output?
expect_message()	displays specified message?
expect_warning()	displays specified warning?
expect_error()	throws specified error?
expect_is()	output inherits from certain class?
expect_false()	returns FALSE?
expect_true()	returns TRUE?

Document (🗀 man/)

🗀 man/ contains the documentation for your functions, the help pages in your package.

- ☑ Use roxygen comments to document each function beside its definition
- ☑ Document the name of each exported data set
- ☑ Include helpful examples for each function

WORKFLOW

1. Add roxygen comments in your .R files
2. Convert roxygen comments into documentation with one of:

   devtools::**document()**

   Converts roxygen comments to .Rd files and places them in 🗀 man/. Builds NAMESPACE.

   Ctrl/Cmd + Shift + D (Keyboard Shortcut)

3. Open help pages with **?** to preview documentation
4. Repeat

.Rd FORMATTING TAGS

```
\emph{italic text}
\strong{bold text}
\code{function(args)}
\pkg{package}

\dontrun{code}
\dontshow{code}
\donttest{code}

\deqn{a + b (block)}
\eqn{a + b (inline)}
```

```
\email{name@@foo.com}
\href{url}{display}
\url{url}

\link[=dest]{display}
\linkS4class{class}
\code{\link{function}}
\code{\link[package]{function}}

\tabular{lcr}{
  left \tab centered \tab right \cr
  cell \tab cell     \tab cell  \cr
}
```

ROXYGEN2

The **roxygen2** package lets you write documentation inline in your .R files with a shorthand syntax. devtools implements roxygen2 to make documentation.

- Add roxygen documentation as comment lines that begin with **#'**.
- Place comment lines directly above the code that defines the object documented.
- Place a roxygen **@** tag (right) after **#'** to supply a specific section of documentation.
- Untagged lines will be used to generate a title, description, and details section (in that order)

```
#' Add together two numbers.
#'
#' @param x A number.
#' @param y A number.
#' @return The sum of \code{x} and \code{y}.
#' @examples
#' add(1, 1)
#' @export
add <- function(x, y) {
  x + y
}
```

COMMON ROXYGEN TAGS

@aliases	@inheritParams	**@seealso**	
@concepts	@keywords	@format	
@describeIn	**@param**	@source	data
@examples	@rdname	@include	
@export	**@return**	@slot	S4
@family	@section	@field	RC

Teach (🗀 vignettes/)

🗀 vignettes/ holds documents that teach your users how to solve real problems with your tools.

- ☑ Create a 🗀 vignettes/ directory and a template vignette with

  devtools::**use_vignette()**

  Adds template vignette as vignettes/my-vignette.Rmd.

- ☑ Append YAML headers to your vignettes (like right)
- ☑ Write the body of your vignettes in R Markdown (rmarkdown.rstudio.com)

```
---
title: "Vignette Title"
author: "Vignette Author"
date: "`r Sys.Date()`"
output: rmarkdown::html_vignette
vignette: >
  %\VignetteIndexEntry{Vignette Title}
  %\VignetteEngine{knitr::rmarkdown}
  \usepackage[utf8]{inputenc}
---
```

Add Data (🗀 data/)

The 🗀 data/ directory allows you to include data with your package.

- ☑ Save data as .Rdata files (suggested)
- ☑ Store data in one of **data/**, **R/Sysdata.rda**, **inst/extdata**
- ☑ Always use **LazyData: true** in your DESCRIPTION file.

devtools::**use_data()**

Adds a data object to data/ (R/Sysdata.rda if **internal = TRUE**)

devtools::**use_data_raw()**

Adds an R Script used to clean a data set to data-raw/. Includes data-raw/ on .Rbuildignore.

Store data in

- **data/** to make data available to package users
- **R/sysdata.rda** to keep data internal for use by your functions.
- **inst/extdata** to make raw data available for loading and parsing examples. Access this data with **system.file()**

Organize (🗎 NAMESPACE)

The 🗎 NAMESPACE file helps you make your package self-contained: it won't interfere with other packages, and other packages won't interfere with it.

- ☑ Export functions for users by placing **@export** in their roxygen comments
- ☑ Import objects from other packages with **package::object** (recommended) or **@import**, **@importFrom**, **@importClassesFrom**, **@importMethodsFrom** (not always recommended)

WORKFLOW

1. Modify your code or tests.
2. Document your package (devtools::**document()**)
3. Check NAMESPACE
4. Repeat until NAMESPACE is correct

SUBMIT YOUR PACKAGE

r-pkgs.had.co.nz/release.html

RStudio

Searching CRAN with packagefinder: : **CHEAT SHEET**

CONSOLE

findPackage(keywords, mode = "or", case.sensitive = FALSE, always.sensitive = NULL, weights = c(2,2,1,2), display = "viewer", results.longdesc = FALSE, limit.results = 15, silent = FALSE, index = NULL, advanced.ranking = TRUE, return.df = FALSE, clipboard = FALSE)

Most important arguments

keywords Word or vector of words to search for

mode Find packages with every keyword ("and") or with any of the keywords ("or")? Will be overruled if keywords contain logical operators like keywords = "X and Y"

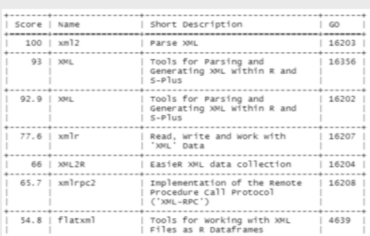
case.sensitive Case-sensitive search?

always.sensitive Vector of words that will always be treated as case-sensitive, e.g. abbreviations

limit.results How many results to display in console or viewer?

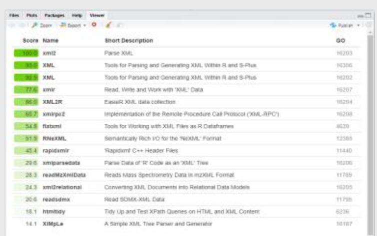
Outputs **display**

display = "console"

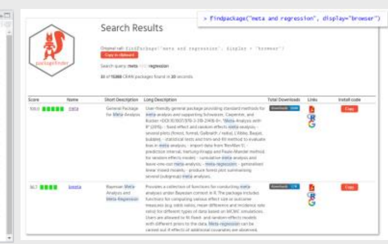


Score	Name	Short Description	GO
100	xml2	Parse XML	16203
93	XML	Tools for Parsing and Generating XML Within R and S-Plus	16356
92.9	XML	Tools for Parsing and Generating XML Within R and S-Plus	16202
77.6	xmlr	Read, Write and Work with 'XML' Data	16207
66	XML2R	EasieR XML data collection	16204
65.7	xmlrpc2	Implementation of the Remote Procedure Call Protocol ('XML-RPC')	16208
54.8	flatxml	Tools for Working with XML Files as R Dataframes	4639

display = "viewer"



display = "browser"



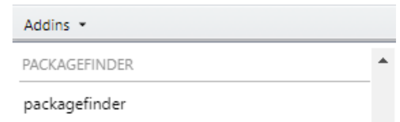
return.df = TRUE Return results as dataframe

clipboard = TRUE Copy results to clipboard

Examples

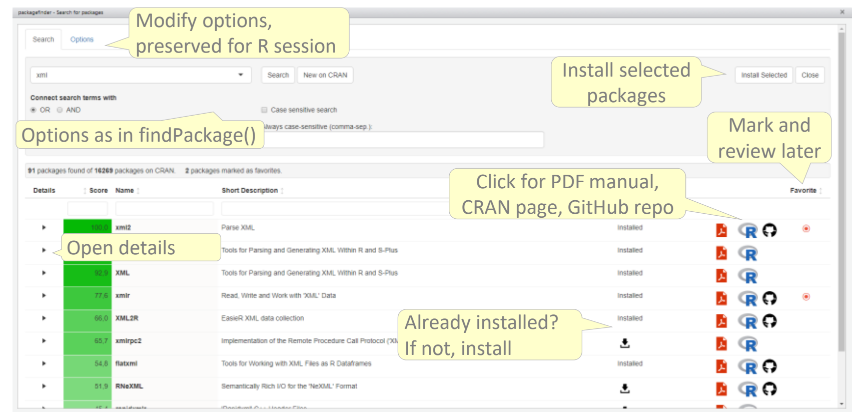
```
> findPackage("parameters", mode = "and", always.sensitive = "SEM")
> findPackage("meta and regression")
> my.resuslts <- findPackage(c("meta", "regression"), "and", return.df = TRUE)
> findPackage("xml", display = "browser")
```

RSTUDIO ADD-IN



Automatically installed with the package.

Provides a graphical interface to the findPackage() and whatsNew() functions



ADDITIONAL FUNCTIONS

whatsNew(last.days = 0)	Show new packages on CRAN
packageDetails(package)	Show details of a CRAN package in the console
lastResults(package = "viewer")	Show results of last search again
fp(…)	Short hand for findPackage(…)
go(package, where.to = "details")	Install CRAN package, show PDF manual, details or package website

Joachim Zuckarelli 2020 joachim@zuckarelli.de jsugarelli github.com/jsugarelli/packagefinder Topics in R

Parallel Computing :: CHEAT SHEET

Splitting :

Splitting a code by :
1. Task (different tasks on same data)
2. Data (one task on different data)

Hardware needs :
CPU (+2 cores)

RAM (shared memory vs distributed memory)

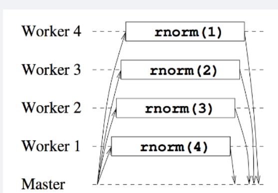
2 ideas in parallel computing :

1. **Map-Reduced Models :**
(distributed data; physically on different devices)
- Hadoop
- Spark

R Packages:
- sparklyr, iotools
- pbdr (programming with big data in R)

2. **Master - Worker Models :**
(M tasks on C cores; usually 1 < C << M)

R Packages:
- snow, snowFT, snowfal
- foreach
- future, future.apply



Not always parallel computing:

stop/start cluster takes time

overhead (communication time b/w master and workers ; not good for repeatedly sending big data!

Sequential vs Parallel:

```
library(microbenchmark)
microbenchmark( FUN1(…), FUN2(…),
times = 10)
```

parallel.R : core package

```
library(parallel)
ncores <- detectCores(logical=F) # physical cores
cl <- makeCluster(ncores)
clusterApply(cl, x = c(…), fun = FUN) # FUN(x,…)
stopCluster(cl)
```

Initialization of workers :

```
clusterCall(cl,FUN)  # calls FUN on workers
clusterEvalQ(cl, exp) # eval an exp. on workers
## clusterEvalQ(cl, library(foo))
clusterExport(cl, varlist) # varlist on workers
## clusterExport(cl, c("mean")) where mean = 10
```

Data Chunk on workers :

1. generated on workers
```
# clusterApply(cl,x, FUN) e.g FUN(){ rnorm()}
```
2. generated on master and pass to workers
```
# ind <- splitIndices(200, 5)
# clusterApply(cl, ind, FUN)
# (-) : not efficient in Big Data : heavy
```
3. chunk on workers # copy of original Data on all workers
```
# clusterExport(cl, M)       e.g. M is a matrix
# clusterApply(cl, x, FUN)   FUN contains subset M
```

foreach.R : Sequential

```
library(foreach)        # by default return a list
foreach(n = rep(5,3), m = 10^(0:2)) %do% FUN(n,m)
foreach(n, .packages = "X") %do% FUN(n)
# FUN needs package X to be run
foreach(n, .export = c("Y") ) %do% FUN(n,b=Y)
# FUN needs outside object/function "Y"
foreach(n,.combine = rbind) %do% FUN(n) #row bind
foreach(n,.combine = '+') %do% FUN(n) #rbind + colSum
foreach(n,.combine = c) %do% FUN(n) # vector
foreach(n,.combine = c) %:% when(n > 2) %do% FUN(n)
```

future.R : asynchronously

```
library(future) (variables run as soon as created)
plan(multicore)
# plans : sequential, cluster, multicore, multiprocess
x %<-% mean(rnorm(100))
y %<-% mean(rnorm(100))
```

future.apply.R : parallel _apply

```
library(future.apply) (parallel _apply functions)
plan(multicore)     # can be other plans
future_apply(n,FUN),future_lapply(…),future_sapply(…)
```

foreach.R : Parallel

needs backend packages support parallel computing
- doParallel(parallel.R),doFuture (future.R),doSEQ

doParallel.R : backend of foreach

```
library(doParallel)
cl <- makeCluster(ncores)     # ncores = 2,3,…
registerDoParallel(cl)     # register the backend
foreach(…) %dopar% FUN(…)
```

doFuture.R : backend of foreach

```
library(doFuture)
registerDoFuture()
plan(cluster , workers = 3) # can be other plans
foreach(…) %dopar% FUN(…)
```

Load Balancing: for uneven task times

```
clusterApplyLB(cl,x,FUN) # not for small task time
clusterApply(cl, x = splitIndices(10,2), FUN)
library(itertools)
foreach(s=isplitVector(1:10,chunks =2))%dopar% FUN
# e.g. FUN = sapply(s,"*",100)
future_sapply(…, future.scheduling = 1)
```

REST APIs with plumber: : CHEAT SHEET

Introduction to REST APIs

Web APIs use **HTTP** to communicate between **client** and **server**.

HTTP

HTTP is built around a **request** and a **response**. A **client** makes a request to a **server**, which handles the request and provides a response. Requests and responses are specially formatted text containing details and data about the exchange between client and server.

REQUEST

Path · HTTP Method · HTTP Version · Headers · Message body

```
curl -v "http://httpbin.org/get"
#> GET  /  get HTTP/1.1
#> Host: httpbin.org
#> User-Agent: curl/7.55.1
#> Accept: */*
#
# Request Body
```

RESPONSE

HTTP Version · Status code · Reason phrase · Headers · Message body

```
#< HTTP/1.1 200 OK
#< Connection: keep-alive
#< Date: Thu, 02 Aug 2018 18:22:22 GMT
#
# Response Body
```

Plumber: Build APIs with R

Plumber uses special comments to turn any arbitrary R code into API endpoints. The example below defines a function that takes the `msg` argument and returns it embedded in additional text.

Plumber comments begin with #* · **@ decorators define API characteristics** · **HTTP Method** · **/<path> is used to define the location of the endpoint**

```
library(plumber)
#* @apiTitle Plumber Example API

#* Echo back the input
#* @param msg The message to echo
#* @get /echo
function(msg = "") {
  list(
    msg = paste0(
      "The message is: '", msg, "'")
  )
}
```

Plumber pipeline

Plumber endpoints contain R code that is executed in response to an HTTP request. Incoming requests pass through a set of mechanisms before a response is returned to the client.

FILTERS

Filters can forward requests (after potentially mutating them), throw errors, or return a response without forwarding the request. Filters are defined similarly to endpoints using the `@filter [name]` tag. By default, filters apply to all endpoints. Endpoints can opt out of filters using the `@preempt` tag.

PARSER

Parsers determine how Plumber parses the incoming request body. By default Plumber parses the request body as JavaScript Object Notation (JSON). Other parsers, including custom parsers, are identified using the `@parser [parser name]` tag. All registered parsers can be viewed with `registered_parsers()`.

ENDPOINT

Endpoints define the R code that is executed in response to incoming requests. These endpoints correspond to HTTP methods and respond to incoming requests that match the defined method.

METHODS

- **`@get`** - request a resource
- **`@post`** - send data in body
- **`@put`** - store / update data
- **`@delete`** - delete resource
- **`@head`** - no request body
- **`@options`** - describe options
- **`@patch`** - partial changes
- **`@use`** - use all methods

SERIALIZER

Serializers determine how Plumber returns results to the client. By default Plumber serializes the R object returned into JavaScript Object Notation (JSON). Other serializers, including custom serializers, are identified using the `@serializer [serializer name]` tag. All registered serializers can be viewed with `registered_serializers()`.

Identify as filter · **Filter name** · **Forward request** · **Endpoint description** · **Opt out of the log filter** · **Parser** · **HTTP Method** · **Endpoint path** · **Serializer**

```
library(plumber)
#* @filter log
function(req, res) {
  print(req$HTTP_USER_AGENT)
  forward()
}

#* Convert request body to uppercase
#* @preempt log
#* @parser json
#* @post /uppercase
#* @serializer json
function(req, res) {
  toupper(req$body)
}
```

Running Plumber APIs

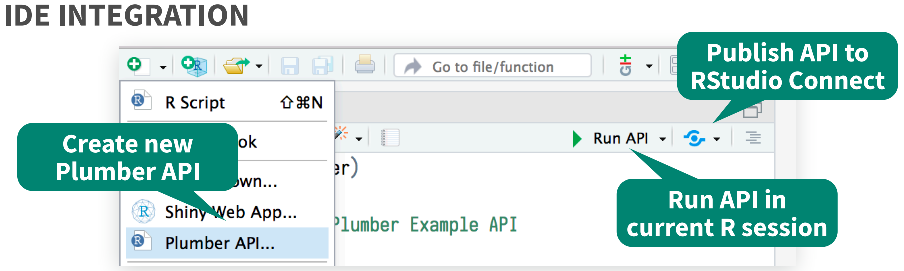
Plumber APIs can be run programmatically from within an R session.

Path to API definition · **Specify API port**

```
library(plumber)
plumb("plumber.R") %>%
  pr_run(port = 5762)
```

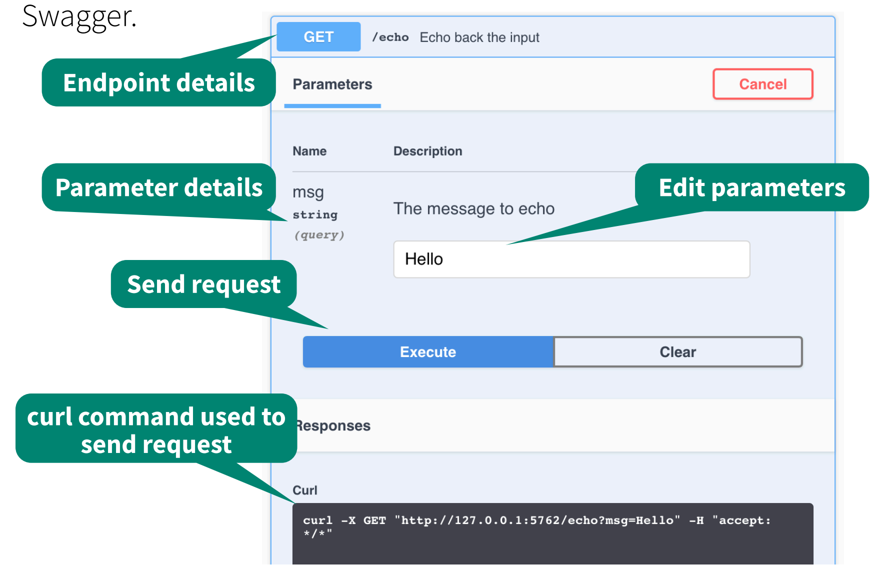
This runs the API on the host machine supported by the current R session.

IDE INTEGRATION



Documentation

Plumber APIs automatically generate an OpenAPI specification file. This specification file can be interpreted to generate a dynamic user-interface for the API. The default interface is generated via Swagger.



Interact with the API

Once the API is running, it can be interacted with using any HTTP client. Note that using `httr` requires using a separate R session from the one serving the API.

```
(resp <- httr::GET("localhost:5762/echo?msg=Hello"))
#> Response [http://localhost:5762/echo?msg=Hello]
#>   Date: 2018-08-07 20:06
#>   Status: 200
#>   Content-Type: application/json
#>   Size: 35 B
httr::content(resp, as = "text")
#> [1] "{\"msg\":[\"The message is: 'Hello'\"]}"
```

RStudio

Programmatic Plumber

Tidy Plumber

Plumber is exceptionally customizable. In addition to using special comments to create APIs, APIs can be created entirely programatically. This exposes additional features and functionality. Plumber has a convenient "tidy" interface that allows API routers to be built piece by piece. The following example is part of a standard `plumber.R` file.

```r
library(plumber)

#* @plumber
function(pr) {
  pr %>%
    pr_get(path = "/echo",
           handler = function(msg = "") {
             list(msg = paste0(
               "The message is: '",
               msg,
               "'")
             )
           }) %>%
    pr_get(path = "/plot",
           handler = function() {
             rand <- rnorm(100)
             hist(rand)
           },
           serializer = serializer_png()) %>%
    pr_post(path = "/sum",
            handler = function(a, b) {
              as.numeric(a) + as.numeric(b)
            })
}
```

Use @plumber tag

Function that accepts and modifies a plumber router

"Tidy" functions for building out Plumber API

OpenAPI

Plumber automatically creates an OpenAPI specification file based on Plumber comments. This file can be further modified using `pr_set_api_spec()` with either a function that modifies the existing specification or a path to a `.yaml` or `.json` specification file.

```r
library(plumber)

#* @param msg The message to echo
#* @get /echo
function(msg = "") {
  list(
    msg = paste0(
      "The message is: '", msg, "'")
  )
}

#* @plumber
function(pr) {
  pr %>%
    pr_set_api_spec(function(spec) {
      spec$paths[["/echo"]]$get$summary <-
        "Echo back the input"
      spec
    })
}
```

Function that receives and modifies the existing specification

Return the updated specification

By default, Swagger is used to interpret the OpenAPI specification file and generate the user interface for the API. Other interpreters can be used to adjust the look and feel of the user interface via `pr_set_docs()`.

Advanced Plumber

REQUEST and RESPONSE

Plumber provides access to special `req` and `res` objects that can be passed to Plumber functions. These objects provide access to the request submitted by the client and the response that will be sent to the client. Each object has several components, the most helpful of which are outlined below:

Name	Example	Description
req		
`req$pr`	`plumber::pr()`	The Plumber router processing the request
`req$body`	`list(a=1)`	Typically the same as `argsBody`
`req$argsBody`	`list(a=1)`	The parsed body output
`req$argsPath`	`list(c=3)`	The values of the path arguments
`req$argsQuery`	`list(e=5)`	The parsed output from `req$QUERY_STRING`
`req$cookies`	`list(cook = "a")`	A list of cookies
`req$REQUEST_METHOD`	`"GET"`	The method used for the HTTP request
`req$PATH_INFO`	`"/"`	The path of the incoming HTTP request
`req$HTTP_*`	`"HTTP_USER_AGENT"`	All of the HTTP headers sent with the request
`req$bodyRaw`	`charToRaw("a=1")`	The `raw()` contents of the request body
res		
`res$headers`	`list(header = "abc")`	HTTP headers to include in the response
`res$setHeader()`	`setHeader("foo", "bar")`	Sets an HTTP header
`res$setCookie()`	`setCookie("foo", "bar")`	Sets an HTTP cookie on the client
`res$removeCookie`	`removeCookie("foo")`	Removes an HTTP cookie
`res$body`	`"{\"a\":[1]}"`	Serialized output
`res$status`	`200`	The response HTTP status code
`res$toResponse()`	`toResponse()`	A list of `status`, `headers`, and `body`

ASYNC PLUMBER

Plumber supports asynchronous execution via the `future` R package. This pattern allows Plumber to concurrently process multiple requests.

```r
library(plumber)
future::plan("multisession")

#* @get /slow
function() {
  promises::future_promise({
    slow_calc()
  })
}
```

Set the execution plan

Slow calculation

MOUNTING ROUTERS

Plumber routers can be combined by mounting routers into other routers. This can be beneficial when building routers that involve several different endpoints and you want to break each component out into a separate router. These separate routers can even be separate files loaded using `plumb()`.

```r
library(plumber)

route <- pr() %>%
  pr_get("/foo", function() "foo")

#* @plumber
function(pr) {
  pr %>%
    pr_mount("/bar", route)
}
```

Create an initial router

Mount one router into another

In the above example, the final route is `/bar/foo`.

RUNNING EXAMPLES

Some packages, like the Plumber package itself, may include example Plumber APIs. Available APIs can be viewed using `available_apis()`. These example APIs can be run with `plumb_api()` combined with `pr_run()`.

```r
library(plumber)

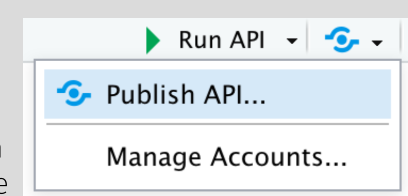
plumb_api(package = "plumber",
          name = "01-append",
          edit = TRUE) %>%
  pr_run()
```

Identify the package name and API name

Optionally open the file for editing

Run the example API

Deploying Plumber APIs



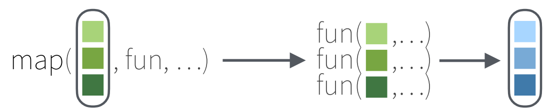
Once Plumber APIs have been developed, they often need to be deployed somewhere to be useful. Plumber APIs can be deployed in a variety of different ways. One of the easiest way to deploy Plumber APIs is using RStudio Connect, which supports push button publishing from the RStudio IDE.

Apply functions with purrr : : CHEAT SHEET

Map Functions

ONE LIST

map(.x, .f, …**)** Apply a function to each element of a list or vector, return a list.
x <- list(1:10, 11:20, 21:30)
l1 <- list(x = c("a", "b"), y = c("c", "d"))
map(l1, sort, decreasing = TRUE)



map_dbl(.x, .f, …**)**
Return a double vector.
map_dbl(x, mean)

map_int(.x, .f, ...**)**
Return an integer vector.
map_int(x, length)

map_chr(.x, .f, …**)**
Return a character vector.
map_chr(l1, paste, collapse = "")

map_lgl(.x, .f, …**)**
Return a logical vector.
map_lgl(x, is.integer)

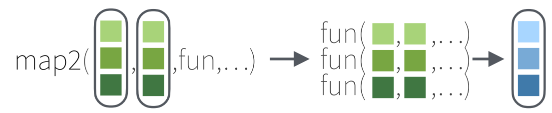
map_dfc(.x, .f, ...**)**
Return a data frame created by column-binding.
map_dfc(l1, rep, 3)

map_dfr(.x, .f, ..., .id = NULL**)**
Return a data frame created by row-binding.
map_dfr(x, summary)

walk(.x, .f, ...**)** Trigger side effects, return invisibly.
walk(x, print)

TWO LISTS

map2(.x, .y, .f, …**)** Apply a function to pairs of elements from two lists or vectors, return a list.
y <- list(1, 2, 3); z <- list(4, 5, 6); l2 <- list(x = "a", y = "z")
map2(x, y, ~ .x * .y)



map2_dbl(.x, .y, .f, …**)**
Return a double vector.
map2_dbl(y, z, ~ .x / .y)

map2_int(.x, .y, .f, …**)**
Return an integer vector.
map2_int(y, z, \`+\`)

map2_chr(.x, .y, .f, …**)**
Return a character vector.
map2_chr(l1, l2, paste, collapse = ",", sep = ":")

map2_lgl(.x, .y, .f, …**)**
Return a logical vector.
map2_lgl(l2, l1, \`%in%\`)

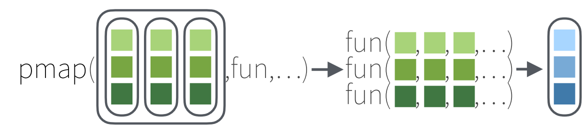
map2_dfc(.x, .y, .f, ...**)**
Return a data frame created by column-binding.
map2_dfc(l1, l2,
~ as.data.frame(c(.x, .y)))

map2_dfr(.x, .y, .f, ..., .id = NULL**)** Return a data frame created by row-binding.
map2_dfr(l1, l2,
~ as.data.frame(c(.x, .y)))

walk2(.x, .y, .f, ...**)** Trigger side effects, return invisibly.
walk2(objs, paths, save)

MANY LISTS

pmap(.l, .f, …**)** Apply a function to groups of elements from a list of lists or vectors, return a list.
pmap(list(x, y, z), ~ ..1 * (..2 + ..3))



pmap_dbl(.l, .f, …**)**
Return a double vector.
pmap_dbl(list(y, z), ~ .x / .y)

pmap_int(.l, .f, …**)**
Return an integer vector.
pmap_int(list(y, z), \`+\`)

pmap_chr(.l, .f, …**)**
Return a character vector.
pmap_chr(list(l1, l2), paste, collapse = ",", sep = ":")

pmap_lgl(.l, .f, …**)**
Return a logical vector.
pmap_lgl(list(l2, l1), \`%in%\`)

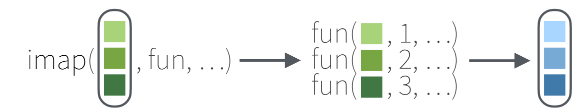
pmap_dfc(.l, .f, ...**)** Return a data frame created by column-binding.
pmap_dfc(list(l1, l2),
~ as.data.frame(c(.x, .y)))

pmap_dfr(.l, .f, ..., .id = NULL**)** Return a data frame created by row-binding.
pmap_dfr(list(l1, l2),
~ as.data.frame(c(.x, .y)))

pwalk(.l, .f, ...**)** Trigger side effects, return invisibly.
pwalk(list(objs, paths), save)

LISTS AND INDEXES

imap(.x, .f, ...**)** Apply .f to each element and its index, return a list.
imap(y, ~ paste0(.y, ": ", .x))



imap_dbl(.x, .f, …**)**
Return a double vector.
imap_dbl(y, ~ .y)

imap_int(.x, .f, ...**)**
Return an integer vector.
imap_int(y, ~ .y)

imap_chr(.x, .f, …**)**
Return a character vector.
imap_chr(y, ~ paste0(.y, ": ", .x))

imap_lgl(.x, .f, …**)**
Return a logical vector.
imap_lgl(l1, ~ is.character(.y))

imap_dfc(.x, .f, ...**)**
Return a data frame created by column-binding.
imap_dfc(l2,
~ as.data.frame(c(.x, .y)))

imap_dfr(.x, .f, ..., .id = NULL**)**
Return a data frame created by row-binding.
imap_dfr(l2,
~ as.data.frame(c(.x, .y)))

iwalk(.x, .f, ...**)** Trigger side effects, return invisibly.
iwalk(z, ~ print(paste0(.y, ": ", .x)))

Function Shortcuts

Use **~ .** with functions like **map()** that have single arguments.

map(l, ~ . + 2)
becomes
map(l, function(x) x + 2))

Use **~ .x .y** with functions like **map2()** that have two arguments.

map2(l, p, ~ .x +.y)
becomes
map2(l, p, function(l, p) l + p)

Use **~ ..1 ..2 ..3** etc with functions like **pmap()** that have many arguments.

pmap(list(a, b, c), ~ ..3 + ..1 - ..2)
becomes
pmap(list(a, b, c), function(a, b, c) c + a -b)

Use **~ .x .y** with functions like **imap()**. .x will get the list value and .y will get the index, or name if available.

imap(list(a, b, c), ~ paste0(.y, ": ", .x)
outputs **"index: value"** for each item

Use a **string** or an **integer** with any map function to index list elements by name or position. **map(l, "name")** becomes **map(l, function(x) x[["name"]])**

RStudio

Work with Lists

Filter

keep(.x, .p, …)
Select elements that pass a logical test.
Conversely, **discard()**.
keep(x, is.na)

compact(.x, .p = identity)
Drop empty elements.
compact(x)

head_while(.x, .p, …)
Return head elements until one does not pass.
Also **tail_while()**.
head_while(x, is.character)

detect(.x, .f, ..., dir = c("forward", "backward"), .right = NULL, .default = NULL)
Find first element to pass.
detect(x, is.character)

detect_index(.x, .f, ..., dir = c("forward", "backward"), .right = NULL) Find index of first element to pass.
detect_index(x, is.character)

every(.x, .p, …)
Do all elements pass a test?
every(x, is.character)

some(.x, .p, …)
Do some elements pass a test?
some(x, is.character)

none(.x, .p, …)
Do no elements pass a test?
none(x, is.character)

has_element(.x, .y)
Does a list contain an element?
has_element(x, "foo")

vec_depth(x)
Return depth (number of levels of indexes).
vec_depth(x)

Index

pluck(.x, ..., .default=NULL)
Select an element by name or index. Also **attr_getter()** and **chuck()**.
pluck(x, "b")
x %>% pluck("b")

assign_in(x, where, value)
Assign a value to a location using pluck selection.
assign_in(x, "b", 5)
x %>% assign_in("b", 5)

modify_in(.x, .where, .f)
Apply a function to a value at a selected location.
modify_in(x, "b", abs)
x %>% modify_in("b", abs)

Reshape

flatten(.x) Remove a level of indexes from a list.
Also **flatten_chr()** etc.
flatten(x)

array_tree(array, margin = NULL) Turn array into list.
Also **array_branch()**.
array_tree(x, margin = 3)

cross2(.x, .y, .filter = NULL)
All combinations of .x and .y.
Also **cross()**, **cross3()**, and **cross_df()**.
cross2(1:3, 4:6)

transpose(.l, .names = NULL)
Transposes the index order in a multi-level list.
transpose(x)

set_names(x, nm = x)
Set the names of a vector/list directly or with a function.
set_names(x, c("p", "q", "r"))
set_names(x, tolower)

Modify

modify(.x, .f, ...) Apply a function to each element. Also **modify2()**, and **imodify()**.
modify(x, ~.+ 2)

modify_at(.x, .at, .f, ...) Apply a function to selected elements.
Also **map_at()**.
modify_at(x, "b", ~.+ 2)

modify_if(.x, .p, .f, ...) Apply a function to elements that pass a test. Also **map_if()**.
modify_if(x, is.numeric,~.+2)

modify_depth(.x, .depth, .f, ...)
Apply function to each element at a given level of a list. Also **map_depth()**.
modify_depth(x, 2, ~.+ 2)

Combine

append(x, values, after = length(x)) Add values to end of list.
append(x, list(d = 1))

prepend(x, values, before = 1)
Add values to start of list.
prepend(x, list(d = 1))

splice(…) Combine objects into a list, storing S3 objects as sub-lists.
splice(x, y, "foo")

List-Columns

max	seq
3	<int [3]>
4	<int [4]>
5	<int [5]>

List-columns are columns of a data frame where each element is a list or vector instead of an atomic value. Columns can also be lists of data frames. See **tidyr** for more about nested data and list columns.

WORK WITH LIST-COLUMNS

Manipulate list-columns like any other kind of column, using **dplyr** functions like **mutate()** and **transmute()**. Because each element is a list, use **map functions** within a column function to manipulate each element.

map(), **map2()**, or **pmap()** return lists and will **create new list-columns**.

list function, return list
list-columns

```
starwars %>%
  transmute(ships = map2(vehicles,
                         starships,
                         append)
```

column function

Suffixed map functions like **map_int()** return an atomic data type and will **simplify list-columns into regular columns**.

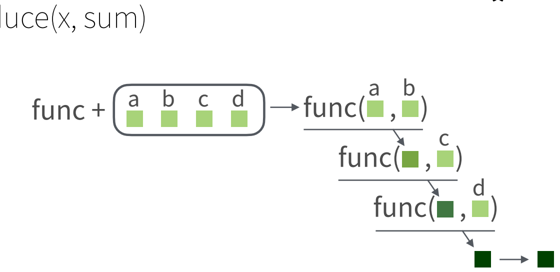
list function, return int

```
starwars %>%
  mutate(n_films = map_int(films, length))
```

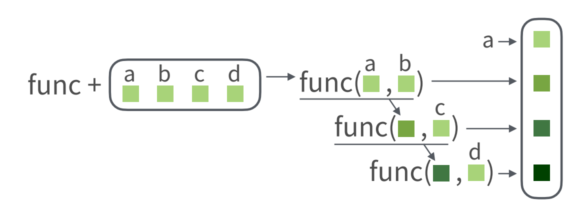
column function
list-column

Reduce

reduce(.x, .f, ..., .init, .dir = c("forward", "backward")) Apply function recursively to each element of a list or vector. Also **reduce2()**.
reduce(x, sum)



accumulate(.x, .f, ..., .init) Reduce a list, but also return intermediate results. Also **accumulate2()**.
accumulate(x, sum)



quanteda Cheat Sheet

Quantitative Analysis of Textual Data

General syntax

- **corpus_*** manage text collections/metadata
- **tokens_*** create/modify tokenized texts
- **dfm_*** create/modify doc-feature matrices
- **fcm_*** work with co-occurrence matrices
- **textstat_*** calculate text-based statistics
- **textmodel_*** fit (un-)supervised models
- **textplot_*** create text-based visualizations

Consistent grammar:

- **object()** constructor for the object type
- **object_verb()** inputs & returns object type

Extensions

quanteda works well with these companion packages:

- **quanteda.textmodels**: Text scaling and classification models
- **readtext**: an easy way to read text data
- **spacyr**: NLP using the spaCy library
- **quanteda.corpora**: additional text corpora
- **stopwords**: multilingual stopword lists in R

Create a corpus from texts (corpus_*)

Read texts (txt, pdf, csv, doc, docx, json, xml)

```
my_texts <- readtext::readtext("~/link/to/path/*")
```

Construct a corpus from a character vector

```
x <- corpus(data_char_ukimmig2010, text_field = "text")
```

Explore a corpus

```
summary(data_corpus_inaugural, n = 2)
## Corpus consisting of 58 documents, showing 2 documents:
##
##             Text Types Tokens Sentences Year  President FirstName Party
##  1789-Washington   625   1537        23 1789 Washington    George  none
##  1793-Washington    96    147         4 1793 Washington    George  none
```

Extract or add document-level variables

```
party <- data_corpus_inaugural$Party
x$serial_number <- seq_len(ndoc(x))
docvars(x, "serial_number") <- seq_len(ndoc(x)) # alternative
```

Bind or subset corpora

```
corpus(x[1:5]) + corpus(x[7:9])
corpus_subset(x, Year > 1990)
```

Change units of a corpus

```
corpus_reshape(x, to = "sentences")
```

Segment texts on a pattern match

```
corpus_segment(x, pattern, valuetype, extract_pattern = TRUE)
```

Take a random sample of corpus texts

```
corpus_sample(x, size = 10, replace = FALSE)
```

Extract features (dfm_*; fcm_*)

Create a document-feature matrix (dfm) from a corpus

```
x <- dfm(data_corpus_inaugural,
         tolower = TRUE, stem = FALSE, remove_punct = TRUE,
         remove = stopwords("english"))

print(x, max-_ndoc = 2, max_nfeat = 4)
## Document-feature matrix of: 58 documents, 9,210 features (92.6% sparse) and 4 docvars.
##                  features
## docs               fellow-citizens senate house representatives
##   1789-Washington                1      1     2               2
##   1793-Washington                0      0     0               0
## [ reached max_ndoc ... 56 more documents, reached max_nfeat ... 9,206 more features ]
```

Create a dictionary

```
dictionary(list(negative = c("bad", "awful", "sad"),
                positive = c("good", "wonderful", "happy")))
```

Apply a dictionary

```
dfm_lookup(x, dictionary = data_dictionary_LSD2015)
```

Select features

```
dfm_select(x, pattern = data_dictionary_LSD2015, selection = "keep")
```

Randomly sample documents or features

```
dfm_sample(x, what = c("documents", "features"))
```

Weight or smooth the feature frequencies

```
dfm_weight(x, scheme = "prop") | dfm_smooth(x, smoothing = 0.5)
```

Sort or group a dfm

```
dfm_sort(x, margin = c("features", "documents", "both"))
dfm_group(x, groups = "President")
```

Combine identical dimension elements of a dfm

```
dfm_compress(x, margin = c("both", "documents", "features"))
```

Create a feature co-occurrence matrix (fcm)

```
x <- fcm(data_corpus_inaugural, context = "window", size = 5)
```

`fcm_compress`/`remove`/`select`/`toupper`/`tolower` are also available

Useful additional functions

Locate keywords-in-context

```
kwic(data_corpus_inaugural, pattern = "america*")
```

Utility functions

texts(*corpus*)	*Show texts of a corpus*
ndoc(*corpus / dfm / tokens*)	*Count documents/features*
nfeat(*corpus / dfm / tokens*)	*Count features*
summary(*corpus / dfm*)	*Print summary*
head(*corpus / dfm*)	*Return first part*
tail(*corpus / dfm*)	*Return last part*

Tokenize a set of texts (tokens_*)

Tokenize texts from a character vector or corpus

```
x <- tokens("Powerful tool for text analysis.",
            remove_punct = TRUE)
```

Convert sequences into compound tokens

```
myseqs <- phrase(c("text analysis"))
tokens_compound(x, myseqs)
```

Select tokens

```
tokens_select(x, c("powerful", "text"), selection = "keep")
```

Create ngrams and skipgrams from tokens

```
tokens_ngrams(x, n = 1:3)
tokens_skipgrams(x, n = 2, skip = 0:1)
```

Convert case of tokens or features

```
tokens_tolower(x) tokens_toupper(x) dfm_tolower(x)
```

Stem tokens or features

```
tokens_wordstem(x) dfm_wordstem(x)
```

Calculate text statistics (textstat_*)

Tabulate feature frequencies from a dfm

```
textstat_frequency(x) topfeatures(x)
```

Identify and score collocations from a tokenized text

```
toks <- tokens(c("quanteda is a pkg for quant text analysis",
                 "quant text analysis is a growing field"))
textstat_collocations(toks, size = 3, min_count = 2)
```

Calculate readability of a corpus

```
textstat_readability(x, measure = c("Flesch", "FOG"))
```

Calculate lexical diversity of a dfm

```
textstat_lexdiv(x, measure = "TTR")
```

Measure distance or similarity from a dfm

```
textstat_simil(x, "2017-Trump", method = "cosine",
               margin = c("documents", "features"))
textstat_dist(x, "2017-Trump",
              margin = c("documents", "features"))
```

Calculate keyness statistics

```
textstat_keyness(x, target = "2017-Trump")
```

Fit text models based on a dfm (textmodel_*)

*These functions require the **quanteda.textmodels** package*

Correspondence Analysis (CA)

```
textmodel_ca(x, threads = 2, sparse = TRUE, residual_floor = 0.1)
```

Naïve Bayes classifier for texts

```
textmodel_nb(x, y = training_labels, distribution = "multinomial")
```

SVM classifier for texts

```
textmodel_svm(x, y = training_labels)
```

Wordscores text model

```
refscores <- c(seq(-1.5, 1.5, .75), NA))
textmodel_wordscores(data_dfm_lbgexample, refscores)
```

Wordfish Poisson scaling model

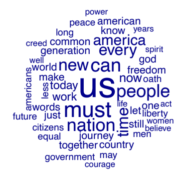
```
textmodel_wordfish(dfm(data_corpus_irishbudget2010), dir = c(6,5))
```

Textmodel methods: `predict(), coef(), summary(), print()`

Plot features or models (textplot_*)

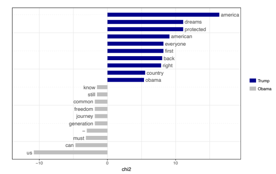
Plot features as a wordcloud

```
data_corpus_inaugural %>%
  corpus_subset(President == "Obama") %>%
  dfm(remove = stopwords("en")) %>%
  textplot_wordcloud()
```



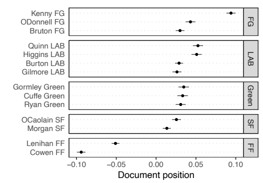
Plot word keyness

```
data_corpus_inaugural %>%
  corpus_subset(President %in%
                c("Obama", "Trump")) %>%
  dfm(groups = "President",
      remove = stopwords("en")) %>%
  textstat_keyness(target = "Trump") %>%
  textplot_keyness()
```



Plot Wordfish, Wordscores or CA models
(requires the **quanteda.textmodels** package)

```
scaling_model %>%
  textplot_scale1d(groups = party,
                   margin = "documents")
```



Convert dfm to a non-quanteda format

```
convert(x, to = c("lda", "tm", "stm", "austin", "topicmodels",
                  "lsa", "matrix", "data.frame"))
```

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Learn more at: http://quanteda.io • updated: 05/2020

PGS Catalog access with quincunx

Introduction

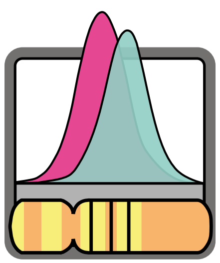
The **PGS Catalog** is a service provided by the EMBL-EBI and University of Cambridge that offers a manually curated and freely available database of published polygenic scores (PGS): `https://www.pgscatalog.org/`.

The PGS Catalog data provided by the **REST API** is organised around five core entities:

- PGS **Polygenic Scores**
- PGP **PGS Publications**
- PSS **PGS Sample Sets**
- PPM **PGS Performance Metrics**
- EFO **EFO traits**

Get PGS Catalog Entities

quincunx facilitates the access to the Catalog via the REST API, allowing you to programmatically retrieve data directly into R. Each of the five entities is mapped to an S4 object of a class of the same name.

PGS CATALOG	RETRIEVAL FUNCTIONS	S4 CLASSES
	`get_scores()`	scores
	`get_publications()`	publications
	`get_sample_sets()`	sample_sets
	`get_performance_metrics()`	performance_metrics
	`get_traits()`	traits

Query criteria for retrieval functions, e.g., PGS can be queried by either `pgs_id`, `efo_id` or `pubmed_id`. These correspond to the criteria exposed by the PGS Catalog REST API: `https://www.pgscatalog.org/rest/`.

Search by	Example	PGS	PGP	PSS	PPM	EFO
pgs_id	"PGS000001"	✓	✓	✓	✓	
pgp_id	"PGP000001"		✓			
pss_id	"PSS000001"			✓		
ppm_id	"PPM000001"				✓	
efo_id	"EFO_0000249"	✓				✓
pubmed_id	"25855707"	✓	✓			
author	"Mavaddat"		✓			
trait_term	"Alzheimer"					✓

PGS Catalog Entities in R

PGS Catalog entities are represented as S4 classes in R. Each class represents a relational database of tidy data tables. All objects start with a table with the same name as the class. Combination of variables indicated in bold renders each row unique in each table.

S4 class scores

`scores`
- **pgs_id**
- pgs_name
- scoring_file
- matches_publication
- reported_trait
- trait_additional_description
- pgs_method_name
- pgs_method_params
- n_variants
- n_variants_interactions
- assembly
- license
- beta_unit

`publications`
- **pgs_id**
- **pgp_id**
- pubmed_id
- publication_date
- publication
- title
- author_fullname
- doi

`samples`
- **pgs_id**
- **sample_id**
- stage
- sample_size
- sample_cases
- sample_controls
- sample_percent_male
- phenotype_description
- ancestry_category
- ancestry
- country
- ancestry_additional_description
- study_id
- pubmed_id
- cohorts_additional_description

`traits`
- **pgs_id**
- **efo_id**
- trait
- description
- url

`demographics`
- **pgs_id**
- **sample_id**
- **variable**
- estimate_type
- estimate
- unit
- variability_type
- variability
- interval_type
- interval_lower
- interval_upper

`cohorts`
- **pgs_id**
- **sample_id**
- **cohort_symbol**
- cohort_name

S4 class publications

`publications`
- **pgp_id**
- pubmed_id
- publication_date
- publication
- title
- author_fullname
- doi
- authors

`pgs_ids`
- **pgp_id**
- **pgs_id**
- stage

S4 class traits

`traits`
- **efo_id**
- **parent_efo_id**
- is_child
- trait
- description
- url

`pgs_ids`
- **efo_id**
- **parent_efo_id**
- is_child
- pgs_id

`child_pgs_ids`
- **efo_id**
- **parent_efo_id**
- is_child
- child_pgs_id

3x `trait_{categories, synonyms, mapped_terms}`
- **efo_id**
- **parent_efo_id**
- is_child
- trait_{category, synonyms, mapped_terms}

S4 class sample_sets

`sample_sets`
- **pss_id**
- pgs_name
- scoring_file
- matches_publication
- reported_trait
- trait_additional_description
- pgs_method_name
- pgs_method_params
- n_variants
- n_variants_interactions
- assembly
- license
- beta_unit

`cohorts`
- **pss_id**
- **sample_id**
- **cohort_symbol**
- cohort_name

`samples`
- **pss_id**
- **sample_id**
- stage
- sample_size
- sample_cases
- sample_controls
- sample_percent_male
- phenotype_description
- ancestry_category
- ancestry
- country
- ancestry_additional_description
- study_id
- pubmed_id
- cohorts_additional_description

`demographics`
- **pss_id**
- **sample_id**
- **variable**
- estimate_type
- estimate
- unit
- variability_type
- variability
- interval_type
- interval_lower
- interval_upper

S4 class performance_metrics

`performance_metrics`
- **ppm_id**
- pgs_id
- reported_trait
- covariates
- comments

`publications`
- **ppm_id**
- **pgp_id**
- pubmed_id
- publication_date
- publication
- title
- author_fullname
- doi

`sample_sets`
- **ppm_id**
- **pss_id**

`samples`
- **ppm_id**
- **pss_id**
- **sample_id**
- stage
- sample_size
- sample_cases
- sample_controls
- sample_percent_male
- phenotype_description
- ancestry_category
- ancestry
- country
- ancestry_additional_description
- study_id
- pubmed_id
- cohorts_additional_description

`demographics`
- **ppm_id**
- **pss_id**
- **sample_id**
- **variable**
- estimate_type
- estimate
- unit
- variability_type
- variability
- interval_type
- interval_lower
- interval_upper

`cohorts`
- **ppm_id**
- **pss_id**
- **sample_id**
- **cohort_symbol**
- cohort_name

3x `pgs_{effect_sizes,classification_metrics,other_metrics}`
- **ppm_id**
- **{effect_size_id, classification_metrics_id, other_metrics_id}**
- estimate_type_long
- estimate_type
- estimate
- unit
- variability_type
- variability
- interval_type
- interval_lower
- interval_upper

Other S4 Entities

Besides the five PGS Catalog entities, there are three other objects that can be retrieved from the REST API: `trait_categories`, `cohorts` and `releases`.

S4 class trait_categories

`trait_categories`
- **trait_category**

`trait`
- **trait_category**
- **efo_id**
- trait
- description
- url

S4 class cohorts

`cohorts`
- **cohort_symbol**
- cohort_name

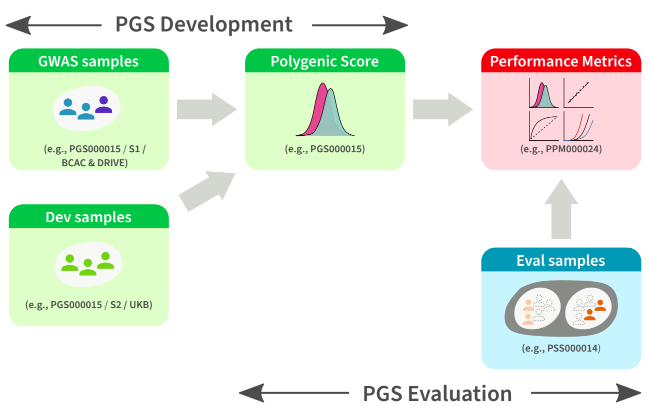
`pgs_ids`
- **cohort_symbol**
- **pgs_id**
- stage

S4 class releases

`releases`
- **date**
- n_pgs
- n_ppm
- n_pgp
- notes

3x `{pgs_ids, ppm_ids,pgp_ids}`
- **date**
- **{pgs_id, ppm_id, pgp_id}**

PGS Construction Process



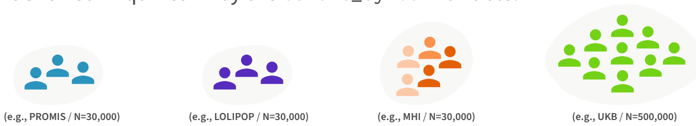
Samples and Polygenic Scores (PGS) are annotated according to their utilisation context in the PGS construction process, i.e. the `stage` variable in quincunx:

- Source of Variant Associations (GWAS): `stage="gwas"`
- Score Development/Training: `stage="dev"`
- Development: `stage="gwas/dev"` (`"gwas"` and `"dev"`)
- PGS Evaluation: `stage="eval"`

Cohorts, Samples and Sample Sets

Cohorts

A cohort is a group of individuals with a shared characteristic. Cohorts are identified in quincunx by the `cohort_symbol` variable.



Samples

A sample is a group of participants associated with none, one or more catalogued cohorts. The selection from a cohort can be either a subset or its totality. Samples are not identified in PGS Catalog with a global unique identifier, but quincunx assigns a surrogate identifier (`sample_id`) to allow relations between tables.

Possible compositions of samples:

Admixture of cohorts. (e.g., PGS000011 / S2 / PROMIS & LOLIPOP / N=8,653)

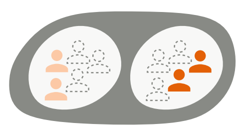
A cohort subset. (e.g., PSS000020 / S1 / MHI / N=862)

Another but disjoint subset. (e.g., PSS000020 / S2 / MHI / N=2,333)

Not associated with any cohort.

Sample Sets

A sample set is a group of samples **used in a polygenic score evaluation.** Each sample set is identified in the PGS Catalog by a unique sample set identifier (PSS ID).



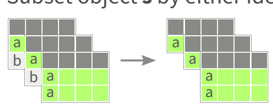
A sample set of two samples.
(e.g., PSS000020: S1 and S2)

Manipulate Cases of S4 Entities

Get a **scores** object **s** consisting of two polygenic scores (PGS):

```
s <- get_scores(pgs_id = c('a', 'b'))
```

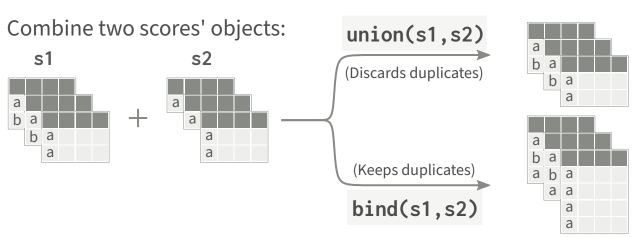
Subset object **s** by either identifier or position using `` `[` ``:



```
s['a'] # Subset by identifier
```

```
s[1] # Subset by position
```

Combine two scores' objects:



Polygenic scoring file

PGS scoring files are provided by the PGS Catalog to allow computation of polygenic scores by users. These files are hosted at the PGS Catalog FTP server: `http://ftp.ebi.ac.uk/pub/databases/spot/pgs/scores/`. They are labelled by their respective PGS Score ID (e.g. `PGS000001.txt.gz`). For more details please visit: `https://maialab.org/quincunx/articles/pgs-scoring-file.html`.

File Format

Each scoring file contains variant identification, effect alleles and respective score weights. The file is formatted as a gzipped tab-delimited text file, with a header containing brief metada about the score. You can read PGS scoring files into R with `read_scoring_file()`.

`PGS000117.txt.gz`

```
### PGS CATALOG SCORING FILE - see www.pgscatalog.org/downloads/#dl_ftp for…
## POLYGENIC SCORE (PGS) INFORMATION
# PGS ID = PGS000117
# Reported Trait = Cardiovascular Disease
# Original Genome Build = GRCh37
# Number of Variants = 267863
## SOURCE INFORMATION
# PGP ID = PGP000054
# Citation = Elliott J et al. JAMA (2020). doi:10.1001/jama.2019.22241
rsID       chr_name chr_position effect_allele reference_allele effect_weight
rs11240779 1        808631       A             G                0.00077622
rs1921     1        949608       A             G                -0.00583829
rs2710890  1        958905       G             A                -0.00182583
rs4970349  1        967658       T             C                -0.001855691
…
```

Columns

The following table lists all possible columns in a PGS scoring file. A few columns are required (R), and most are optional (O); either the `rsID` alone or the combination of `chr_name` and `chr_position` are required, with the other being optional.

Column (Requirement)	Description	Example
rsID (R/O)	dbSNP Accession ID	"rs554219"
chr_name (R/O)	Chromosome name	"11"
chr_position (R/O)	Chromosome position	69516874
effect_allele (R)	Effect allele	"G"
reference_allele (O)	Reference allele	"C"
effect_weight (R)	Variant weight	0.117
locus_name (O)	Locus name	"CCND1"
weight_type (O)	Type of weight	"log(OR)", "beta_cox"
allelefrequency_effect (O)	Effect allele frequency	0.410
is_interaction (O)	Variant interaction?	TRUE or FALSE
is_recessive (O)	Recessive inheritance model?	TRUE or FALSE
is_haplotype (O)	Is effect allele a haplotype?	TRUE or FALSE
is_diplotype (O)	Is effect allele a diplotype?	TRUE or FALSE
imputation_method (O)	Imputation method	TODO
variant_description (O)	Variant description	TODO
inclusion_criteria (O)	Score inclusion criteria	TODO
OR (O)	Odds Ratio	1.12
HR (O)	Hazard Ratio	1.08

randomizr: : CHEAT SHEET

Two Arm Trials

Simple random assignment is like flipping coins for each unit separately.

```
simple_ra(N = 100, prob = 0.5)
```

Complete random assignment allocates a fixed number of units to each condition.

```
complete_ra(N = 100, m = 50)
complete_ra(N = 100, prob = 0.5)
```

Block random assignment conducts complete random assignment separately for groups of units.

```
blocks <- rep(c("A", "B", "C"),
              c(50, 100, 200))

# defaults to half of each block
block_ra(blocks = blocks)

# can change with block_m
block_ra(blocks = blocks,
         block_m = c(20, 30, 40))
```

Cluster random assignment allocates whole groups of units to conditions together.

```
clusters <- rep(letters, times = 1:26
cluster_ra(clusters = clusters)
```

Block and cluster random assignment conducts cluster random assignment separately for groups of clusters.

```
clusters <- rep(letters, times = 1:26)
blocks <- rep(paste0("block_", 1:5),
              c(15, 40, 65, 90, 141))
block_and_cluster_ra(blocks = blocks,
                     clusters = clusters)
```

Multi Arm Trials

Set the number of arms with `num_arms` or with `conditions`.

```
complete_ra(N = 100, num_arms = 3)
complete_ra(N = 100, conditions = c("control",
"placebo", "treatment"))
```

The `*_each` arguments in randomizr functions specify design parameters for each arm separately.

```
complete_ra(N = 100, m_each = c(20, 30, 50))
complete_ra(N = 100,
            prob_each = c(0.2, 0.3, 0.5))
```

If the design is the **same** for all blocks, use `prob_each`:

```
blocks <- rep(c("A", "B","C"),
              c(50, 100, 200))
block_ra(blocks = blocks,
         prob_each = c(.1, .1, .8))
```

If the design is **different** in different blocks, use `block_m_each` or `block_prob_each`:

```
block_m_each <- rbind(c(10, 20, 20),
                      c(30, 50, 20),
                      c(50, 75, 75))
block_ra(blocks = blocks,
         block_m_each = block_m_each)

block_prob_each <- rbind(c(.1, .1, .8),
                         c(.2, .2, .6),
                         c(.3, .3, .4))
block_ra(blocks = blocks,
         block_prob_each = block_prob_each)
```

If `conditions` is numeric, the output will be **numeric**.
If `conditions` is not numeric, the output will be a **factor** with levels in the order provided to conditions.

```
complete_ra(N = 100, conditions = -2:2)
complete_ra(N = 100, conditions = c("A", "B"))
```

randomizr is part of the DeclareDesign suite of packages for designing, implementing, and analyzing social science research designs.

Declaration

Learn about assignment procedures by "declaring" them with `declare_ra()`

```
declaration <-
  declare_ra(N = 100, m_each = c(30, 30, 40))

declaration # print design information
```

Conduct a random assignment:

```
conduct_ra(declaration)
```

Obtain observed condition probabilities (useful for inverse probability weighting if probabilities of assignment are not constant)

```
Z <- conduct_ra(declaration)
obtain_condition_probabilities(declaration, Z)
```

Sampling

All assignment functions have sampling analogues: Sampling is identical to a two arm trial where the treatment group is sampled.

Assignment	Sampling
`simple_ra()`	`simple_rs()`
`complete_ra()`	`complete_rs()`
`block_ra()`	`strata_rs()`
`cluster_ra()`	`cluster_rs()`
`block_and_cluster_ra()`	`strata_and_cluster_rs()`
`declare_ra()`	`declare_rs()`
`conduct_ra()`	`draw_rs()`

Stata

A Stata version of randomizr is available, with the same arguments but different syntax:

```
ssc install randomizr
set obs 100
complete_ra, m(50)
```

Basic Regular Expressions in R

Cheat Sheet

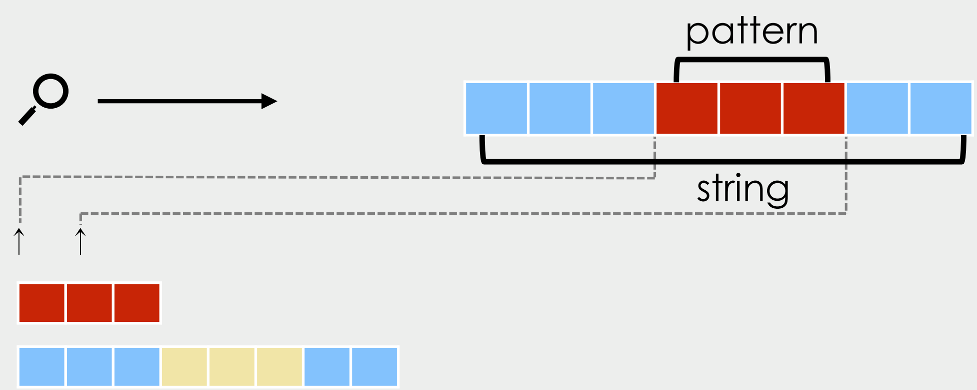
Functions for Pattern Matching

Detect pattern

Locate pattern

Extract pattern

Replace pattern




```
> string <- c("Hiphopopotamus", "Rhymenoceros", "time for bottomless lyrics")
> pattern <- "t.m"
```

Detect Patterns

grep(pattern, string)
`[1] 1 3`

grep(pattern, string, value = TRUE)
`[1] "Hiphopopotamus"`
`[2] "time for bottomless lyrics“`

grepl(pattern, string)
`[1]  TRUE FALSE  TRUE`

stringr::str_detect(string, pattern)
`[1]  TRUE FALSE  TRUE`

Locate Patterns

regexpr(pattern, string)
find starting position and length of first match

gregexpr(pattern, string)
find starting position and length of all matches

stringr::**str_locate(string, pattern)**
find starting and end position of first match

stringr::**str_locate_all(string, pattern)**
find starting and end position of all matches

Split a String using a Pattern

strsplit(string, pattern) or stringr::**str_split(string, pattern)**

Extract Patterns

regmatches(string, regexpr(pattern, string))
extract first match `[1] "tam" "tim"`

regmatches(string, gregexpr(pattern, string))
extract all matches, outputs a list
`[[1]] "tam" [[2]] character(0) [[3]] "tim" "tom"`

stringr::**str_extract(string, pattern)**
extract first match `[1] "tam" NA  "tim"`

stringr::**str_extract_all(string, pattern)**
extract all matches, outputs a list

stringr::**str_extract_all(string, pattern, simplify = TRUE)**
extract all matches, outputs a matrix

stringr::**str_match(string, pattern)**
extract first match + individual character groups

stringr::**str_match_all(string, pattern)**
extract all matches + individual character groups

Replace Patterns

sub(pattern, replacement, string)
replace first match

gsub(pattern, replacement, string)
replace all matches

stringr::**str_replace(string, pattern, replacement)**
replace first match

stringr::**str_replace_all(string, pattern, replacement)**
replace all matches

Character Classes

[[:digit:]] or \\d	Digits; `[0-9]`
\\D	Non-digits; `[^0-9]`
[[:lower:]]	Lower-case letters; `[a-z]`
[[:upper:]]	Upper-case letters; `[A-Z]`
[[:alpha:]]	Alphabetic characters; `[A-z]`
[[:alnum:]]	Alphanumeric characters `[A-z0-9]`
\\w	Word characters; `[A-z0-9_]`
\\W	Non-word characters
[[:xdigit:]] or \\x	Hexadec. digits; `[0-9A-Fa-f]`
[[:blank:]]	Space and tab
[[:space:]] or \\s	Space, tab, vertical tab, newline, form feed, carriage return
\\S	Not space; `[^[:space:]]`
[[:punct:]]	Punctuation characters; `!"#$%&’()*+,-./:;<=>?@[]^_`{|}~`
[[:graph:]]	Graphical characters; `[[:alnum:][:punct:]]`
[[:print:]]	Printable characters; `[[:alnum:][:punct:]\\s]`
[[:cntrl:]] or \\c	Control characters; `\n`, `\r` etc.

Special Metacharacters

\n	New line
\r	Carriage return
\t	Tab
\v	Vertical tab
\f	Form feed

Lookaraounds and Conditionals*

(?=)	Lookahead (requires PERL = TRUE), e.g. `(?=yx)`: position followed by `'xy'`
(?!)	Negative lookahead (PERL = TRUE); position NOT followed by pattern
(?<=)	Lookbehind (PERL = TRUE), e.g. `(?<=yx)`: position following `'xy'`
(?<!)	Negative lookbehind (PERL = TRUE); position NOT following pattern
?(if)then	If-then-condition (PERL = TRUE); use lookaheads, optional char. etc in if-clause
?(if)then|else	If-then-else-condition (PERL = TRUE)

*see, e.g. http://www.regular-expressions.info/lookaround.html
http://www.regular-expressions.info/conditional.html

Character Classes and Groups

.	Any character except `\n`
|	Or, e.g. `(a|b)`
[...]	List permitted characters, e.g. `[abc]`
[a-z]	Specify character ranges
[^...]	List excluded characters
(...)	Grouping, enables back referencing using `\\N` where `N` is an integer

Anchors

^	Start of the string
$	End of the string
\\b	Empty string at either edge of a word
\\B	NOT the edge of a word
\\<	Beginning of a word
\\>	End of a word

Quantifiers

*	Matches at least 0 times
+	Matches at least 1 time
?	Matches at most 1 time; optional string
{n}	Matches exactly n times
{n,}	Matches at least n times
{n,m}	Matches between n and m times

General Modes

By default R uses *extended* regular expressions. You can switch to *PCRE regular expressions* using `PERL = TRUE` for base or by wrapping patterns with `perl()` for stringr.

All functions can be used with literal searches using `fixed = TRUE` for base or by wrapping patterns with `fixed()` for stringr.

All base functions can be made case insensitive by specifying `ignore.case = TRUE`.

Escaping Characters

Metacharacters (`. * +` etc.) can be used as literal characters by escaping them. Characters can be escaped using `\\` or by enclosing them in `\\Q...\\E`.

Case Conversions

Regular expressions can be made case insensitive using `(?i)`. In backreferences, the strings can be converted to lower or upper case using `\\L` or `\\U` (e.g. `\\L\\1`). This requires `PERL = TRUE`.

Greedy Matching

By default the asterisk `*` is greedy, i.e. it always matches the longest possible string. It can be used in lazy mode by adding `?`, i.e. `*?`.

Greedy mode can be turned off using `(?U)`. This switches the syntax, so that `(?U)a*` is lazy and `(?U)a*?` is greedy.

Note

Regular expressions can conveniently be created using e.g. the packages rex or rebus.

Updated: 07/19

Use Python with R with reticulate : : CHEAT SHEET

The **reticulate** package lets you use Python and R together seamlessly in R code, in R Markdown documents, and in the RStudio IDE.

Python in R Markdown

(Optional) Build Python env to use.

Add **knitr::knit_engines$set(python = reticulate::eng_python)** to the setup chunk to set up the reticulate Python engine (not required for knitr >= 1.18).

Suggest the Python environment to use, in your setup chunk.

Begin Python chunks with **```{python}**. Chunk options like **echo**, **include**, etc. all work as expected.

Use the **py** object to access objects created in Python chunks from R chunks.

Python chunks all execute within a **single** Python session so you have access to all objects created in previous chunks.

Use the **r** object to access objects created in R chunks from Python chunks.

Output displays below chunk, including matplotlib plots.

python.Rmd

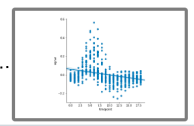
````
```{r setup, include = FALSE}
library(reticulate)
virtualenv_create("fmri-proj")
py_install("seaborn", envname = "fmri-proj")
use_virtualenv("fmri-proj")
```

```{python, echo = FALSE}
import seaborn as sns
fmri = sns.load_dataset("fmri")
```

```{r}
f1 <- subset(py$fmri, region == "parietal")
```

```{python}
import matplotlib as mpl
sns.lmplot("timepoint","signal", data=r.f1)
mpl.pyplot.show()
```
````

R Console



21:4 (Top Level) R Markdown

python.r

```
library(reticulate)
py_install("seaborn")
use_virtualenv("r-reticulate")

sns <- import("seaborn")

fmri <- sns$load_dataset("fmri")
dim(fmri)

# creates tips
source_python("python.py")
dim(tips)

# creates tips in main
py_run_file("python.py")
dim(py$tips)

py_run_string("print(tips.shape)")
```

19:1 (Top Level) R Script

Python in R

Call Python from R code in three ways:

IMPORT PYTHON MODULES

Use **import()** to import any Python module. Access the attributes of a module with **$**.

- **import**(module, as = NULL, convert = TRUE, delay_load = FALSE) Import a Python module. If convert = TRUE, Python objects are converted to their equivalent R types. Also **import_from_path()**. import("pandas")
- **import_main**(convert = TRUE) Import the main module, where Python executes code by default. import_main()
- **import_builtins**(convert = TRUE) Import Python's built-in functions. import_builtins()

SOURCE PYTHON FILES

Use **source_python()** to source a Python script and make the Python functions and objects it creates available in the calling R environment.

- **source_python**(file, envir = parent.frame(), convert = TRUE) Run a Python script, assigning objects to a specified R environment. source_python("file.py")

RUN PYTHON CODE

Execute Python code into the **main** Python module with **py_run_file()** or **py_run_string()**.

- **py_run_string**(code, local = FALSE, convert = TRUE) Run Python code (passed as a string) in the main module. py_run_string("x = 10"); py$x
- **py_run_file**(file, local = FALSE, convert = TRUE) Run Python file in the main module. py_run_file("script.py")
- **py_eval**(code, convert = TRUE) Run a Python expression, return the result. Also **py_call()**. py_eval("1 + 1")

Access the results, and anything else in Python's **main** module, with **py**.

- **py** An R object that contains the Python main module and the results stored there. py$x

Object Conversion

Tip: To index Python objects begin at 0, use integers, e.g. 0L

Reticulate provides **automatic** built-in conversion between Python and R for many Python types.

R ⟷	Python
Single-element vector	Scalar
Multi-element vector	List
List of multiple types	Tuple
Named list	Dict
Matrix/Array	NumPy ndarray
Data Frame	Pandas DataFrame
Function	Python function
NULL, TRUE, FALSE	None, True, False

Or, if you like, you can convert manually with

py_to_r(x) Convert a Python object to an R object. Also **r_to_py()**. py_to_r(x)

tuple(..., convert = FALSE) Create a Python tuple. tuple("a", "b", "c")

dict(..., convert = FALSE) Create a Python dictionary object. Also **py_dict()** to make a dictionary that uses Python objects as keys. dict(foo = "bar", index = 42L)

np_array(data, dtype = NULL, order = "C") Create NumPy arrays. np_array(c(1:8), dtype = "float16")

array_reshape(x, dim, order = c("C", "F")) Reshape a Python array. x <- 1:4; array_reshape(x, c(2, 2))

py_func(f) Wrap an R function in a Python function with the same signature. py_func(xor)

py_main_thread_func(f) Create a function that will always be called on the main thread.

iterate(it, f = base::identity, simplify = TRUE) Apply an R function to each value of a Python iterator or return the values as an R vector, draining the iterator as you go. Also **iter_next()** and **as_iterator()**. iterate(iter, print)

py_iterator(fn, completed = NULL) Create a Python iterator from an R function. seq_gen <- function(x){ n <- x; function() {n <<- n + 1; n}}; py_iterator(seq_gen(9))

Helpers

py_capture_output(expr, type = c("stdout", "stderr")) Capture and return Python output. Also **py_suppress_warnings()**. py_capture_output("x")

py_get_attr(x, name, silent = FALSE) Get an attribute of a Python object. Also **py_set_attr()**, **py_has_attr()**, and **py_list_attributes()**. py_get_attr(x)

py_help(object) Open the documentation page for a Python object. py_help(sns)

py_last_error() Get the last Python error encountered. Also **py_clear_last_error()** to clear the last error. py_last_error()

py_save_object(object, filename, pickle = "pickle", ...) Save and load Python objects with pickle. Also **py_load_object()**. py_save_object(x, "x.pickle")

with(data, expr, as = NULL, ...) Evaluate an expression within a Python context manager.
py <- import_builtins();
with(py$open("output.txt", "w") %as% file,
{ file$write("Hello, there!")})

RStudio

Python in the IDE

Requires reticulate plus RStudio v1.2+. Some features require v1.4+.

Syntax highlighting for Python scripts and chunks.

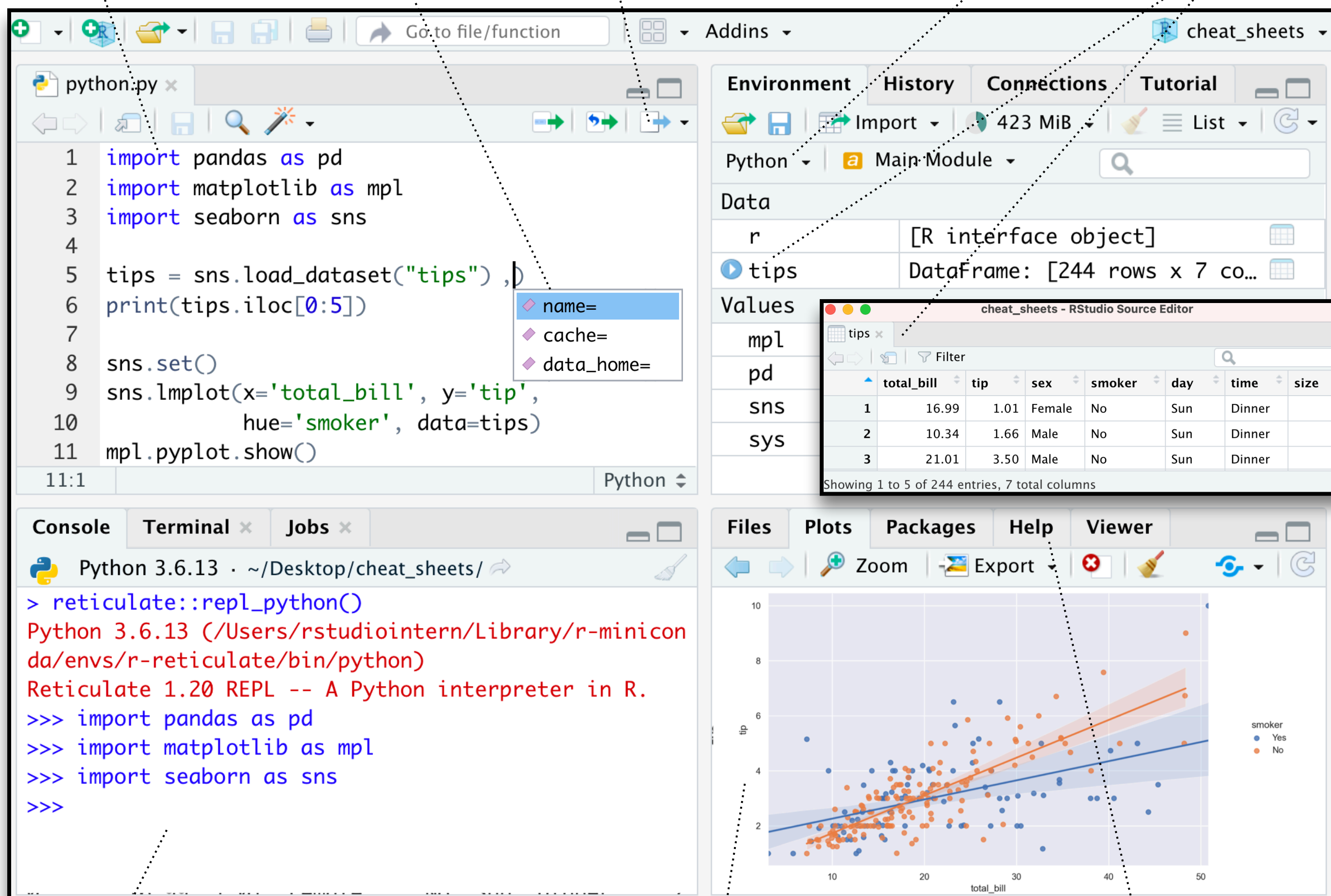
Tab completion for Python functions and objects (and Python modules imported in R scripts).

Source Python scripts.

Execute Python code line by line with **Cmd + Enter** (**Ctrl + Enter**).

View Python objects in the Environment Pane.

View Python objects in the Data Viewer.



A Python REPL opens in the console when you run Python code with a keyboard shortcut. Type **exit** to close.

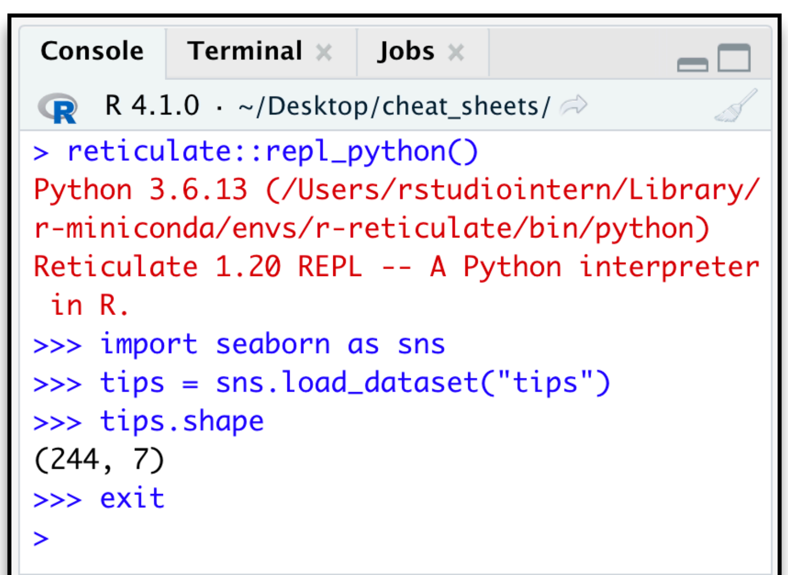
matplotlib plots display in plots pane.

Press **F1** over a Python symbol to display the help topic for that symbol.

Python REPL

A REPL (Read, Eval, Print Loop) is a command line where you can run Python code and view the results.

1. Open in the console with **repl_python()**, or by running code in a Python script with **Cmd + Enter** (**Ctrl + Enter**).
   - **repl_python(**module = NULL, quiet = getOption("reticulate.repl.quiet", default = FALSE), input = NULL) Launch a Python REPL. Run **exit** to close. repl_python()
2. Type commands at >>> prompt.
3. Press **Enter** to run code.
4. Type **exit** to close and return to R console.



Configure Python

Reticulate binds to a local instance of Python when you first call **import()** directly or implicitly from an R session. To control the process, find or build your desired Python instance. Then suggest your instance to reticulate. **Restart R to unbind.**

Find Python

- **install_python(**version, list = FALSE, force = FALSE) Download and install Python. install_python("3.6.13")
- **py_available(**initialize = FALSE) Check if Python is available on your system. Also **py_module_available()** and **py_numpy_module().** py_available()
- **py_discover_config()** Return all detected versions of Python. Use **py_config()** to check which version has been loaded. py_config()
- **virtualenv_list()** List all available virtualenvs. Also **virtualenv_root().** virtualenv_list()
- **conda_list(**conda = "auto") List all available conda envs. Also **conda_binary()** and **conda_version().** conda_list()

Create a Python env

- **virtualenv_create(**envname = NULL, ...) Create a new virtual environment. virtualenv_create("r-pandas")
- **conda_create(**envname = NULL, ...) Create a new conda environment. conda_create("r-pandas", packages = "pandas")

Install Packages

Install Python packages with R (below) or the shell:

pip install SciPy
conda install SciPy

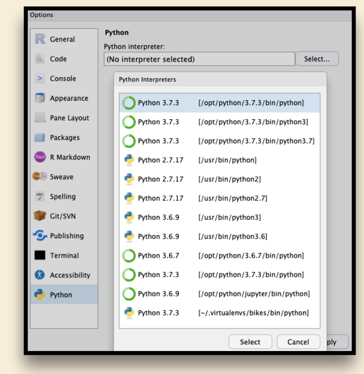
- **py_install(**packages, envname, ...) Installs Python packages into a Python env. py_install("pandas")
- **virtualenv_install(**envname, packages, ...) Install a package within a virtualenv. Also **virtualenv_remove().** virtualenv_install("r-pandas", packages = "pandas")
- **conda_install(**envname, packages, ...) Install a package within a conda env. Also **conda_remove().** conda_install("r-pandas", packages = "plotly")

Suggest an env to use

Set a default Python interpreter in the RStudio IDE Global or Project Options.

Go to **Tools > Global Options... > Python** for Global Options.

Within a project, go to **Tools > Project Options... >Python.**



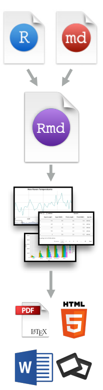
Otherwise, to choose an instance of Python to bind to, reticulate scans the instances on your computer in the following order, **stopping at the first instance that contains the module called by import().**

1. The instance referenced by the environment variable **RETICULATE_PYTHON** (if specified). **Tip: set in .Renviron file.**
   - **Sys.setenv(**RETICULATE_PYTHON = PATH) Set default Python binary. Persists across sessions! Undo with **Sys.unsetenv().** Sys.setenv(RETICULATE_PYTHON = "/usr/local/bin/python")
2. The instances referenced by **use_** functions if called before import(). Will fail silently if called after import unless **required = TRUE.**
   - **use_python(**python, required = FALSE) Suggest a Python binary to use by path. use_python("/usr/local/bin/python")
   - **use_virtualenv(**virtualenv = NULL, required = FALSE) Suggest a Python virtualenv. use_virtualenv("~/myenv")
   - **use_condaenv(**condaenv = NULL, conda = "auto", required = FALSE) Suggest a conda env to use. use_condaenv(condaenv = "r-nlp", conda = "/opt/anaconda3/bin/conda")
3. Within virtualenvs and conda envs that carry the same name as the imported module. e.g. ~/anaconda/envs/nltk for import("nltk")
4. At the location of the Python binary discovered on the system PATH (i.e. Sys.which("python"))
5. At customary locations for Python, e.g. /usr/local/bin/python, /opt/local/bin/python...

RStudio

rmarkdown : : CHEAT SHEET

What is rmarkdown?



.Rmd files · Develop your code and ideas side-by-side in a single document. Run code as individual chunks or as an entire document.

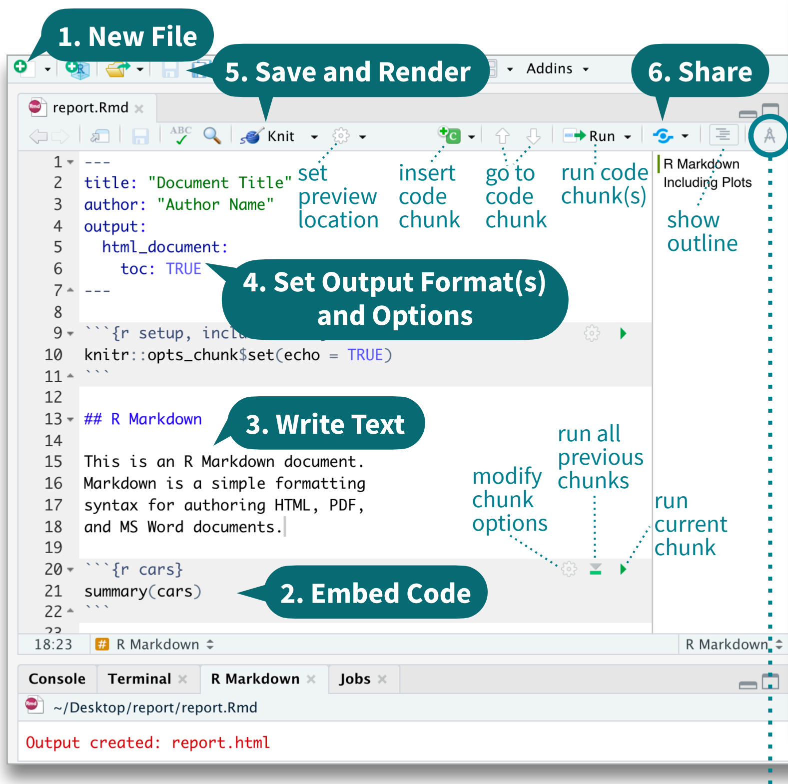
Dynamic Documents · Knit together plots, tables, and results with narrative text. Render to a variety of formats like HTML, PDF, MS Word, or MS Powerpoint.

Reproducible Research · Upload, link to, or attach your report to share. Anyone can read or run your code to reproduce your work.

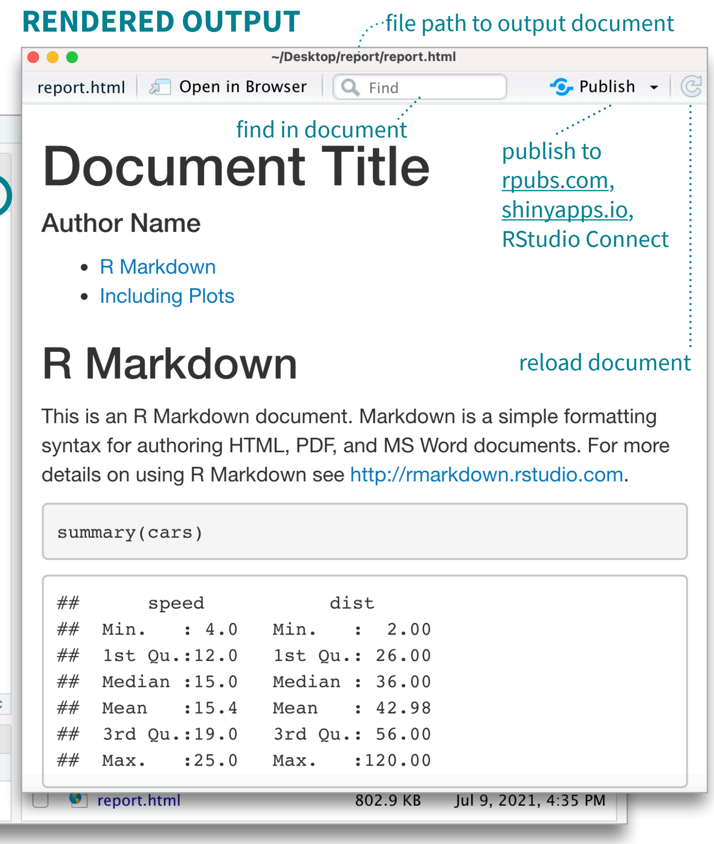
Workflow

1. Open a **new .Rmd file** in the RStudio IDE by going to *File > New File > R Markdown*.
2. **Embed code** in chunks. Run code by line, by chunk, or all at once.
3. **Write text** and add tables, figures, images, and citations. Format with Markdown syntax or the RStudio Visual Markdown Editor.
4. **Set output format(s) and options** in the YAML header. Customize themes or add parameters to execute or add interactivity with Shiny.
5. **Save and render** the whole document. Knit periodically to preview your work as you write.
6. **Share your work!**

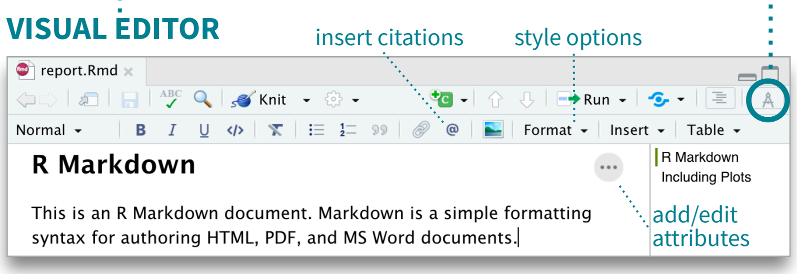
SOURCE EDITOR



RENDERED OUTPUT



VISUAL EDITOR

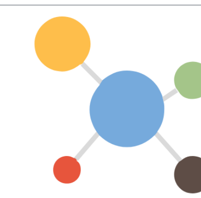
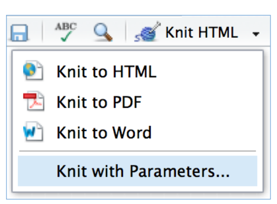
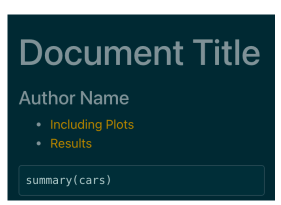
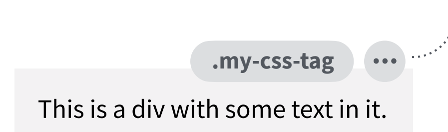
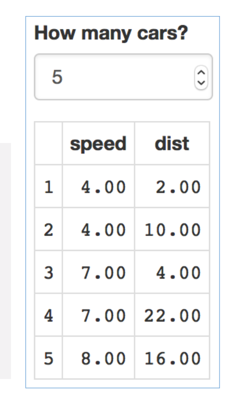
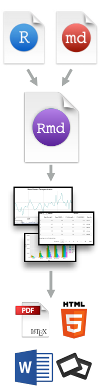
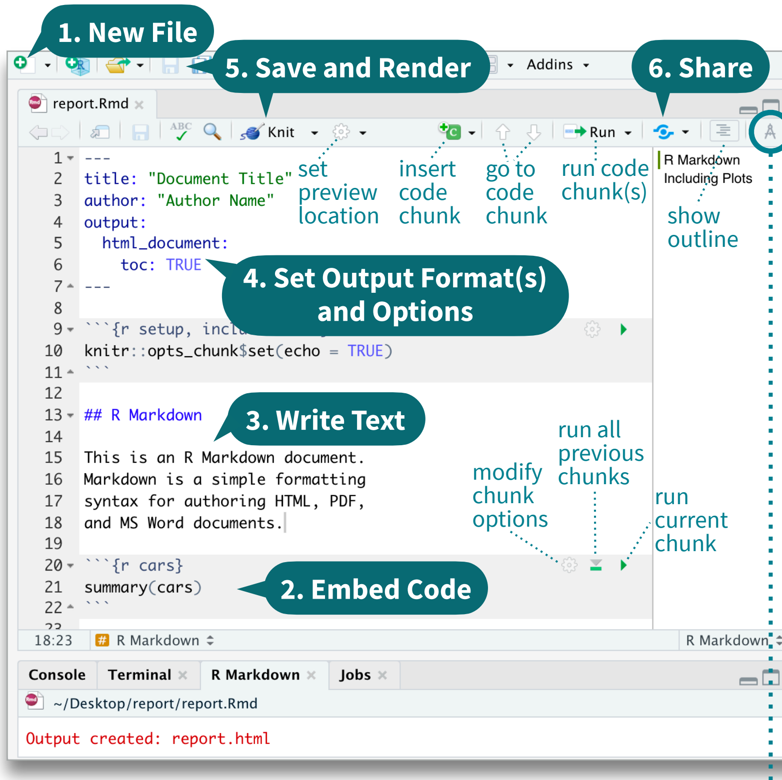
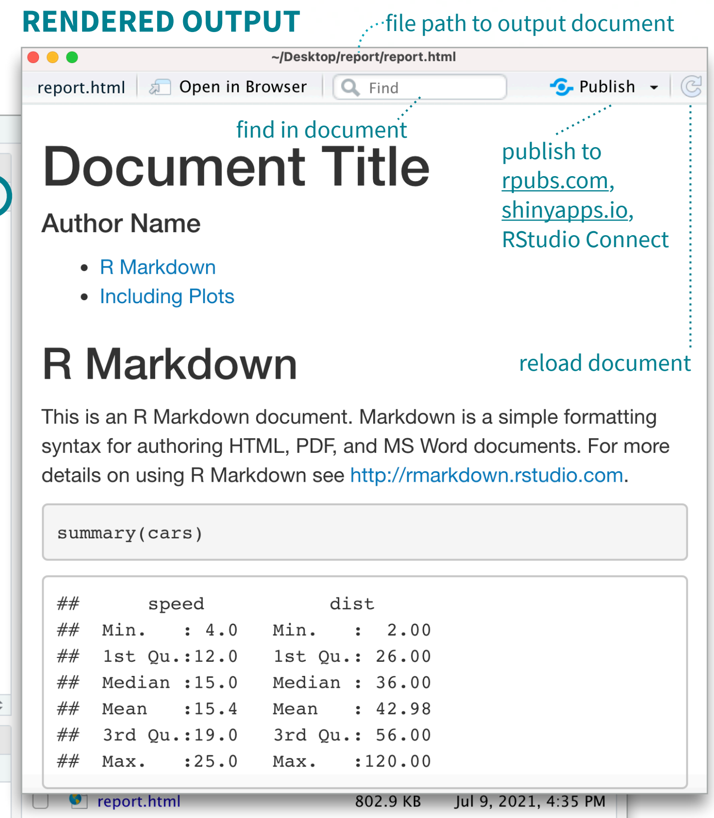
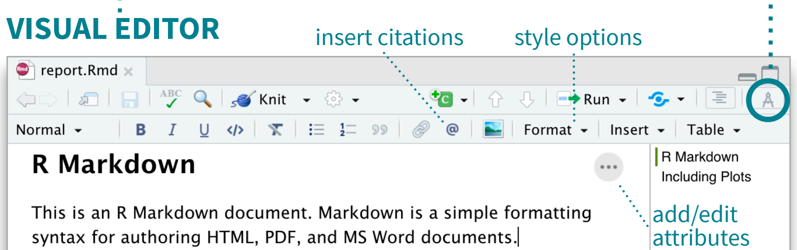
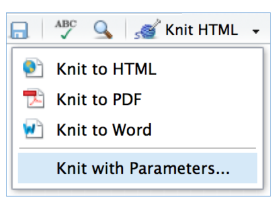
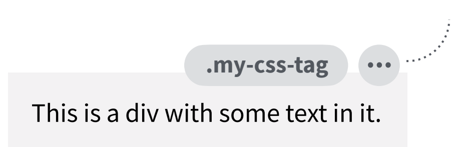


Embed Code with knitr

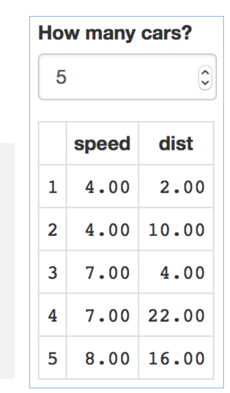
CODE CHUNKS

Surround code chunks with ```{r} and ``` or use the Insert Code Chunk button. Add a chunk label and/or chunk options inside the curly braces after **r**.

```
```{r chunk-label, include=FALSE}
summary(mtcars)
```
```

SET GLOBAL OPTIONS

Set options for the entire document in the first chunk.

```
```{r include=FALSE}
knitr::opts_chunk$set(message = FALSE)
```
```

INLINE CODE

Insert `` `r <code>` `` into text sections. Code is evaluated at render and results appear as text.

"Built with `r getRversion()`" --> "Built with 4.1.0"

OPTION	DEFAULT	EFFECTS
echo	TRUE	display code in output document
error	FALSE	TRUE (display error messages in doc) FALSE (stop render when error occurs)
eval	TRUE	run code in chunk
include	TRUE	include chunk in doc after running
message	TRUE	display code messages in document
warning	TRUE	display code warnings in document
results	"markup"	"asis" (passthrough results) "hide" (don't display results) "hold" (put all results below all code)
fig.align	"default"	"left", "right", or "center"
fig.alt	NULL	alt text for a figure
fig.cap	NULL	figure caption as a character string
fig.path	"figure/"	prefix for generating figure file paths
fig.width & fig.height	7	plot dimensions in inches
out.width		rescales output width, e.g. "75%", "300px"
collapse	FALSE	collapse all sources & output into a single block
comment	"##"	prefix for each line of results
child	NULL	files(s) to knit and then include
purl	TRUE	include or exclude a code chunk when extracting source code with knitr::purl()

See more options and defaults by running **str(knitr::opts_chunk$get())**

Insert Citations

Create citations from a bibliography file, a Zotero library, or from DOI references.

BUILD YOUR BIBLIOGRAPHY

- Add BibTeX or CSL bibliographies to the YAML header.

```
---
title: "My Document"
bibliography: references.bib
link-citations: TRUE
---
```

- If Zotero is installed locally, your main library will automatically be available.
- Add citations by DOI by searching "from DOI" in the **Insert Citation** dialog.

INSERT CITATIONS

- Access the **Insert Citations** dialog in the Visual Editor by clicking the **@** symbol in the toolbar or by clicking **Insert > Citation**.
- Add citations with markdown syntax by typing **[@cite]** or **@cite**.

Insert Tables

Output data frames as tables using **kable**(data, caption).

Table with kable	
eruptions	waiting
3.600	79
1.800	54
3.333	74
2.283	62

```
```{r}
data <- faithful[1:4, ]
knitr::kable(data,
        caption = "Table with kable")
```
```

Other table packages include **flextable**, **gt**, and **kableExtra**.

Write with Markdown

The syntax on the left renders as the output on the right.

Plain text.	Plain text.
End a line with two spaces to start a new paragraph.	End a line with two spaces to start a new paragraph.
Also end with a backslash\ to make a new line.	Also end with a backslash to make a new line.
italics and **bold**	*italics* and **bold**
superscript^2^/subscript~2~	superscript^2/subscript$_2$
~~strikethrough~~	~~strikethrough~~
escaped: * _ \\\\	escaped: * _ \
endash: --, emdash: ---	endash: –, emdash: —
# Header 1	**Header 1**
## Header 2	**Header 2**
...	...
###### Header 6	**Header 6**

- unordered list
- item 2
  - item 2a (indent 1 tab)
  - item 2b
	• unordered list
	• item 2
	  • item 2a (indent 1 tab)
	  • item 2b

1. ordered list
2. item 2
  - item 2a (indent 1 tab)
  - item 2b
	1. ordered list
	2. item 2
	  • item 2a (indent 1 tab)
	  • item 2b

<link url>	http://www.rstudio.com/
[This is a link.](link url)	This is a link.
[This is another link][id]. At the end of the document: [id]: link url	This is another link.
![Caption](image.png) or ![Caption][id2] At the end of the document: [id2]: image.png	Caption.
\`verbatim code\`	`verbatim code`
\`\`\` multiple lines of verbatim code \`\`\`	`multiple lines of verbatim code`
> block quotes	block quotes
equation: \$e^{i \pi} + 1 = 0\$	equation: $e^{i\pi} + 1 = 0$
equation block: \$\$E = mc^{2}\$\$	equation block: $$E = mc^2$$
horizontal rule: ---	horizontal rule:

```
| Right | Left | Default | Center |
|-------:|:------|-----------|:---------:|
| 12 | 12 | 12 | 12 |
| 123 | 123 | 123 | 123 |
| 1 | 1 | 1 | 1 |
```

Right	Left	Default	Center
12	12	12	12
123	123	123	123
1	1	1	1

HTML Tabsets
```
# Results {.tabset}
## Plots
text

## Tables
more text
```

Results

Plots | Tables

text

RStudio

Set Output Formats and their Options in YAML

Use the document's YAML header to set an **output format** and customize it with **output options**.

```
---
title: "My Document"
author: "Author Name"
output:
  html_document:
    toc: TRUE
---
```

Indent format 2 characters, indent options 4 characters

OUTPUT FORMAT	CREATES
html_document	.html
pdf_document*	.pdf
word_document	Microsoft Word (.docx)
powerpoint_presentation	Microsoft Powerpoint (.pptx)
odt_document	OpenDocument Text
rtf_document	Rich Text Format
md_document	Markdown
github_document	Markdown for Github
ioslides_presentation	ioslides HTML slides
slidy_presentation	Slidy HTML slides
beamer_presentation*	Beamer slides

* Requires LaTeX, use **tinytex::install_tinytex()**
Also see **flexdashboard**, **bookdown**, **distill**, and **blogdown**.

IMPORTANT OPTIONS	DESCRIPTION	HTML	PDF	MS Word	MS PPT
anchor_sections	Show section anchors on mouse hover (TRUE or FALSE)	X			
citation_package	The LaTeX package to process citations ("default", "natbib", "biblatex")		X		
code_download	Give readers an option to download the .Rmd source code (TRUE or FALSE)	X			
code_folding	Let readers to toggle the display of R code ("none", "hide", or "show")	X			
css	CSS or SCSS file to use to style document (e.g. "style.css")	X			
dev	Graphics device to use for figure output (e.g. "png", "pdf")	X	X		
df_print	Method for printing data frames ("default", "kable", "tibble", "paged")	X	X	X	X
fig_caption	Should figures be rendered with captions (TRUE or FALSE)	X	X	X	X
highlight	Syntax highlighting ("tango", "pygments", "kate", "zenburn", "textmate")	X	X	X	
includes	File of content to place in doc ("in_header", "before_body", "after_body")	X	X		
keep_md	Keep the Markdown .md file generated by knitting (TRUE or FALSE)	X	X	X	X
keep_tex	Keep the intermediate TEX file used to convert to PDF (TRUE or FALSE)		X		
latex_engine	LaTeX engine for producing PDF output ("pdflatex", "xelatex", or "lualatex")		X		
reference_docx/_doc	docx/pptx file containing styles to copy in the output (e.g. "file.docx", "file.pptx")			X	X
theme	Theme options (see Bootswatch and Custom Themes below)	X			
toc	Add a table of contents at start of document (TRUE or FALSE)	X	X	X	X
toc_depth	The lowest level of headings to add to table of contents (e.g. 2, 3)	X	X	X	X
toc_float	Float the table of contents to the left of the main document content (TRUE or FALSE)	X			

Use **?<output format>** to see all of a format's options, e.g. **?html_document**

Render

When you render a document, rmarkdown:

1. Runs the code and embeds results and text into an .md file with knitr.
2. Converts the .md file into the output format with Pandoc.

Save, then **Knit** to preview the document output. The resulting HTML/PDF/MS Word/etc. document will be created and saved in the same directory as the .Rmd file.

Use **rmarkdown::render()** to render/knit in the R console. See **?render** for available options.

Share



Publish on RStudio Connect
to share R Markdown documents securely, schedule automatic updates, and interact with parameters in real time.
rstudio.com/products/connect/

More Header Options

PARAMETERS

Parameterize your documents to reuse with new inputs (e.g., data, values, etc.).

1. **Add parameters** in the header as sub-values of params.

```
---
params:
  state: "hawaii"
---
```

2. **Call parameters** in code using params$<name>.

````
```{r}
data <- df[, params$state]
summary(data)
```
````

3. **Set parameters** with Knit with Parameters or the params argument of **render()**.



REUSABLE TEMPLATES

1. **Create a new package** with a inst/rmarkdown/ templates directory.
2. **Add a folder** containing **template.yaml** (below) and **skeleton.Rmd** (template contents).

```
---
name: "My Template"
---
```

3. **Install** the package to access template by going to **File > New R Markdown > From Template**.

BOOTSWATCH THEMES

Customize HTML documents with Bootswatch themes from the **bslib** package using the theme output option.

Use **bslib::bootswatch_themes()** to list available themes.




```
---
title: "Document Title"
author: "Author Name"
output:
  html_document:
    theme:
      bootswatch: solar
---
```

CUSTOM THEMES

Customize individual HTML elements using bslib variables. Use **?bs_theme** to see more variables.

```
---
output:
  html_document:
    theme:
      bg: "#121212"
      fg: "#E4E4E4"
      base_font:
        google: "Prompt"
---
```

More on **bslib** at **pkgs.rstudio.com/bslib/**.

STYLING WITH CSS AND SCSS

Add CSS and SCSS to your document by adding a path to a file with the **css** option in the YAML header.

```
---
title: "My Document"
author: "Author Name"
output:
  html_document:
    css: "style.css"
---
```

Apply CSS styling by writing HTML tags directly or:

- Use markdown to apply style attributes inline.

Bracketed Span
A [green]{.my-color} word.

A green word.

Fenced Div
::: {.my-color}
All of these words
are green.
:::

All of these words are green.

- Use the Visual Editor. Go to **Format > Div/Span** and add CSS styling directly with Edit Attributes.



INTERACTIVITY

Turn your report into an interactive Shiny document in 4 steps:

1. Add **runtime: shiny** to the YAML header.
2. Call Shiny input functions to embed input objects.
3. Call Shiny render functions to embed reactive output.
4. Render with **rmarkdown::run()** or click **Run Document** in RStudio IDE.

```
---
output: html_document
runtime: shiny
---
```

````
```{r, echo = FALSE}
numericInput("n",
  "How many cars?", 5)

renderTable({
  head(cars, input$n)
})
```
````



Also see Shiny Prerendered for better performance. **rmarkdown.rstudio.com/authoring_shiny_prerendered**

Embed a complete app into your document with **shiny::shinyAppDir()**. More at **bookdown.org/yihui/rmarkdown/shiny-embedded.html**.

RStudio

rmarkdown : : CHEAT SHEET

What is rmarkdown?



.Rmd files · Develop your code and ideas side-by-side in a single document. Run code as individual chunks or as an entire document.

Dynamic Documents · Knit together plots, tables, and results with narrative text. Render to a variety of formats like HTML, PDF, MS Word, or MS Powerpoint.

Reproducible Research · Upload, link to, or attach your report to share. Anyone can read or run your code to reproduce your work.

Workflow

1. Open a **new .Rmd file** in the RStudio IDE by going to *File > New File > R Markdown*.
2. **Embed code** in chunks. Run code by line, by chunk, or all at once.
3. **Write text** and add tables, figures, images, and citations. Format with Markdown syntax or the RStudio Visual Markdown Editor.
4. **Set output format(s) and options** in the YAML header. Customize themes or add parameters to execute or add interactivity with Shiny.
5. **Save and render** the whole document. Knit periodically to preview your work as you write.
6. **Share your work!**

SOURCE EDITOR



RENDERED OUTPUT



VISUAL EDITOR



Embed Code with knitr

CODE CHUNKS

Surround code chunks with ```` ```{r} ```` and ```` ``` ```` or use the Insert Code Chunk button. Add a chunk label and/or chunk options inside the curly braces after **r**.

```
```{r chunk-label, include=FALSE}
summary(mtcars)
```
```

SET GLOBAL OPTIONS

Set options for the entire document in the first chunk.

```
```{r include=FALSE}
knitr::opts_chunk$set(message = FALSE)
```
```

INLINE CODE

Insert `` `r <code>` `` into text sections. Code is evaluated at render and results appear as text.

"Built with `r getRversion()`" --> "Built with 4.1.0"

OPTION	DEFAULT	EFFECTS
echo	TRUE	display code in output document
error	FALSE	TRUE (display error messages in doc) FALSE (stop render when error occurs)
eval	TRUE	run code in chunk
include	TRUE	include chunk in doc after running
message	TRUE	display code messages in document
warning	TRUE	display code warnings in document
results	"markup"	"asis" (passthrough results) "hide" (don't display results) "hold" (put all results below all code)
fig.align	"default"	"left", "right", or "center"
fig.alt	NULL	alt text for a figure
fig.cap	NULL	figure caption as a character string
fig.path	"figure/"	prefix for generating figure file paths
fig.width & fig.height	7	plot dimensions in inches
out.width		rescales output width, e.g. "75%", "300px"
collapse	FALSE	collapse all sources & output into a single block
comment	"##"	prefix for each line of results
child	NULL	files(s) to knit and then include
purl	TRUE	include or exclude a code chunk when extracting source code with knitr::purl()

See more options and defaults by running **str(knitr::opts_chunk$get())**

Insert Citations

Create citations from a bibliography file, a Zotero library, or from DOI references.

BUILD YOUR BIBLIOGRAPHY

- Add BibTeX or CSL bibliographies to the YAML header.

```
---
title: "My Document"
bibliography: references.bib
link-citations: TRUE
---
```

- If Zotero is installed locally, your main library will automatically be available.
- Add citations by DOI by searching "from DOI" in the **Insert Citation** dialog.

INSERT CITATIONS

- Access the **Insert Citations** dialog in the Visual Editor by clicking the **@** symbol in the toolbar or by clicking **Insert > Citation**.
- Add citations with markdown syntax by typing **[@cite]** or **@cite**.

Insert Tables

Output data frames as tables using **kable**(data, caption).

Table with kable

eruptions	waiting
3.600	79
1.800	54
3.333	74
2.283	62

```
```{r}
data <- faithful[1:4, ]
knitr::kable(data,
        caption = "Table with kable")
```
```

Other table packages include **flextable**, **gt**, and **kableExtra**.

Write with Markdown

The syntax on the left renders as the output on the right.

Markdown	Output
Plain text.	Plain text.
End a line with two spaces to start a new paragraph.	End a line with two spaces to start a new paragraph.
Also end with a backslash\ to make a new line.	Also end with a backslash to make a new line.
italics and **bold**	*italics* and **bold**
superscript^2^/subscript~2~	superscript^2/subscript$_2$
\~\~strikethrough\~\~	~~strikethrough~~
escaped: * _ \\\\	escaped: * _ \
endash: --, emdash: ---	endash: –, emdash: —
# Header 1	**Header 1**
## Header 2	**Header 2**
...	...
###### Header 6	**Header 6**

- unordered list
- item 2
  - item 2a (indent 1 tab)
  - item 2b
	• unordered list
	• item 2
	  • item 2a (indent 1 tab)
	  • item 2b

1. ordered list
2. item 2
  - item 2a (indent 1 tab)
  - item 2b
	1. ordered list
	2. item 2
	  • item 2a (indent 1 tab)
	  • item 2b

<link url>	http://www.rstudio.com/
[This is a link.](link url)	This is a link.
[This is another link][id]. At the end of the document: [id]: link url	This is another link.
![Caption](image.png) or ![Caption][id2] At the end of the document: [id2]: image.png	Caption.
\`verbatim code\`	`verbatim code`
\`\`\` multiple lines of verbatim code \`\`\`	`multiple lines of verbatim code`
> block quotes	block quotes
equation: \$e^{i \pi} + 1 = 0\$	equation: $e^{i\pi} + 1 = 0$
equation block: \$\$E = mc^{2}\$\$	equation block: $$E = mc^2$$
horizontal rule: ---	horizontal rule:

```
| Right | Left | Default | Center |
|-------:|:------|-----------|:---------:|
| 12 | 12 | 12 | 12 |
| 123 | 123 | 123 | 123 |
| 1 | 1 | 1 | 1 |
```

Right	Left	Default	Center
12	12	12	12
123	123	123	123
1	1	1	1

HTML Tabsets

```
# Results {.tabset}
## Plots
text

## Tables
more text
```

Results

Plots | Tables

text

Set Output Formats and their Options in YAML

Use the document's YAML header to set an **output format** and customize it with **output options**.

```
---
title: "My Document"
author: "Author Name"
output:
  html_document:
    toc: TRUE
---
```

Indent format 2 characters, indent options 4 characters

OUTPUT FORMAT	CREATES
html_document	.html
pdf_document*	.pdf
word_document	Microsoft Word (.docx)
powerpoint_presentation	Microsoft Powerpoint (.pptx)
odt_document	OpenDocument Text
rtf_document	Rich Text Format
md_document	Markdown
github_document	Markdown for Github
ioslides_presentation	ioslides HTML slides
slidy_presentation	Slidy HTML slides
beamer_presentation*	Beamer slides

* Requires LaTeX, use **tinytex::install_tinytex()**

Also see **flexdashboard**, **bookdown**, **distill**, and **blogdown**.

IMPORTANT OPTIONS	DESCRIPTION	HTML	PDF	MS Word	MS PPT
anchor_sections	Show section anchors on mouse hover (TRUE or FALSE)	X			
citation_package	The LaTeX package to process citations ("default", "natbib", "biblatex")		X		
code_download	Give readers an option to download the .Rmd source code (TRUE or FALSE)	X			
code_folding	Let readers to toggle the display of R code ("none", "hide", or "show")	X			
css	CSS or SCSS file to use to style document (e.g. "style.css")	X			
dev	Graphics device to use for figure output (e.g. "png", "pdf")	X	X		
df_print	Method for printing data frames ("default", "kable", "tibble", "paged")	X	X	X	X
fig_caption	Should figures be rendered with captions (TRUE or FALSE)	X	X	X	X
highlight	Syntax highlighting ("tango", "pygments", "kate", "zenburn", "textmate")	X	X	X	
includes	File of content to place in doc ("in_header", "before_body", "after_body")	X	X		
keep_md	Keep the Markdown .md file generated by knitting (TRUE or FALSE)	X	X	X	X
keep_tex	Keep the intermediate TEX file used to convert to PDF (TRUE or FALSE)		X		
latex_engine	LaTeX engine for producing PDF output ("pdflatex", "xelatex", or "lualatex")		X		
reference_docx/_doc	docx/pptx file containing styles to copy in the output (e.g. "file.docx", "file.pptx")			X	X
theme	Theme options (see Bootswatch and Custom Themes below)	X			
toc	Add a table of contents at start of document (TRUE or FALSE)	X	X	X	X
toc_depth	The lowest level of headings to add to table of contents (e.g. 2, 3)	X	X	X	X
toc_float	Float the table of contents to the left of the main document content (TRUE or FALSE)	X			

Use **?<output format>** to see all of a format's options, e.g. **?html_document**

Render

When you render a document, rmarkdown:

1. Runs the code and embeds results and text into an .md file with knitr.
2. Converts the .md file into the output format with Pandoc.

Save, then **Knit** to preview the document output. The resulting HTML/PDF/MS Word/etc. document will be created and saved in the same directory as the .Rmd file.

Use **rmarkdown::render()** to render/knit in the R console. See **?render** for available options.

Share

Publish on RStudio Connect to share R Markdown documents securely, schedule automatic updates, and interact with parameters in real time.

rstudio.com/products/connect/

More Header Options

PARAMETERS

Parameterize your documents to reuse with new inputs (e.g., data, values, etc.).

1. **Add parameters** in the header as sub-values of params.

```
---
params:
  state: "hawaii"
---
```

2. **Call parameters** in code using params$<name>.

````
```{r}
data <- df[, params$state]
summary(data)
```
````

3. **Set parameters** with Knit with Parameters or the params argument of **render()**.



REUSABLE TEMPLATES

1. **Create a new package** with a inst/rmarkdown/templates directory.
2. **Add a folder** containing **template.yaml** (below) and **skeleton.Rmd** (template contents).

```
---
name: "My Template"
---
```

3. **Install** the package to access template by going to **File > New R Markdown > From Template**.

BOOTSWATCH THEMES

Customize HTML documents with Bootswatch themes from the **bslib** package using the theme output option.

Use **bslib::bootswatch_themes()** to list available themes.


```
---
title: "Document Title"
author: "Author Name"
output:
  html_document:
    theme:
      bootswatch: solar
---
```

CUSTOM THEMES

Customize individual HTML elements using bslib variables. Use **?bs_theme** to see more variables.

```
---
output:
  html_document:
    theme:
      bg: "#121212"
      fg: "#E4E4E4"
      base_font:
        google: "Prompt"
---
```

More on **bslib** at **pkgs.rstudio.com/bslib/**.

STYLING WITH CSS AND SCSS

Add CSS and SCSS to your document by adding a path to a file with the **css** option in the YAML header.

```
---
title: "My Document"
author: "Author Name"
output:
  html_document:
    css: "style.css"
---
```

Apply CSS styling by writing HTML tags directly or:

- Use markdown to apply style attributes inline.

Bracketed Span

A [green]{.my-color} word.

Fenced Div

::: {.my-color}
All of these words
are green.
:::

A green word.

All of these words are green.

- Use the Visual Editor. Go to **Format > Div/Span** and add CSS styling directly with Edit Attributes.



INTERACTIVITY

Turn your report into an interactive Shiny document in 4 steps:

1. Add **runtime: shiny** to the YAML header.
2. Call Shiny input functions to embed input objects.
3. Call Shiny render functions to embed reactive output.
4. Render with **rmarkdown::run()** or click **Run Document** in RStudio IDE.

```
---
output: html_document
runtime: shiny
---
```

````
```{r, echo = FALSE}
numericInput("n",
  "How many cars?", 5)

renderTable({
  head(cars, input$n)
})
```
````



Also see Shiny Prerendered for better performance. **rmarkdown.rstudio.com/authoring_shiny_prerendered**

Embed a complete app into your document with **shiny::shinyAppDir()**. More at **bookdown.org/yihui/rmarkdown/shiny-embedded.html**.

Add silhouettes with rphylopic : : CHEAT SHEET

Install rphylopic

rphylopic allows you to add species' silhouettes from phylopic to ggplot2 or base plots:

CRAN version
```
install.packages("rphylopic")
```

Development version
```
install.packages("remotes")
remotes::install_github("sckott/rphylopic")

library('rphylopic')
```

uuid

Universally unique identifier (uuid) is a 128-bit number. It has 32 alphanumeric characters in the form of 8-4-4-4-12. Every silhouette has a uuid to uniquely identify it.

Find silhouettes

1. Work with names.

- **name_search**(text, options)[[1]]

Searches the uuid code based on common name or taxonomy of a species. The options can be namebankID, type, names, root, uri.

- **name_get**(uuid, options)

Get information on a name using the uuid code. The options can be citationStart, html, namebakID, root.

- **name_images**(uuid, options = 'credit')

Searches for different images for a taxonomic name.

- **name_taxonomy**(uuid, options, as)

Returns taxonomic name based on uuid code. Options can be string, and as can be list, table, json.

- **name_taxonomy_many**(uuid, options, as)

Returns taxonomic names for two or more concatenated (c()) uuid codes.

- **name_taxonomy_sources**(uuid)

Gives information on the sources for a name's taxonomy given a uuid.

2. Work with uBio data

- **ubio_get**(namebankID)

Retrieve the uuid code based on the namebankID number .

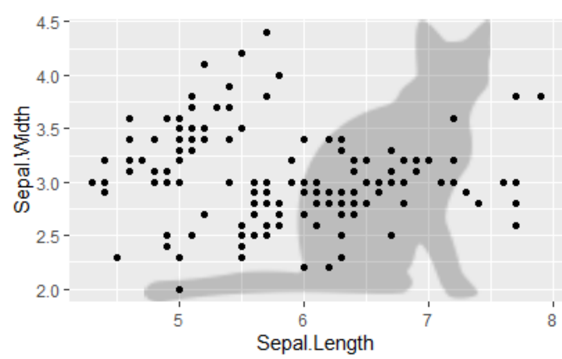
Plot silhouettes

1. Plot a silhouette behind a plot

- **ggplot**

```
library(ggplot2)
cat <- image_data("23cd6aa4-9587-4a2e-8e26-de42885004c9", size = 128)[[1]]

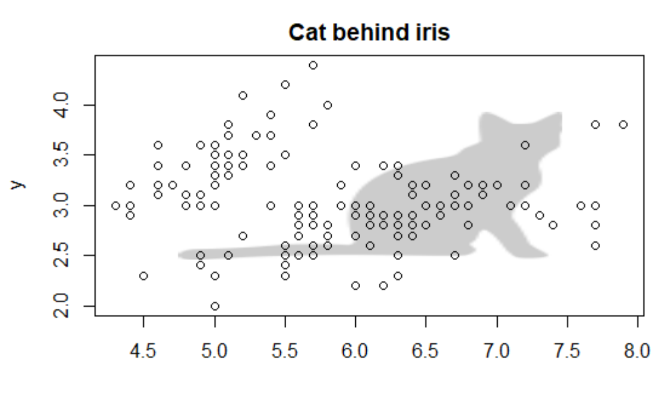
ggplot(data = iris,
       aes(x = Sepal.Length,
           y = Sepal.Width))+
  geom_point()+
  add_phylopic(cat, alpha = 0.2)
```



- **Base plot**

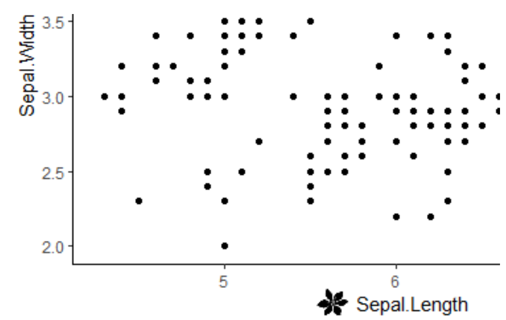
```
cat <- image_data("23cd6aa4-9587-4a2e-8e26-de42885004c9", size = 128)[[1]]

plot(1, 1,
     type = 'n',
     main = "Cat behind iris")
add_phylopic_base(cat,
                  x = 0.5,
                  y = 0.5,
                  ysize = 0.8,
                  alpha = 0.2)
```



2. Plot a silhouette anywhere in a plot

```
ggpubr::ggarrange(plot) +
        add_phylopic(irisimg,
                     alpha = 1,
                     x = 0.43,
                     y = 0.05,
                     ysize = 0.06)
```

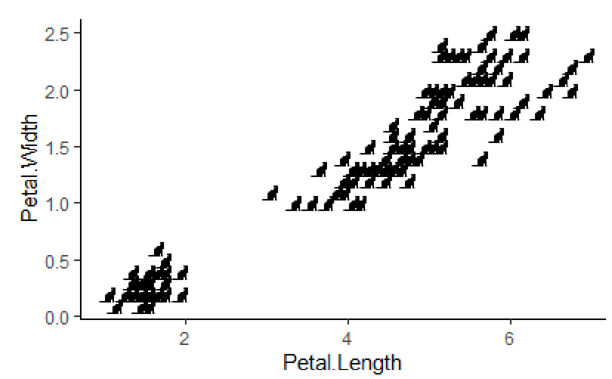


3. Plot silhouettes as points in a plot

- **ggplot2**

```
p <- ggplot(iris,
            aes(Petal.Length,
                Petal.Width)) +
       geom_blank() +
       theme_classic()

for (i in 1:nrow(iris)) {
  p <- p +
       add_phylopic(cat,
                    alpha = 1,
                    iris$Petal.Length[i],
                    iris$Petal.Width[i],
                    ysize = 0.2)
                    }
p
```



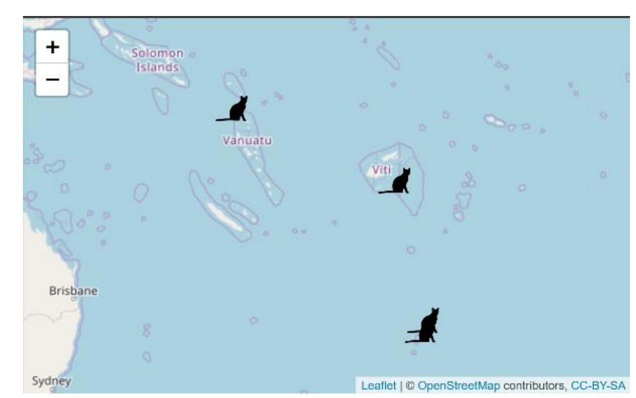
4. Save PNG file to disk

- Download a silhouette from http://phylopic.org/ and save it in your working directory.

```
img <- png::readPNG("img.png")
```

5. Use silhouettes as icons in leaflet plots

```
library(leaflet)
data(quakes) ## this is a table
# get an image
cat <- image_data("23cd6aa4-9587-4a2e-8e26-de42885004c9", size = 128)[[1]]
# save to disk
catimg <- save_png(cat)
# make an icon. See ?makeIcon for more
# iconwidth is in pixels
cat_icon <- makeIcon(iconUrl = catimg,
                     iconWidth = 30)
# make the plot, just 7:10 rows
leaflet(data = quakes[7:10,]) %>%
        addTiles() %>%
        addMarkers(~long, ~lat,
                   icon = cat_icon)
```



Citation
```
Don't forget to cite rphylopic. See how here:

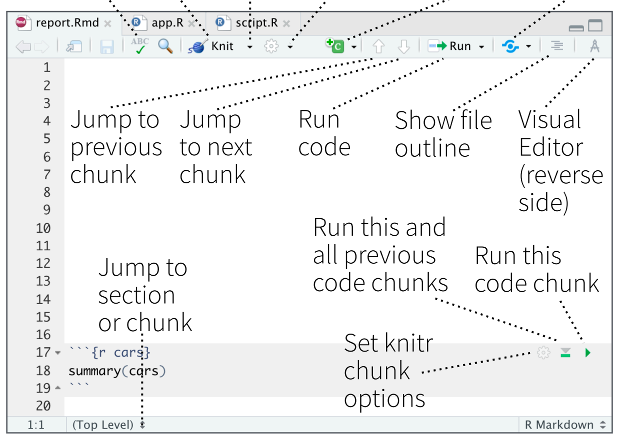
citation("rphylopic")
```

RStudio IDE : : CHEAT SHEET

Documents and Apps

Open Shiny, R Markdown, knitr, Sweave, LaTeX, .Rd files and more in Source Pane

Check spelling · Render output · Choose output format · Configure render options · Insert code chunk · Publish to server

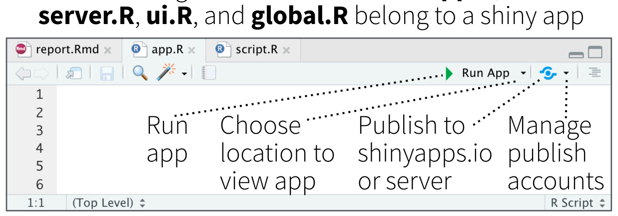


Jump to previous chunk · Jump to next chunk · Run code · Show file outline · Visual Editor (reverse side)

Jump to section or chunk · Run this and all previous code chunks · Run this code chunk · Set knitr chunk options

Access markdown guide at
Help > Markdown Quick Reference
See reverse side for more on **Visual Editor**

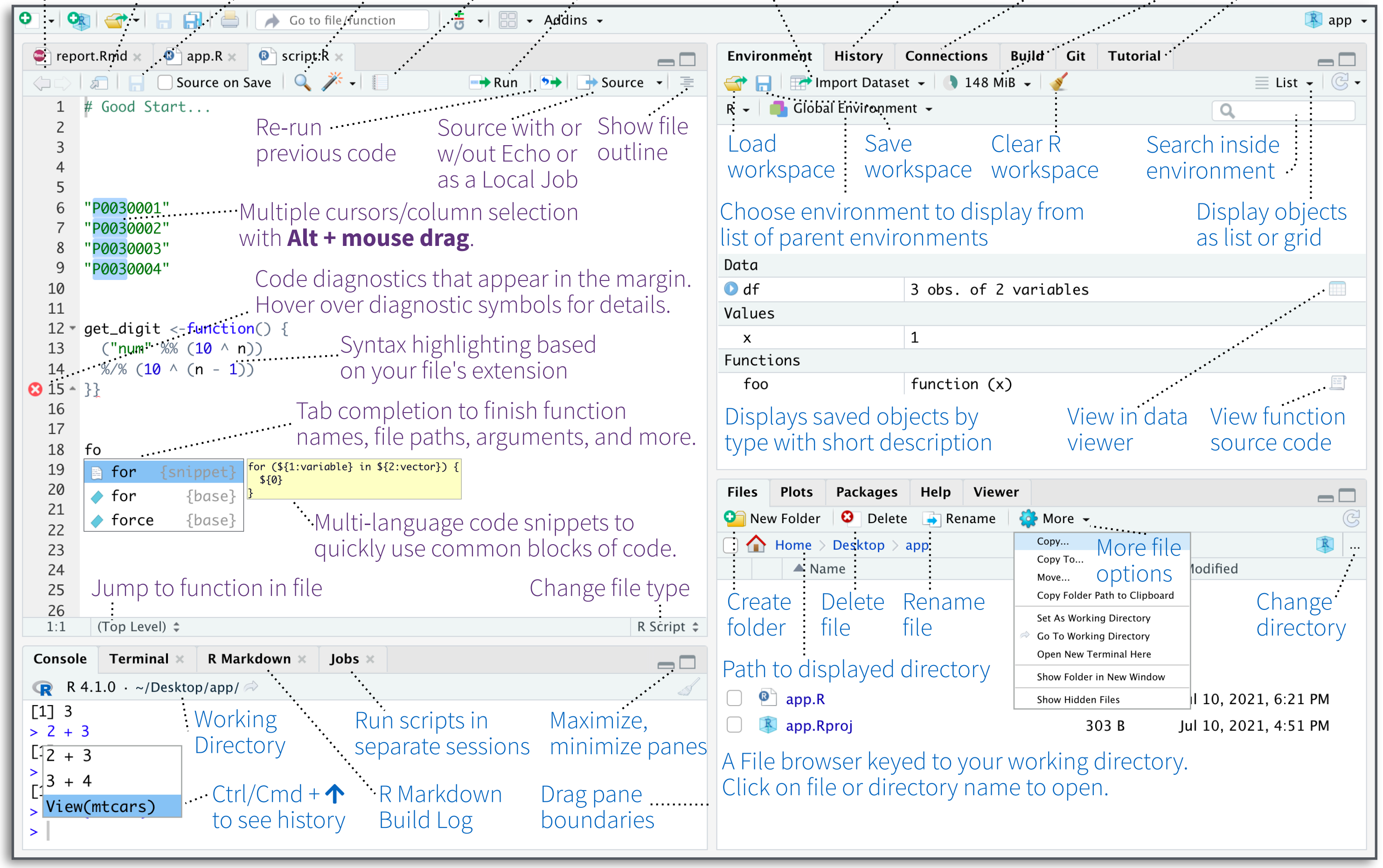
RStudio recognizes that files named **app.R**, **server.R**, **ui.R**, and **global.R** belong to a shiny app



Run app · Choose location to view app · Publish to shinyapps.io or server · Manage publish accounts

Source Editor

Navigate backwards/ forwards · Open in new window · Save · Find and replace · Compile as notebook · Run selected code



Re-run previous code · Source with or w/out Echo or as a Local Job · Show file outline

Multiple cursors/column selection with **Alt + mouse drag**.

Code diagnostics that appear in the margin. Hover over diagnostic symbols for details.

Syntax highlighting based on your file's extension

Tab completion to finish function names, file paths, arguments, and more.

Multi-language code snippets to quickly use common blocks of code.

Jump to function in file · Change file type

Working Directory · Run scripts in separate sessions · Maximize, minimize panes

Ctrl/Cmd + ↑ to see history · R Markdown Build Log · Drag pane boundaries

Tab Panes

Import data with wizard · History of past commands to run/copy · Manage external databases · View memory usage · R tutorials

Load workspace · Save workspace · Clear R workspace · Search inside environment

Choose environment to display from list of parent environments · Display objects as list or grid

Displays saved objects by type with short description · View in data viewer · View function source code

Create folder · Delete file · Rename file · More file options · Change directory

Path to displayed directory

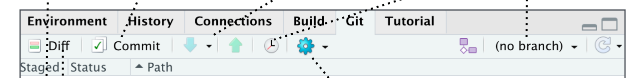
A File browser keyed to your working directory. Click on file or directory name to open.

Version Control

Turn on at **Tools > Project Options > Git/SVN**

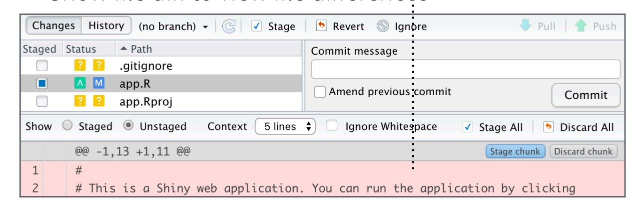
A Added · D Deleted · M Modified · R Renamed · ? Untracked

Stage files: · Commit staged files · Push/Pull to remote · View History · Current branch



Open shell to type commands

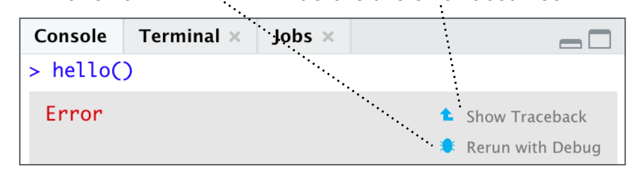
Show file diff to view file differences



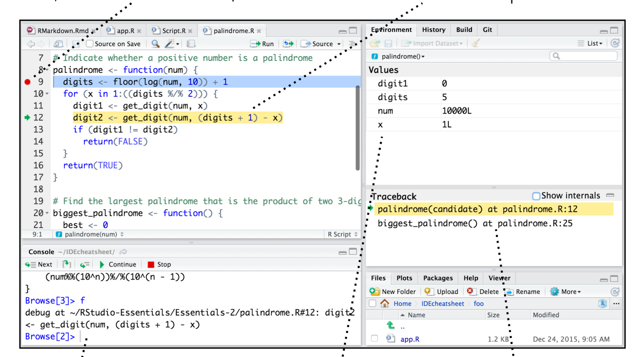
Debug Mode

Use **debug()**, **browser()**, or a breakpoint and execute your code to open the debugger mode.

Launch debugger mode from origin of error · Open traceback to examine the functions that R called before the error occurred



Click next to line number to add/remove a breakpoint. · Highlighted line shows where execution has paused



Run commands in environment where execution has paused · Examine variables in executing environment · Select function in traceback to debug

Step through code one line at a time · Step into and out of functions to run · Resume execution · Quit debug mode

Package Development

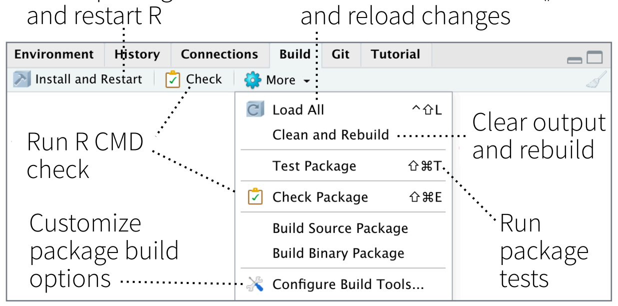
Create a new package with
File > New Project > New Directory > R Package

Enable roxygen documentation with
Tools > Project Options > Build Tools

Roxygen guide at **Help > Roxygen Quick Reference**

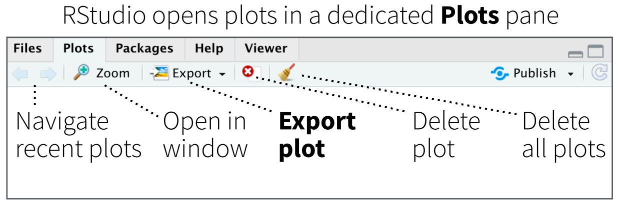
See package information in the **Build Tab**

Install package and restart R · Run devtools::load_all() and reload changes



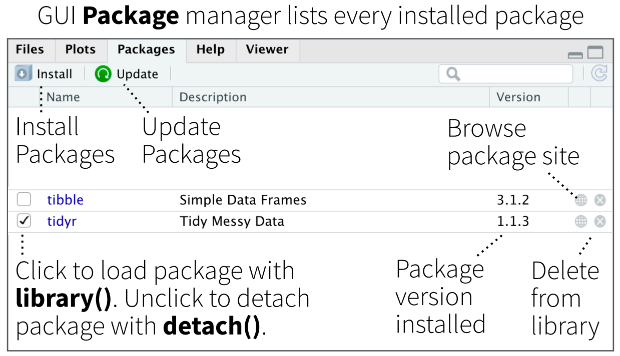
Run R CMD check · Clear output and rebuild · Customize package build options · Run package tests

RStudio opens plots in a dedicated **Plots** pane



Navigate recent plots · Open in window · **Export plot** · Delete plot · Delete all plots

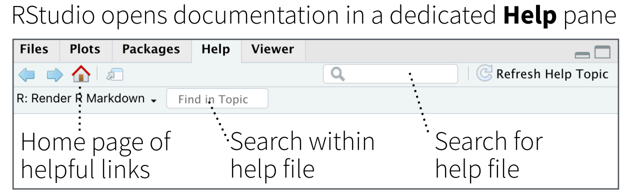
GUI **Package** manager lists every installed package



Install Packages · Update Packages · Browse package site

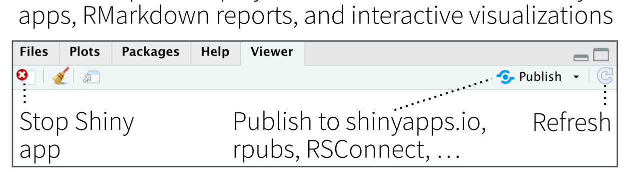
Click to load package with **library()**. Unclick to detach package with **detach()**. · Package version installed · Delete from library

RStudio opens documentation in a dedicated **Help** pane



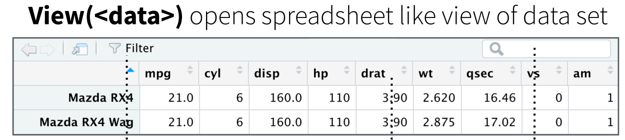
Home page of helpful links · Search within help file · Search for help file

Viewer pane displays HTML content, such as Shiny apps, RMarkdown reports, and interactive visualizations



Stop Shiny app · Publish to shinyapps.io, rpubs, RSConnect, … · Refresh

View(<data>) opens spreadsheet like view of data set



Filter rows by value or value range · Sort by values · Search for value

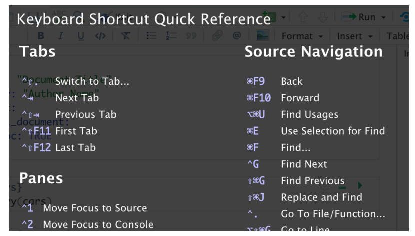
Keyboard Shortcuts

RUN CODE	Windows/Linux	Mac
Search command history	Ctrl+↑	Cmd+↑
Interrupt current command	Esc	Esc
Clear console	Ctrl+L	Ctrl+L
NAVIGATE CODE		
Go to File/Function	Ctrl+.	Ctrl+.
WRITE CODE		
Attempt completion	Tab or Ctrl+Space	Tab or Ctrl+Space
Insert <– (assignment operator)	Alt+-	Option+-
Insert %>% (pipe operator)	Ctrl+Shift+M	Cmd+Shift+M
(Un)Comment selection	Ctrl+Shift+C	Cmd+Shift+C

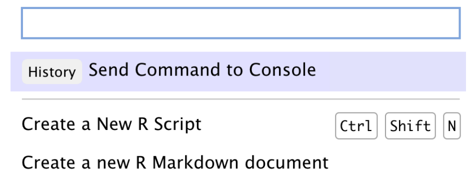
MAKE PACKAGES	Windows/Linux	Mac
Load All (devtools)	Ctrl+Shift+L	Cmd+Shift+L
Test Package (Desktop)	Ctrl+Shift+T	Cmd+Shift+T
Document Package	Ctrl+Shift+D	Cmd+Shift+D

DOCUMENTS AND APPS		
Knit Document (knitr)	Ctrl+Shift+K	Cmd+Shift+K
Insert chunk (Sweave & Knitr)	Ctrl+Alt+I	Cmd+Option+I
Run from start to current line	Ctrl+Alt+B	Cmd+Option+B
MORE KEYBOARD SHORTCUTS		
Keyboard Shortcuts Help	Alt+Shift+K	Option+Shift+K
Show Command Palette	Ctrl+Shift+P	Cmd+Shift+P

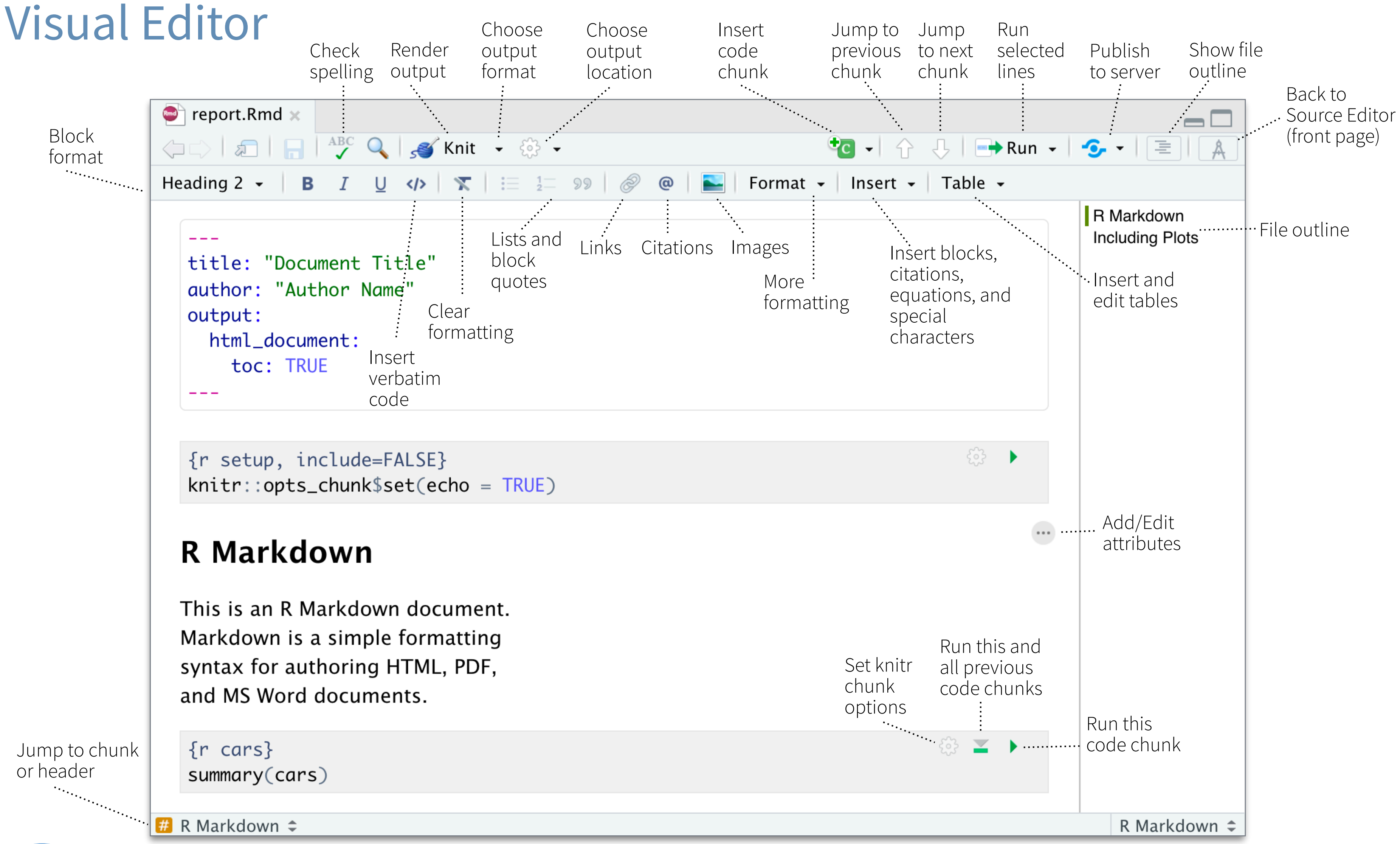
View the Keyboard Shortcut Quick Reference with **Tools > Keyboard Shortcuts** or **Alt/Option + Shift + K**



Search for keyboard shortcuts with **Tools > Show Command Palette** or **Ctrl/Cmd + Shift + P.**



Visual Editor



RStudio Workbench

WHY RSTUDIO WORKBENCH?

Extend the open source server with a commercial license, support, and more:

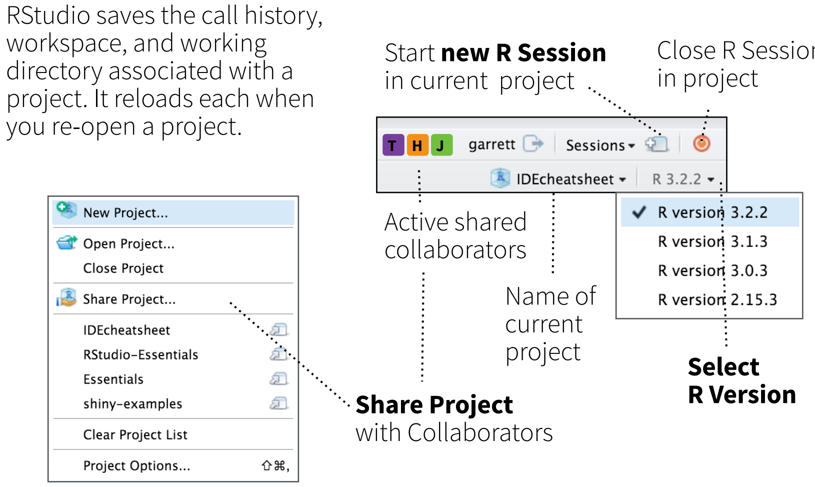
- open and run multiple R sessions at once
- tune your resources to improve performance
- administrative tools for managing user sessions
- collaborate real-time with others in shared projects
- switch easily from one version of R to a different version
- integrate with your authentication, authorization, and audit practices
- work in the RStudio IDE, JupyterLab, Jupyter Notebooks, or VS Code

Download a free 45 day evaluation at **www.rstudio.com/products/workbench/evaluation/**

Share Projects

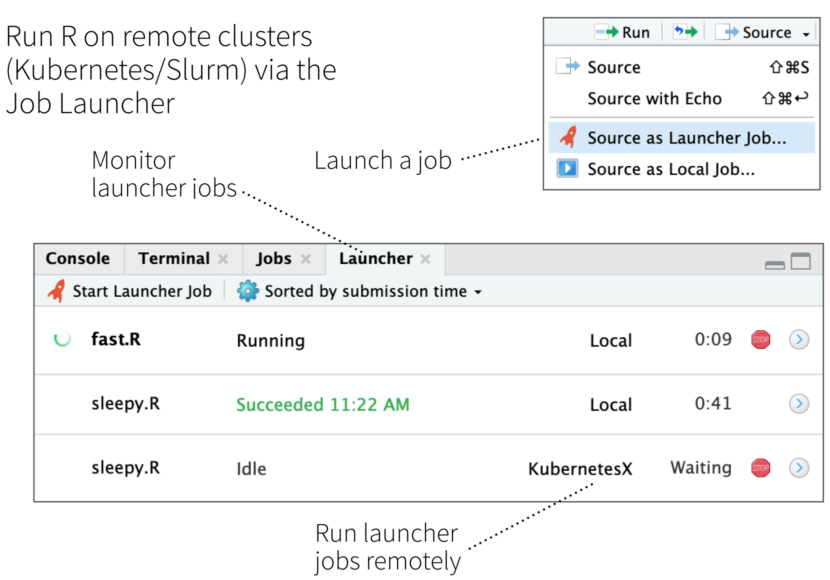
File > New Project

RStudio saves the call history, workspace, and working directory associated with a project. It reloads each when you re-open a project.



Run Remote Jobs

Run R on remote clusters (Kubernetes/Slurm) via the Job Launcher



SAS <-> R :: CHEAT SHEET

Introduction

This guide aims to familiarise SAS users with R.
R examples make use of tidyverse collection of packages.

Install tidyverse: **install.packages("tidyverse")**
Attach tidyverse packages for use: **library(tidyverse)**

R data here in 'data frames', and occasionally vectors (via **c( )**)
Other R structures (lists, matrices...) are not explored here.

Keyboard shortcuts: **<-** Alt + - **%>%** Ctrl + Shift + m

Datasets; drop, keep & rename variables

```
data new_data;
 set old_data;
run;
```

```
new_data <- old_data
```

```
data new_data (keep=id);
 set old_data (drop=job_title) ;
run;
```

```
new_data <- old_data %>%
 select(-job_title) %>%
 select(id)
```

```
data new_data (drop= temp: );
 set old_data;
run;
```

```
new_data <- old_data %>%
 select( -starts_with("temp")
```

C.f. contains( ) , ends_with( )

```
data new_data;
 set old_data;
 rename old_name = new_name;
run;
```

```
new_data <- old_data %>%
 rename(new_name = old_name)
```

Note order differs

Conditional filtering

```
data new_data;
 set old_data;
 if Sex = "M";
run;
```

```
new_data <- old_data %>%
 filter(Sex == "M")
```

```
data new_data;
 set old_data;
 if year in (2010,2011,2012);
run;
```

```
new_data <- old_data %>%
 filter(year %in%
c(2010,2011,2012))
```

```
data new_data;
 set old_data;
 by id ;
 if first.id ;
run;
```

```
new_data <- old_data %>%
 group_by( id ) %>%
 slice(1)
```

Could use slice(n( )) *for last*

```
data new_data;
 set old_data;
 if dob > "25APR1990"d;
run;
```

```
new_data <- old_data %>%
 filter(dob > as.Date("1990-04-25"))
```

New variables, conditional editing

```
data new_data;
 set old_data;
 total_income = wages + benefits ;
run;
```

```
new_data <- old_data %>%
 mutate(total_income = wages + benefits)
```

```
data new_data;
 set old_data;
 if hours > 30 then full_time = "Y";
 else full_time = "N";
run;
```

```
new_data <- old_data %>%
 mutate(full_time = if_else(hours > 30 , "Y" , "N"))
```

```
data new_data;
 set old_data;
 if temp > 20 then weather = "Warm";
 else if temp > 10 then weather = "Mild";
 else weather = "Cold";
run;
```

```
new_data <- old_data %>%
 mutate(weather = case_when(
  temp > 20 ~ "Warm",
  temp > 10 ~"Mild",
  TRUE ~ "Cold" ) )
```

Counting and Summarising

```
proc freq data = old_data ;
 table job_type ;
run;
```

```
old_data %>%
 count( job_type )
```

For percent, add:
%>% mutate(percent = n*100/sum(n))

```
proc freq data = old_data ;
 table job_type*region ;
run;
```

```
old_data %>%
 count( job_type , region )
```

```
proc summary data = old_data nway ;
 class job_type region ;
 output out = new_data ;
run;
```

```
new_data <- old_data %>%
 group_by( job_type , region ) %>%
 summarise( Count = n( ) )
```

Equivalent without nway not trivially produced

```
proc summary data = old_data nway ;
 class job_type region ;
 var salary ;
 output out = new_data
  sum( salary ) = total_salaries ;
run;
```

```
new_data <- old_data %>%
 group_by( job_type , region ) %>%
 summarise( total_salaries = sum( salary ) ,
  Count = n( ) )
```

Lots of summary functions in both languages
Swap summarise( ) *for* mutate( ) *to add summary data to original data*

Combining datasets

```
data new_data ;
 set data_1 data_2 ;
run;
```

```
new_data <- bind_rows( data_1 , data_2 )
```

C.f. rbind( ) *which produces error if columns are not identical*

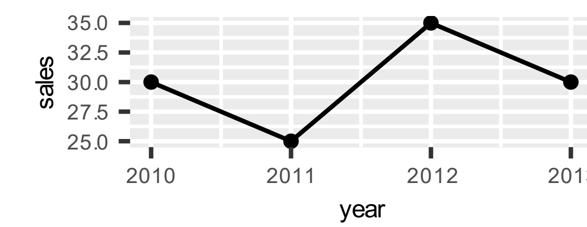
```
data new_data ;
 merge data_1 (in= in_1) data_2 ;
 by id ;
 if in_1 ;
run;
```

```
new_data <- left_join( data_1 , data_2 , by = "id")
```

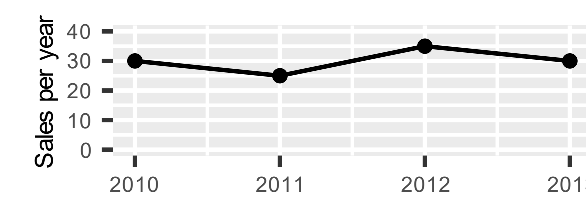
C.f. full_join( ) , right_join( ) , inner_join( )

Some plotting in R

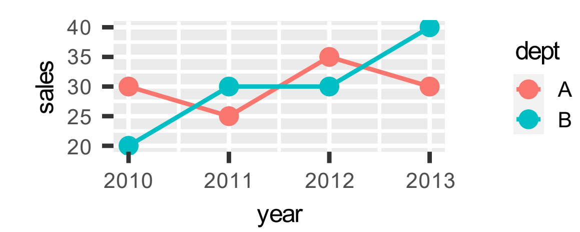
```
ggplot( my_data , aes( year , sales ) ) +
 geom_point( ) + geom_line( )
```



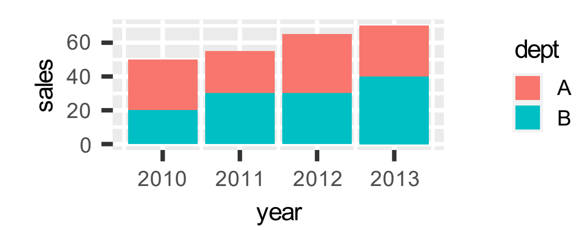

```
ggplot( my_data , aes( year , sales ) ) +
 geom_point( ) + geom_line( ) + ylim(0, 40) +
 labs(x = "" , y = "Sales per year")
```




```
ggplot(my_data, aes( year, sales, colour = dept) ) +
 geom_point( ) + geom_line( )
```

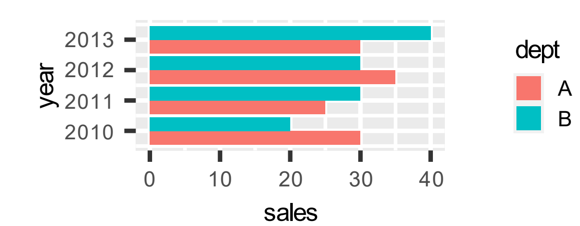



```
ggplot( my_data , aes( year, sales, fill = dept) ) +
 geom_col( )
```



Note 'colour' for lines & points, 'fill' for shapes

```
ggplot( my_data , aes( year, sales, fill = dept) ) +
 geom_col( position = "dodge" ) + coord_flip( )
```



C.f. position = "fill" *for 100% stacked bars/cols*

Sorting and Row-Wise Operations

```
proc sort data=old_data out=new_data;
 by id descending income ;
run;
```

```
new_data <- old_data %>%
 arrange( id , desc( income ) )
```

```
proc sort data=old_data nodup;
 by id job_type;
run;
```

```
old_data <- old_data %>%
 arrange( id , job_type)) %>%
 distinct( )
```

Note nodup relies on adjacency of duplicate rows, distinct( ) *does not*

```
proc sort data=old_data nodupkey;
 by id ;
run;
```

```
old_data <- old_data %>%
 arrange( id ) %>%
 group_by( id ) %>%
 slice( 1 )
```

```
data new_data;
 set old_data;
 by id descending income ;
 if first.id ;
run;
```

```
new_data <- old_data %>%
 group_by( id ) %>%
 slice(which.max( income ))
```

C.f.which.min( )

Swap to preserve duplicate maxima: … slice.max(income)

Alternatively: … filter(income==max(income))

```
data new_data;
 set old_data;
 prev_id= lag( id );
run;
```

```
new_data <- old_data %>%
 mutate( prev_id = lag( id , 1 ))
```

C.f. lead( ) *for subsequent rows*

```
data new_data;
 set old_data;
 by id;
 counter +1 ;
 if first.id then counter = 1;
run;
```

```
new_data <- old_data %>%
 group_by( id ) %>%
 mutate( counter = row_number( ) )
```

Converting and Rounding

```
data new_data;
 set old_data ;
 num_var = input("5" , 8. );
 text_var = put( 5 , 8. );
run;
```

```
new_data <- old_data %>%
 mutate(num_var = as.numeric("5" )) %>%
 mutate(text_var = as.character( 5 ))
```

```
data new_data ;
 set old_data;
 nearest_5 = round( x , 5 )
 two_decimals = round( x , 0.01)
run;
```

```
new_data <- old_data %>%
 mutate(nearest_5 = round(x/5)*5) %>%
 mutate(two_decimals = round( x , digits = 2)
```

Creating functions to modify datasets

```
%macro add_variable(dataset_name);
data &dataset_name;
 set &dataset_name;
 new_variable = 1;
run;
%mend;
%add_variable( my_data );
```

```
add_variable <- function( dataset_name ){
 dataset_name <- dataset_name %>%
  mutate(new_variable = 1)
 return( dataset_name )
}
my_data <- add_variable( my_data )
```

Note SAS can modify within the macro, whereas R creates a copy within the function

Dealing with strings

```
data new_data;
 set old_data;
 if find( job_title , "Health" );
run;
```

```
new_data <- old_data %>%
 filter( str_detect( job_title , "Health" ))
```

```
data new_data;
 set old_data;
 if job_title =: "Health" ;
run;
```

```
new_data <- old_data %>%
 filter( str_detect( job_title , "^Health" ))
```

Use ^ for start of string, $ for end of string, e.g. "Health$"

```
data new_data;
 set old_data;
 substring = substr( big_string , 3 , 4 );
run;
```

```
new_data <- old_data %>%
 mutate( substring = str_sub( big_string , 3 , 6 ))
```

Returns characters 3 to 6. Note SAS uses <start>, <length>, R uses <start>, <end>

```
data new_data;
 set old_data;
 address = tranwrd( address , "Street" , "St" );
run;
```

```
new_data <- old_data %>%
 mutate( address = str_replace_all( address , "Street" , "St" ))
```

C.f. str_replace( ) *for first instance of pattern only*

```
data new_data;
 set old_data;
 full_name = catx(" " , first_name , surname );
run;
```

```
new_data <- old_data %>%
 mutate( full_name = str_c( first_name , surname , sep = " " ))
```

Drop sep = " " *for equivalent to* cats( ) *in SAS*

```
data new_data;
 set old_data;
 first_word = scan( sentence , 1 );
run;
```

```
new_data <- old_data %>%
 mutate( first_word = word( sentence , 1 ))
```

R example preserves punctuation at the end of words, SAS doesn't

```
data new_data;
 set old_data;
 house_number = compress( address , , "dk" );
run;
```

```
new_data <- old_data %>%
 mutate( house_number = str_extract( address , "\\d*" ))
```

Wide range of regexps in both languages, this example extracts digits only

File operations

Operate in 'Work' library.
Use **libname** to define file locations

Operate in a particular 'working directory' (identify using **getwd( )**)
Move to other locations using **setwd( )**

```
libname library_name "file_location";
data library_name.saved_data;
 set data_in_use;
run;
```

```
save(data_in_use , file="file_location/saved_data.rda")
or
setwd("file_location")
save( data_in_use , file = "saved_data.rda")
```

```
libname library_name "file_location";
data data_in_use ;
 set library_name.saved_data ;
run;
```

```
load("file_location/saved_data.rda" )
or
setwd("file_location")
load("saved_data.rda")
```

save( ) *can store multiple data frames in a single .rda file,* load( ) *will restore all of these*

```
proc import datafile = "my_file.csv"
 out = my_data dbms = csv;
run;
```

```
my_data <- read_csv("my_file.csv")
```

Both examples assume column headers in csv file

Spatial manipulation with sf: : CHEAT SHEET

The sf package provides a set of tools for working with geospatial vectors, i.e. points, lines, polygons, etc.

Geometric confirmation

st_contains(x, y, ...) Identifies if y is within x (i.e. point within polygon)

st_covered_by(x, y, ...) Identifies if x is completely within y (i.e. polygon completely within polygon)

st_covers(x, y, ...) Identifies if any point from x is outside of y (i.e. polygon outside polygon)

st_crosses(x, y, ...) Identifies if any geometry of x have commonalities with y

st_disjoint(x, y, ...) Identifies when geometries from x do not share space with y

st_equals(x, y, ...) Identifies if x and y share the same geometry

st_intersects(x, y, ...) Identifies if x and y geometry share any space

st_overlaps(x, y, ...) Identifies if geometries of x and y share space, are of the same dimension, but are not completely contained by each other

st_touches(x, y, ...) Identifies if geometries of x and y share a common point but their interiors do not intersect

st_within(x, y, ...) Identifies if x is in a specified distance to y

Geometric operations

st_boundary(x) Creates a polygon that encompasses the full extent of the geometry

st_buffer(x, dist, nQuadSegs) Creates a polygon covering all points of the geometry within a given distance

st_centroid(x, ..., of_largest_polygon) Creates a point at the geometric centre of the geometry

st_convex_hull(x) Creates geometry that represents the minimum convex geometry of x

st_line_merge(x) Creates linestring geometry from sewing multi linestring geometry together

st_node(x) Creates nodes on overlapping geometry where nodes do not exist

st_point_on_surface(x) Creates a point that is guarenteed to fall on the surface of the geometry

st_polygonize(x) Creates polygon geometry from linestring geometry

st_segmentize(x, dfMaxLength, ...) Creates linesting geometry from x based on a specified length

st_simplify(x, preserveTopology, dTolerance) Creates a simplified version of the geometry based on a specified tolerance

Geometry creation

st_triangulate(x, dTolerance, bOnlyEdges) Creates polygon geometry as triangles from point geometry

st_voronoi(x, envelope, dTolerance, bOnlyEdges) Creates polygon geometry covering the envolope of x, with x at the centre of the geometry

st_point(x, c(numeric vector), dim = "XYZ") Creating point geometry from numeric values

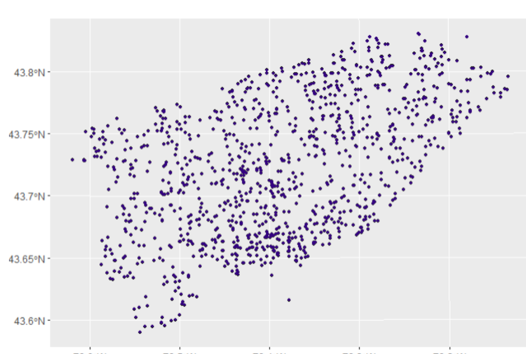
st_multipoint(x = matrix(numeric values in rows), dim = "XYZ") Creating multi point geometry from numeric values

st_linestring(x = matrix(numeric values in rows), dim = "XYZ") Creating linestring geometry from numeric values

st_multilinestring(x = list(numeric matricesin rows), dim = "XYZ") Creating multi linestring geometry from numeric values

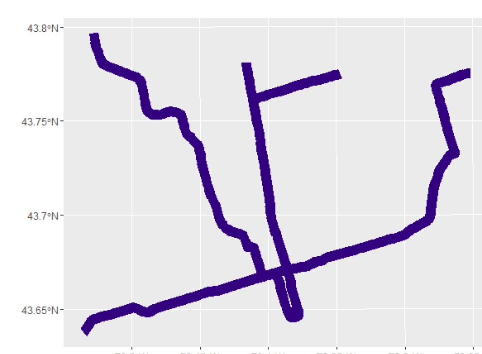
st_polygon(x = list(numeric matrices in rows), dim = "XYZ") Creating polygon geometry from numeric values

st_multipolygon(x = list(numeric matrices in rows), dim = "XYZ") Creating multi polygon geometry from numeric values



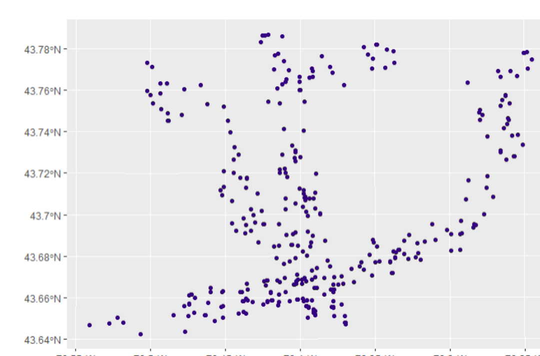
```
ggplot() +
  geom_sf(data = schools)
```

\+



```
ggplot() +
  geom_sf(data = subway)
```

=>



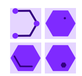
```
ggplot() +
  geom_sf(data = st_intersection(schools, st_buffer(subway, 1000)))
```

This cheatsheet presents the sf package [Edzer Pebesma 2018] in version 0.6.3. See https://github.com/r-spatial/sf for more details.

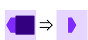
Spatial manipulation with sf: : CHEAT SHEET

The sf package provides a set of tools for working with geospatial vectors, i.e. points, lines, polygons, etc.

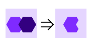
Geometry operations



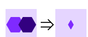
st_contains(x, y, ...) Identifies if y is within x (i.e. point within polygon)



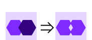
st_crop(x, y, ..., xmin, ymin, xmax, ymax) Creates geometry of x that intersects a specified rectangle



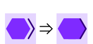
st_difference(x, y) Creates geometry from x that does not intersect with y



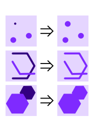
st_intersection(x, y) Creates geometry of the shared portion of x and y



st_sym_difference(x, y) Creates geometry representing portions of x and y that do not intersect



st_snap(x, y, tolerance) Snap nodes from geometry x to geometry y



st_union(x, y, ..., by_feature) Creates multiple geometries into a a single geometry, consisiting of all geometry elements

Geometric measurement

st_area(x) Calculate the surface area of a polygon geometry based on the current coordinate reference system

st_distance(x, y, ..., dist_fun, by_element, which) Calculates the 2D distance between x and y based on the current coordinate system

st_length(x) Calculates the 2D length of a geometry based on the current coordinate system

Misc operations

st_as_sf(x, ...) Create a sf object from a non-geospatial tabular data frame

st_cast(x, to, ...) Change x geometry to a different geometry type

st_coordinates(x, ...) Creates a matrix of coordinate values from x

st_crs(x, ...) Identifies the coordinate reference system of x

st_join(x, y, join, FUN, suffix, ...) Performs a spatial left or inner join between x and y

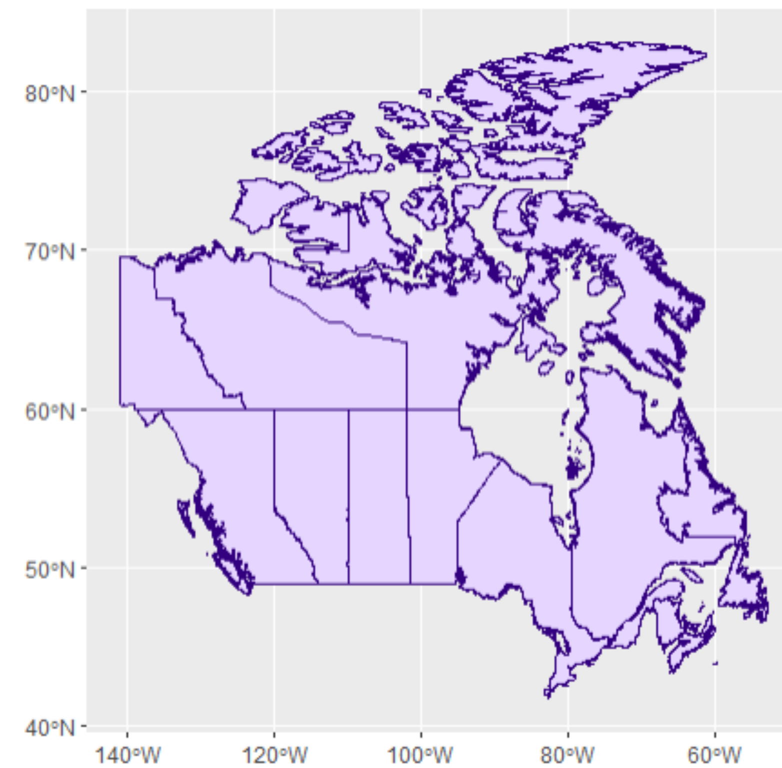
st_make_grid(x, cellsize, offset, n, crs, what) Creates rectangular grid geometry over the bounding box of x

st_nearest_feature(x, y) Creates an index of the closest feature between x and y

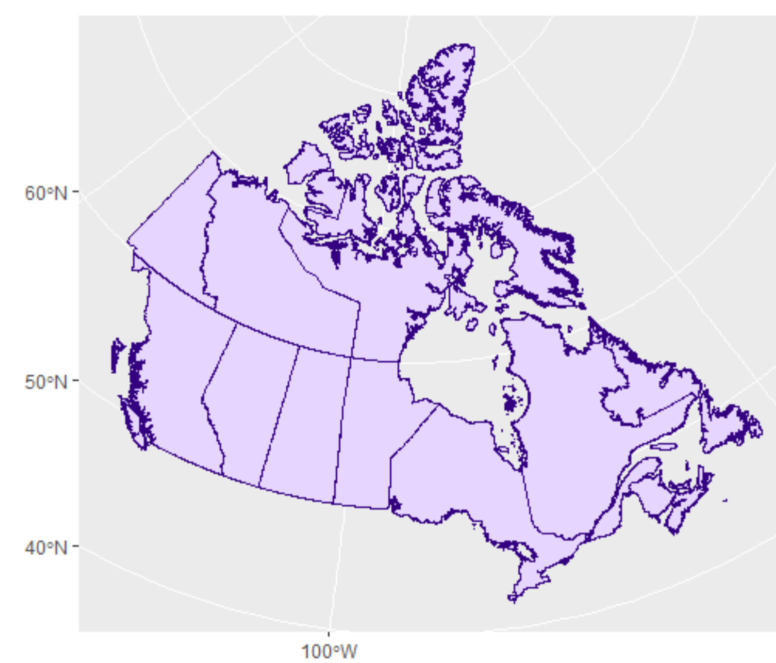
st_nearest_points(x, y, ...) Returns the closest point between x and y

st_read(dsn, layer, ...) Read file or database vector dataset as a sf object

st_transform(x, crs, ...) Convert coordinates of x to a different coordinate reference system




```
ggplot() +
  geom_sf(data = cdn) +
  coord_sf(crs = st_crs(4326))
```




```
ggplot() +
  geom_sf(data = cdn) +
  coord_sf(crs = st_crs(3347))
```

Shiny : : CHEAT SHEET

Building an App

A **Shiny** app is a web page (**ui**) connected to a computer running a live R session (**server**).

Users can manipulate the UI, which will cause the server to update the UI's displays (by running R code).

Save your template as **app.R**. Keep your app in a directory along with optional extra files.

To generate the template, type **shinyapp** and press **Tab** in the RStudio IDE or go to **File > New Project > New Directory > Shiny Web Application**

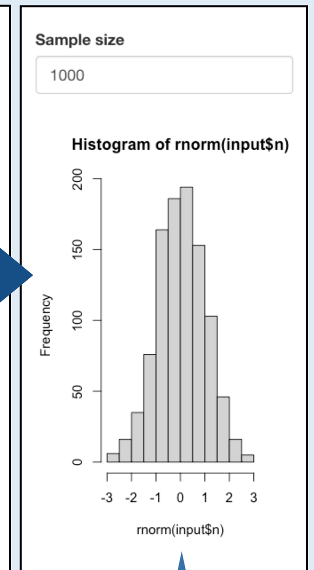
```
# app.R
library(shiny)

ui <- fluidPage(
  numericInput(inputId = "n",
    "Sample size", value = 25),
  plotOutput(outputId = "hist")
)

server <- function(input, output, session) {
  output$hist <- renderPlot({
    hist(rnorm(input$n))
  })
}

shinyApp(ui = ui, server = server)
```

- In **ui** nest R functions to build an HTML interface
- Customize the UI with **Layout Functions**
- Add Inputs with ***Input() functions**
- Add Outputs with ***Output() functions**
- Tell the **server** how to render outputs and respond to inputs with R
- Wrap code in **render*() functions** before saving to output
- Refer to UI inputs with **input$<id>** and outputs with **output$<id>**
- Call **shinyApp()** to combine **ui** and **server** into an interactive app!



- **app-name** — The directory name is the app name
- **app.R**
- **DESCRIPTION** — (optional) used in showcase mode
- **README**
- **R/** — (optional) directory of supplemental .R files that are sourced automatically, must be named **"R"**
- **www/** — (optional) directory of files to share with web browsers (images, CSS, .js, etc.), must be named **"www"**

Launch apps stored in a directory with **runApp(**<path to directory>**)**.

See annotated examples of Shiny apps by running **runExample(**<example name>**)**. Run **runExample()** with no arguments for a list of example names.

Share

Share your app in three ways:

1. **Host it on shinyapps.io**, a cloud based service from RStudio. To deploy Shiny apps:
   - Create a free or professional account at **shinyapps.io**
   - Click the Publish icon in RStudio IDE, or run: **rsconnect::deployApp(**"<path to directory>"**)**
2. **Purchase RStudio Connect**, a publishing platform for R and Python. **rstudio.com/products/connect/**
3. **Build your own Shiny Server** **rstudio.com/products/shiny/shiny-server/**

Outputs

render*() and *Output() functions work together to add R output to the UI.

DT::**renderDataTable(**expr, options, searchDelay, callback, escape, env, quoted, outputArgs**)**	**dataTableOutput(**outputId**)**
renderImage(expr, env, quoted, deleteFile, outputArgs**)**	**imageOutput(**outputId, width, height, click, dblclick, hover, brush, inline**)**
renderPlot(expr, width, height, res, …, alt, env, quoted, execOnResize, outputArgs**)**	**plotOutput(**outputId, width, height, click, dblclick, hover, brush, inline**)**
renderPrint(expr, env, quoted, width, outputArgs**)**	**verbatimTextOutput(**outputId, placeholder**)**
renderTable(expr, striped, hover, bordered, spacing, width, align, rownames, colnames, digits, na, …, env, quoted, outputArgs**)**	**tableOutput(**outputId**)**
renderText(expr, env, quoted, outputArgs, sep**)**	**textOutput(**outputId, container, inline**)**
renderUI(expr, env, quoted, outputArgs**)**	**uiOutput(**outputId, inline, container, …**)** **htmlOutput(**outputId, inline, container, …**)**

These are the core output types. See **htmlwidgets.org** for many more options.

Inputs

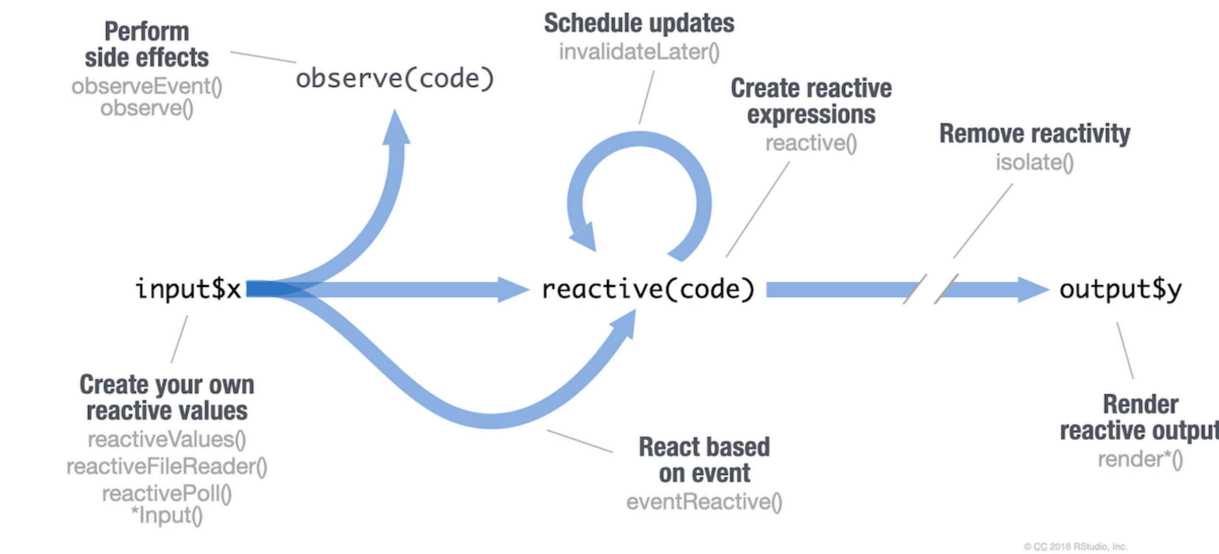
Collect values from the user.

Access the current value of an input object with **input$<inputId>**. Input values are **reactive**.

- **actionButton(**inputId, label, icon, width, …**)**
- **actionLink(**inputId, label, icon, …**)**
- **checkboxGroupInput(**inputId, label, choices, selected, inline, width, choiceNames, choiceValues**)**
- **checkboxInput(**inputId, label, value, width**)**
- **dateInput(**inputId, label, value, min, max, format, startview, weekstart, language, width, autoclose, datesdisabled, daysofweekdisabled**)**
- **dateRangeInput(**inputId, label, start, end, min, max, format, startview, weekstart, language, separator, width, autoclose**)**
- **fileInput(**inputId, label, multiple, accept, width, buttonLabel, placeholder**)**
- **numericInput(**inputId, label, value, min, max, step, width**)**
- **passwordInput(**inputId, label, value, width, placeholder**)**
- **radioButtons(**inputId, label, choices, selected, inline, width, choiceNames, choiceValues**)**
- **selectInput(**inputId, label, choices, selected, multiple, selectize, width, size**)** Also **selectizeInput()**
- **sliderInput(**inputId, label, min, max, value, step, round, format, locale, ticks, animate, width, sep, pre, post, timeFormat, timezone, dragRange**)**
- **submitButton(**text, icon, width**)** (Prevent reactions for entire app)
- **textInput(**inputId, label, value, width, placeholder**)** Also **textAreaInput()**

Reactivity

Reactive values work together with reactive functions. Call a reactive value from within the arguments of one of these functions to avoid the error `Operation not allowed without an active reactive context.`



CREATE YOUR OWN REACTIVE VALUES

```
# *Input() example
ui <- fluidPage(
  textInput("a","","A")
)
```

```
#reactiveValues example
server <-
function(input,output){
  rv <- reactiveValues()
  rv$number <- 5
}
```

***Input() functions** (see front page)

Each input function creates a reactive value stored as **input$<inputId>**.

reactiveValues(...**)**

Creates a list of reactive values whose values you can set.

CREATE REACTIVE EXPRESSIONS

```
library(shiny)
ui <- fluidPage(
  textInput("a","","A"),
  textInput("z","","Z"),
  textOutput("b"))

server <-
function(input,output){
  re <- reactive({
paste(input$a,input$z)})
  output$b <- renderText({
    re()
  })
}
shinyApp(ui, server)
```

reactive(x, env, quoted, label, domain**)**

Reactive expressions:
- **cache** their value to reduce computation
- can be called elsewhere
- notify dependencies when invalidated

Call the expression with function syntax, e.g. `re()`.

REACT BASED ON EVENT

```
library(shiny)
ui <- fluidPage(
  textInput("a","","A"),
  actionButton("go","Go"),
  textOutput("b")
)

server <-
function(input,output){
  re <- eventReactive(
  input$go,{input$a})
  output$b <- renderText({
    re()
  })
}
shinyApp(ui, server)
```

eventReactive(eventExpr, **valueExpr,** event.env, event.quoted, value.env, value.quoted, ..., label, domain, ignoreNULL, ignoreInit**)**

Creates reactive expression with code in 2nd argument that only invalidates when reactive values in 1st argument change.

RENDER REACTIVE OUTPUT

```
library(shiny)
ui <- fluidPage(
  textInput("a","","A"),
  textOutput("b")
)

server <-
function(input,output){
  output$b <-
    renderText({
      input$a
    })
}

shinyApp(ui, server)
```

render*() functions (see front page)

Builds an object to display. Will rerun code in body to rebuild the object whenever a reactive value in the code changes.

Save the results to **output$<outputId>**.

PERFORM SIDE EFFECTS

```
library(shiny)
ui <- fluidPage(
  textInput("a","","A"),
  actionButton("go","Go")
)

server <-
function(input,output){
  observeEvent(input$go,{
    print(input$a)
  })
}

shinyApp(ui, server)
```

observeEvent(eventExpr, **handlerExpr,** event.env, event.quoted, handler.env, handler.quoted, ..., label, suspended, priority, domain, autoDestroy, ignoreNULL, ignoreInit, once**)**

Runs code in 2nd argument when reactive values in 1st argument change. See **observe()** for alternative.

REMOVE REACTIVITY

```
library(shiny)
ui <- fluidPage(
  textInput("a","","A"),
  textOutput("b")
)

server <-
function(input,output){
  output$b <-
    renderText({
      isolate({input$a})
    })
}

shinyApp(ui, server)
```

isolate(expr**)**

Runs a code block. Returns a **non-reactive** copy of the results.

UI - An app's UI is an HTML document.

Use Shiny's functions to assemble this HTML with R.

```
fluidPage(
  textInput("a","")
)
## <div class="container-fluid">
##   <div class="form-group shiny-input-container">
##     <label for="a"></label>
##     <input id="a" type="text"
##        class="form-control" value=""/>
##   </div>
## </div>
```

Returns HTML

HTML

Add static HTML elements with **tags**, a list of functions that parallel common HTML tags, e.g. **tags$a()**. Unnamed arguments will be passed into the tag; named arguments will become tag attributes.

Run **names(tags)** for a complete list.
`tags$h1("Header") -> <h1>Header</h1>`

The most common tags have wrapper functions. You do not need to prefix their names with **tags$**

```
ui <- fluidPage(
  h1("Header 1"),
  hr(),
  br(),
  p(strong("bold")),
  p(em("italic")),
  p(code("code")),
  a(href="", "link"),
  HTML("<p>Raw html</p>")
)
```

CSS

To include a CSS file, use **includeCSS()**, or
1. Place the file in the **www** subdirectory
2. Link to it with:

```
tags$head(tags$link(rel = "stylesheet",
  type = "text/css", href = "<file name>"))
```

JS

To include JavaScript, use **includeScript()** or
1. Place the file in the **www** subdirectory
2. Link to it with:

```
tags$head(tags$script(src = "<file name>"))
```

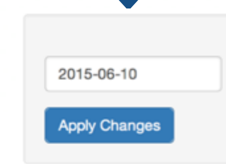
IMAGES

To include an image:
1. Place the file in the **www** subdirectory
2. Link to it with `img(src="<file name>")`

Layouts

Combine multiple elements into a "single element" that has its own properties with a panel function, e.g.

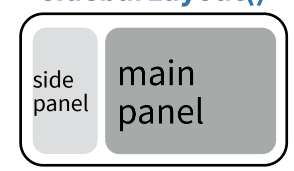
```
wellPanel(
  dateInput("a", ""),
  submitButton()
)
```



absolutePanel()
conditionalPanel()
fixedPanel()
headerPanel()
inputPanel()
mainPanel()
navlistPanel()
sidebarPanel()
tabPanel()
tabsetPanel()
titlePanel()
wellPanel()

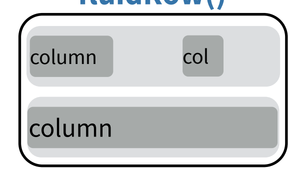
Organize panels and elements into a layout with a layout function. Add elements as arguments of the layout functions.

sidebarLayout()



ui <- fluidPage(
sidebarLayout(
sidebarPanel(),
mainPanel()
)
)

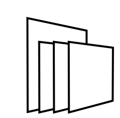
fluidRow()



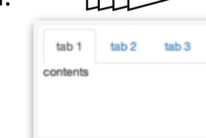
ui <- fluidPage(
fluidRow(column(width = 4**),**
column(width = 2, offset = 3**)),**
fluidRow(column(width = 12**))**
)

Also **flowLayout()**, **splitLayout()**, **verticalLayout()**, **fixedPage()**, and **fixedRow()**.

Layer tabPanels on top of each other, and navigate between them, with:

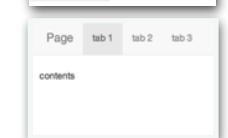


ui <- fluidPage(**tabsetPanel(**
tabPanel("tab 1", "contents"),
tabPanel("tab 2", "contents"),
tabPanel("tab 3", "contents")**))**



ui <- fluidPage(**navlistPanel(**
tabPanel("tab 1", "contents"),
tabPanel("tab 2", "contents"),
tabPanel("tab 3", "contents")**))**

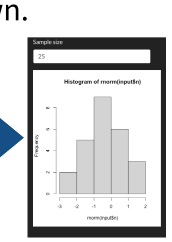
ui <- **navbarPage(**title = "Page",
tabPanel("tab 1", "contents"),
tabPanel("tab 2", "contents"),
tabPanel("tab 3", "contents")**)**



Themes

Use the **bslib** package to add existing themes to your Shiny app ui, or make your own.

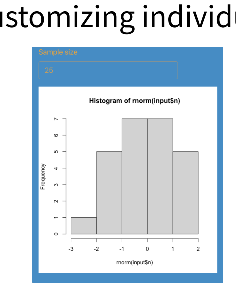
```
library(bslib)
ui <- fluidPage(
  theme = bs_theme(
    bootswatch = "darkly",
    ...
  )
)
```



bootswatch_themes() Get a list of themes.

Build your own theme by customizing individual arguments.

bs_theme(bg = "#558AC5",
fg = "#F9B02D",
...**)**



?bs_theme for a full list of arguments.

bs_themer() Place within the server function to use the interactive theming widget.

Data & Variable Transformation with sjmisc Cheat Sheet

sjmisc complements dplyr, and helps with data transformation tasks and recoding *variables*.

sjmisc works together seamlessly with dplyr and pipes. All functions are designed to support labelled data.

Design Philosophy

The design of sjmisc functions follows the tidyverse-approach: first argument is always the data (either a *data frame* **or** *vector*), followed by variable names to be processed by the functions.

The returned object for each function *equals the type of the data-argument*.

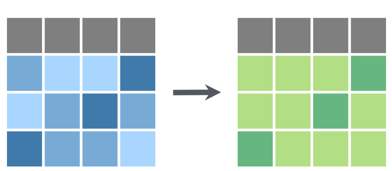
Vector input

- If the data-argument is a *vector*, functions return a *vector*.

rec(mtcars$carb, rec = "1,2=1; 3,4=2; else=3")

Data frame input

- If the data-argument is a *data frame*, functions return a *data frame*.



rec(mtcars, carb, rec = "1,2=1; 3,4=2; else=3")

The …-ellipses Argument

Apply functions to a single variable, selected variables or to a complete data frame.

Variable selection is powered by dplyr's select(): Separate variables with comma, or use dplyr's select-helpers to select variables, e.g. *?rec*:

```
rec(mtcars, one_of(c("gear", "carb")),
    rec = "min:3=1; 4:max=2")
rec(mtcars, gear, carb, rec = "min:3=1; 4:max=2")
```

Descriptives and Summaries

Most of the sjmisc functions (including recode-functions) also work on grouped data frames:

```
library(dplyr)
efc %>%
  group_by(e16sex, c172code) %>%
  frq(e42dep)
```

Frequency Tables

frq(x, ..., sort.frq = c("none", "asc", "desc"), weight.by = NULL, auto.grp = NULL, …)

Print frequency tables of (labelled) vectors. Uses variable labels as table header.

data(efc); frq(efc, e42dep, c161sex)

Use this data set in examples!

flat_table(data, ..., margin = c("counts", "cell", "row", "col"), digits = 2, show.values = FALSE)

Print contingency tables of (labelled) vectors. Uses value labels.

flat_table(efc, e42dep, c172code, e16sex)

count_na(x, ...)

Print frequency table of tagged NA values.

```
library(haven); x <- labelled(c(1:3,
tagged_na("a",   "a", "z")), labels =
c("Refused" = tagged_na("a"), "N/A" =
tagged_na("z")))
count_na(x)
```

Descriptive Summary

descr(x, ..., max.length = NULL)

Descriptive summary of data frames, including variable labels in output.

descr(efc, contains("cop"), max.length = 20)

Finding Variables in a Data Frame

Use find_var() to search for variables by names, value or variable labels. Returns vector/data frame.

```
# variables with "cop" in names and variable labels
find_var(efc, pattern = "cop", out = "df")

# variables with "level" in names and value labels
find_var(efc, "level", search = "name_value")
```

Recode and Transform Variables

Recode functions add a *suffix* to new variables, so original variables are preserved.

By default, original input data frame and new created variables are returned. Use *append = FALSE* to return the recoded variables only.

rec(x, ..., rec, as.num = TRUE, var.label = NULL, val.labels = NULL, append = TRUE, suffix = "_r")

Recode values, return result as numeric, character or categorical (factor).

rec(mtcars, carb, rec = "1,2=1; 3,4=2; else=3")

dicho(x, ..., dich.by = "median", as.num = FALSE, var.label = NULL, val.labels = NULL, append = TRUE, suffix = "_d")

Dichotomise variable by median, mean or specific value.

dicho(mtcars, disp)

split_var(x, ..., n, as.num = FALSE, val.labels = NULL, var.label = NULL, inclusive = FALSE, append = TRUE, suffix = "_g")

Split variable into equal sized groups. Unlike dplyr::ntile(), does not split original categories into different values (see examples in ?split_var).

split_var(mtcars, mpg, disp, n = 3)

group_var(x, ..., size = 5, as.num = TRUE, right.interval = FALSE, n = 30, append = TRUE, suffix = "_gr")

Split variable into groups with equal value range, or into a max. # of groups (value range per group is adjusted to match # of groups).

group_var(mtcars, mpg, disp, size = 5)
group_var(mtcars, mpg, size = "auto", n = 4)

std(x, ..., robust = "sd", include.fac = FALSE, append = TRUE, suffix = "_z")

Z-standardise variables. Also center().

std(efc, e17age, c160age)

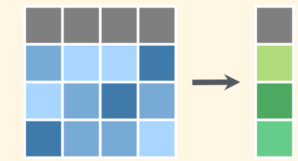
recode_to(x, ..., lowest = 0, highest = -1, append = TRUE, suffix = "_r0")

Shift ("renumber") categories or values.

recode_to(mtcars$gear)

Summarise Variables and Cases

The summary functions mostly mimic base R equivalents, but are designed to work together with pipes and dplyr.



row_sums(x, ..., na.rm = TRUE, var = "rowsums", append = FALSE)

Row sums of data frames.

row_sums(efc, c82cop1:c90cop9)

row_means(x, ..., n, var = "rowmeans", append = FALSE)

Row means, for at least n valid (non-NA) values.

row_means(efc, c82cop1:c90cop9, n = 7)

row_count(x, ..., count, var = "rowcount", append = FALSE)

Row-wise count # of values in data frames. Also col_count().

row_count(efc, c82cop1:c90cop9, count = 2)

Other Useful Functions

- add_columns() and replace_columns() to combine data frames, but either replace or preserve existing columns.
- set_na() and replace_na() to convert regular into missing values, or vice versa. replace_na() also replaces specific tagged NA values only.
- remove_var() and var_rename() to remove variables from data frames, or rename variables.
- group_str() to group similar string values. Useful for variables with similar, but not identically spelled string values that should be "merged".
- merge_df() to full join data frames and preserve value and variable labels.
- to_long() to gather multiple columns in data frames from wide into long format.

Use with %>% and dplyr

```
# use sjmisc-functions in pipes
mtcars %>% select(gear, carb) %>%
  rec(rec = "min:3=1; 4:max=2")

# use sjmisc-function inside mutate
mtcars %>% select(gear, carb) %>% mutate(
  carb2 = rec(carb, rec = "1,2=0;3:8=1"),
  gear2 = rec(gear, rec = "3=1;4:max=2"))
```

slackr : : CHEAT SHEET

Send files, messages, R objects, and images to Slack directly from R

Installation

CRAN version
```
install.packages("slackr")
```
Development version
```
devtools::install_github("mrkaye97/slackr")
```

Setup

i. Go to https://api.slack.com/apps
ii. Click "**Create New App**" and then follow the setup instructions

Multi-channel bot

1. Click "**OAuth & Permissions**" under "**Features**"
2. Enable the following scopes in order to get all of the functionality:
   - `channels:read`
   - `chat:write`
   - `users:read`
   - `chat:write.customize`
   - `files:read`
   - `chat:write.public`
   - `groups:read`
   - `im:write`
   - `groups:write`
   - `incoming-webhook`
   - `channels:history`
3. Click "**Install to Workspace**"
4. Select a channel (for webhook messages)
5. Copy the Bot User OAuth Access Token
6. Click "**Incoming Webhooks**" under "**Features**"
7. Copy the Webhook URL

Single-channel bot

1. Click "**Incoming "Webhooks**" under "**Features**"
2. Turn the "**Activate Incoming Webhooks**" switch on
3. Click "**Add New Webhook to Workspace**"
4. Select the channel you'd like the bot to post to
5. Copy the Webhook URL

Setup environment variables for Slack API access
```
slackr_setup(
  channel = "#general",
  username = "slackr",
  icon_emoji = "",
  incoming_webhook_url = "",
  bot_user_oauth_token = "",
  config_file = "~/.slackr",
  echo = FALSE,
  cacheChannels = TRUE,
  cache_dir = ""
)
```

Generate Config Text (.txt) File (optional)
bot_user_oauth_token: xoxb-[...]
channel: #yourchannel
username: yourusername
incoming_webhook_url: https://hooks.slack.com/services/XXXXX/XXXXX/XXXXX

Common Functions

Post a ggplot to a Slack channel
```
ggslackr(
  plot = last_plot(),
  channels = Sys.getenv("SLACK_CHANNEL"),
  scale = 1,
  width = par("din")[1],
  height = par("din")[2],
  units = c("in", "cm", "mm"),
  dpi = 300,
  limitsize = TRUE,
  bot_user_oauth_token =
    Sys.getenv("SLACK_BOT_USER_OAUTH_TOKEN"),
  file = "ggplot",
  ...
)
```

Save R objects to an RData file on Slack
```
save_slackr(
  ...,
  channels = Sys.getenv("SLACK_CHANNEL"),
  file = "slackr",
  bot_user_oauth_token =
    Sys.getenv("SLACK_BOT_USER_OAUTH_TOKEN"),
  plot_text = ""
)
```

Send result of R expressions to a Slack channel via webhook API
```
slackr_bot(
  ...,
  channel = "",
  username = "",
  icon_emoji = "",
  incoming_webhook_url =
    Sys.getenv("SLACK_INCOMING_URL_PREFIX")
)
```

Delete the specified number of messages from the channel
```
slackr_delete(
  count,
  channel = Sys.getenv("SLACK_CHANNEL"),
  bot_user_oauth_token =
    Sys.getenv("SLACK_BOT_USER_OAUTH_TOKEN")
)
```

Send a message to a Slack channel
```
slackr_msg(
  txt = "",
  channel = Sys.getenv("SLACK_CHANNEL"),
  username = Sys.getenv("SLACK_USERNAME"),
  icon_emoji = Sys.getenv("SLACK_ICON_EMOJI"),
  bot_user_oauth_token =
    Sys.getenv("SLACK_BOT_USER_OAUTH_TOKEN"),
  ...
)
```

Send a file to Slack
```
slackr_upload(
  filename,
  title = basename(filename),
  initial_comment = basename(filename),
  channels = Sys.getenv("SLACK_CHANNEL"),
  bot_user_oauth_token =
    Sys.getenv("SLACK_BOT_USER_OAUTH_TOKEN")
)
```

Other Usages

`auth_test()`	Checks authentication & identity against the Slack API
`call_slack_api()`	A wrapper function to call the Slack API with authentication and pagination
`convert_response_to_tibble()`	Convert Slack API json response to tibble
`register_onexit()`	Append text_slackr as on.exit to functions
`slackr_census_fun()`	Create a cache of the users and channels in the workspace in order to limit API requests
`slackr_channels()`	Get a data frame of Slack channels
`slackr_chtrans()`	Translate vector of channel names to channel IDs for API
`slackr_dev()`	Send the graphics contents of the current device to a Slack channel
`slackr_history()`	Reads history of a channel
`slackr_ims()`	Get a data frame of Slack IM IDs
`slackr_users()`	Get a data frame of Slack users
`text_slackr()`	Sends basic text to a slack channel
`tex_slackr()`	Post a tex output to a Slack channel
`with_pagination()`	Calls the slack API with pagination using cursors

Vignettes

Creating a single-channel bot
```
vignette('webhook-setup', package = 'slackr')
```
Creating a fully-functional multi-channel bot
```
vignette('scoped-bot-setup', package = 'slackr')
```
Usage
```
vignette('using-slackr', package = 'slackr')
```

Data Science in Spark with *sparklyr* : : CHEAT SHEET

Intro

***sparklyr* is an R interface for Apache Spark™.**
It enables us to write all of our analysis code in R, but have the actual processing happen inside Spark clusters. Easily manipulate and model large-scale using R and Spark via *sparklyr.*

Import
- From R (**copy_to()**)
- Read a file (**spark_read_**)
- Read Hive table (**tbl()**)

Wrangle
- **dplyr** verb
- **tidyr** commands
- Feature transformer (**ft_**)
- Direct Spark SQL (**DBI**)

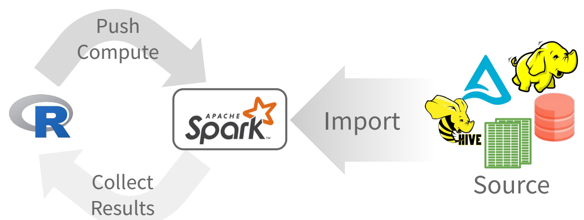
Visualize
- Collect result, plot in R

Model
- Spark MLlib (**ml_**)
- H2O Extension

Communicate
Collect results into R share using **RMarkdown**

R for Data Science, Grolemund & Wickham

Import



Import data into Spark, not R

READ A FILE INTO SPARK

Arguments that apply to all functions:
sc, name, path, options=list(), repartition=0, memory=TRUE, overwrite=TRUE

CSV **spark_read_csv(** header = TRUE, columns=NULL, infer_schema=TRUE, delimiter = ",", quote= "\"", escape = "\\", charset = "UTF-8", null_value = NULL**)**

JSON	**spark_read_json()**
PARQUET	**spark_read_parquet()**
TEXT	**spark_read_text()**
ORC	**spark_read_orc()**
LIBSVM	**spark_read_libsvm()**
DELTA	**spark_read_delta()**
AVRO	**spark_read_avro()**

R DATA FRAME INTO SPARK

dplyr::**copy_to(**dest, df, name**)**

Apache Arrow accelerates data transfer between R and Spark. To use, simply load the library

```
library(sparklyr)
library(arrow)
```

FROM A TABLE IN HIVE

dplyr::**tbl(**scr, …**)** - Creates a reference to the table without loading it into memory

Wrangle

DPLYR VERBS

Translates into Spark SQL statements

```
copy_to(sc, mtcars) %>%
    mutate(trm = ifelse(am == 0,
        "auto", "man")) %>%
    group_by(trm) %>%
    summarise_all(mean)
```

TIDYR

pivot_longer() - Collapse several columns into two.

pivot_wider() - Expand two columns into several.

nest() / unnest() - Convert groups of cells into list-columns, and vice versa.

unite() / separate() - Split a single column into several columns, and vice versa.

fill() - Fill NA with the previous value

FEATURE TRANSFORMERS

ft_binarizer() - Assigned values based on threshold

ft_bucketizer() - Numeric column to discretized column

ft_count_vectorizer() - Extracts a vocabulary from document

ft_discrete_cosine_transform() - 1D discrete cosine transform of a real vector

ft_elementwise_product() - Element-wise product between 2 cols

ft_hashing_tf() - Maps a sequence of terms to their term frequencies using the hashing trick.

ft_idf() - Compute the Inverse Document Frequency (IDF) given a collection of documents.

ft_imputer() - Imputation estimator for completing missing values, uses the mean or the median of the columns.

ft_index_to_string() - Index labels back to label as strings

ft_interaction() - Takes in Double and Vector columns and outputs a flattened vector of their feature interactions.

ft_max_abs_scaler() - Rescale each feature individually to range [-1, 1]

ft_min_max_scaler() - Rescale each feature to a common range [min, max] linearly

ft_ngram() - Converts the input array of strings into an array of n-grams

ft_bucketed_random_projection_lsh()
ft_minhash_lsh() - Locality Sensitive Hashing functions for Euclidean distance and Jaccard distance (MinHash)

ft_normalizer() - Normalize a vector to have unit norm using the given p-norm

ft_one_hot_encoder()- Continuous to binary vectors

ft_pca() - Project vectors to a lower dimensional space of top k principal components.

ft_quantile_discretizer() - Continuous to binned categorical values.

ft_regex_tokenizer() - Extracts tokens either by using the provided regex pattern to split the text.

ft_robust_scaler() - Removes the median and scales according to standard scale.

ft_standard_scaler() - Removes the mean and scaling to unit variance using column summary statistics

ft_stop_words_remover() - Filters out stop words from input

ft_string_indexer() - Column of labels into a column of label indices.

ft_tokenizer() - Converts to lowercase and then splits it by white spaces

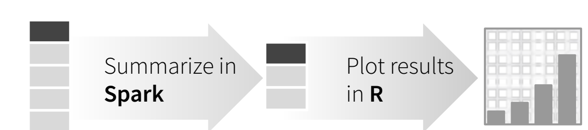
ft_vector_assembler() - Combine vectors into single row-vector

ft_vector_indexer() - Indexing categorical feature columns in a dataset of Vector

ft_vector_slicer() - Takes a feature vector and outputs a new feature vector with a subarray of the original features

ft_word2vec() - Word2Vec transforms a word into a code

Visualize



DPLYR + GGPLOT2

```
copy_to(sc, mtcars) %>%          Summarize in Spark
  group_by(cyl) %>%
  summarise(mpg_m = mean(mpg)) %>%
  collect() %>%                  Collect results in R
  ggplot() +
    geom_col(aes(cyl, mpg_m))    Create plot
```

RStudio

Data Science in Spark with *sparklyr* : : CHEAT SHEET

Modeling

REGRESSION

ml_linear_regression() - Linear regression.

ml_aft_survival_regression() - Parametric survival regression model named accelerated failure time (AFT) model

ml_generalized_linear_regression() - GLM

ml_isotonic_regression() - Currently implemented using parallelized pool adjacent violators algorithm. Only univariate (single feature) algorithm supported

ml_random_forest_regressor() - Regression using random forests.

CLASSIFICATION

ml_linear_svc() - Classification using linear support vector machines

ml_logistic_regression() - Logistic regression

ml_multilayer_perceptron_classifier() - Classification model based on the Multilayer Perceptron.

ml_naive_bayes() - It supports Multinomial NB which can handle finitely supported discrete data

ml_one_vs_rest() - Reduction of Multiclass Classification to Binary Classification. Performs reduction using one against all strategy.

TREE

ml_decision_tree_classifier()|**ml_decision_tree()** |**ml_decision_tree_regressor()** - Classification and regression using decision trees

ml_gbt_classifier()|**ml_gradient_boosted_trees()** | **ml_gbt_regressor()** - Binary classification and regression using gradient boosted trees

ml_random_forest_classifier() - Classification and regression using random forests.

ml_feature_importances() | **ml_tree_feature_importance()** - Feature Importance for Tree Models

CLUSTERING

ml_bisecting_kmeans() - A bisecting k-means algorithm based on the paper

ml_lda() | **ml_describe_topics()** | **ml_log_likelihood()** | **ml_log_perplexity()** | **ml_topics_matrix()** - LDA topic model designed for text documents.

ml_gaussian_mixture() - Expectation maximization for multivariate Gaussian Mixture Models (GMMs)

ml_kmeans() | **ml_compute_cost()** |**ml_compute_silhouette_measure()** - Clustering with support for k-means

ml_power_iteration() - For clustering vertices of a graph given pairwise similarities as edge properties.

FEATURE

ml_chisquare_test(x,features,label) - Pearson's independence test for every feature against the label

ml_default_stop_words() - Loads the default stop words for the given language

STATS

ml_summary() - Extracts a metric from the summary object of a Spark ML model

ml_corr() - Compute correlation matrix

RECOMMENDATION

ml_als() | **ml_recommend()** - Recommendation using Alternating Least Squares matrix factorization

EVALUATION

ml_clustering_evaluator() - Evaluator for clustering

ml_evaluate() - Compute performance metrics

ml_binary_classification_evaluator() | **ml_binary_classification_eval()** | **ml_classification_eval()** - A set of functions to calculate performance metrics for prediction models.

FREQUENT PATTERN

ml_fpgrowth() | **ml_association_rules()** | **ml_freq_itemsets()** - A parallel FP-growth algorithm to mine frequent itemsets.

ml_freq_seq_patterns() | **ml_prefixspan()** - PrefixSpan algorithm for mining frequent itemsets.

UTILITIES

ml_call_constructor() - Identifies the associated sparklyr ML constructor for the JVM

ml_model_data() - Extracts data associated with a Spark ML model

ml_standardize_formula() - Generates a formula string from user inputs, to be used in `ml_model` constructor

ml_uid() - Extracts the UID of an ML object.

ML Pipelines

*Easily create a formal Spark Pipeline models using R. Save the Pipeline in native Sacala. The saved model will have **no dependencies** on R.*

INITIALIZE AND TRAIN

ml_pipeline() - Initializes a new Spark Pipeline

ml_fit() - Trains the model, outputs a Spark Pipeline Model.

SAVE AND RETRIEVE

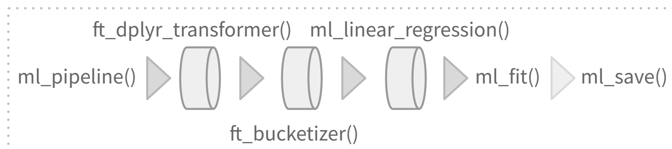
ml_save() - Saves into a format that can be read by Scala and PySpark .

ml_read() - Reads Spark object into sparklyr.

SQL AND DPLYR

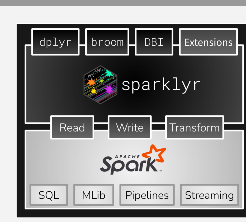
ft_sql_transformer() - Creates a Pipeline step based on the SQL statement passed to the command.

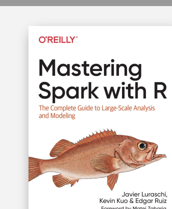
ft_dplyr_transformer() - Creates a Pipeline step based on one or several dplyr commands.



spark.rstudio.com/guides/pipelines

More Info





spark.rstudio.com therinspark.com

Sessions

YARN CLIENT

1. Install RStudio Server on an edge node
2. Locate path to the cluster's Spark Home Directory, it normally is **"/usr/lib/spark"**
3. Basic configuration example

```
conf <- spark_config()
conf$spark.executor.memory <- "300M"
conf$spark.executor.cores <- 2
conf$spark.executor.instances <- 3
conf$spark.dynamicAllocation.enabled<-"false"
```

4. Open a connection

```
sc <- spark_connect(master = "yarn",
             spark_home = "/usr/lib/spark/",
             version = "2.1.0", config = conf)
```

YARN CLUSTER

1. Make sure to have copies of the **yarn-site.xml** and **hive-site.xml** files in the RStudio Server
2. Point environment variables to the correct paths

```
Sys.setenv(JAVA_HOME="[Path]")
Sys.setenv(SPARK_HOME ="[Path]")
Sys.setenv(YARN_CONF_DIR ="[Path]")
```

3. Open a connection

```
sc <- spark_connect(master = "yarn-cluster")
```

STANDALONE CLUSTER

1. Install RStudio Server on one of the existing nodes or a server in the same LAN
2. Open a connection

```
spark_connect(master="spark://host:port",
   version = "2.0.1",
   spark_home = [path to Spark])
```

LOCAL MODE

No cluster required. Use for learning purposes only

1. Install a local version of Spark: `spark_install()`
2. Open a connection

```
sc <- spark_connect(master="local")
```

KUBERNETES

1. Use the following to obtain the Host and Port

```
system2("kubectl", "cluster-info")
```

2. Open a connection

```
sc <- spark_connect(config =
    spark_config_kubernetes(
     "k8s://https://[HOST]>:[PORT]",
      account = "default",
      image = "docker.io/owner/repo:version"))
```

CLOUD

Databricks - `spark_connect(method = "databricks")`

Qubole- `spark_connect(method = "qubole")`

RStudio

Stata to R :: CHEAT SHEET

Introduction

This cheat sheet summarizes common Stata commands for econometric analysis and provides their equivalent expression in R.

References for importing/cleaning data, manipulating variables, and other basic commands include Hanck et al. (2019), *Econometrics with R*, and Wickham and Grolemund (2017), *R for Data Science*.

Example data comes from Wooldridge *Introductory Econometrics: A Modern Approach*. Download Stata data sets here. R data sets can be accessed by installing the `wooldridge` package from CRAN.

All R commands written in base R, unless otherwise noted.

Setup

Note: While it is common to create a `log` file in Stata to store the commands and output of Stata sessions, the equivalent does not exist in R. A more savvy version in R is to create a R-markdown file to capture code and output.

```
ssc install outreg2 // install `outreg2` package. Note: unlike R packages, Stata packages do not have to be loaded each time once installed.
```

```
install.packages("wooldridge") # install `wooldridge` package

data(package = "wooldridge") # list datasets in `wooldridge` package

load(wage1) # load `wage1` dataset into session

?wage1 # consult documentation on `wage1` dataset
```

Summarize Data

example data: `wage1`

Where Stata only allows one to work with one data set at a time, multiple data sets can be loaded into the R environment simultaneously, and hence must be specified with each function call. *Note:* R does not have an equivalent to Stata's `codebook` command.

```
browse // open browser for loaded data

describe // describe structure of loaded data
summarize // display summary statistics for all variables in dataset
list in 1/6 // display first 6 rows

tabulate educ // tabulate `educ` variable frequencies
tabulate educ female // cross-tabulate `educ` and `female` frequencies
```

```
View(wage1) # open browser for loaded `wage1` data

str(wage1) # describe structure of `wage1` data
summary(wage1) # display summary statistics for `wage1` variables
head(wage1) # display first 6 (default) rows data
tail(wage1) # display last 6 rows

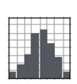
table(wage1$educ) #tabulate `educ` frequencies
table("yrs_edu" = wage1$educ, "female" = wage1$female) # tabulate `educ` frequencies name table columns
```

Tip: The {AER} package will automatically load other useful dependent packages, including: {car}, {lmtest}, {sandwich} which are used for many of the commands listed in this cheat sheet.

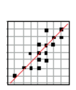
Basic plots

example data: `wage1`

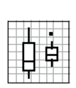
```
hist(wage) // histogram of `wage`
hist(wage), by(nonwhite) //
scatter(wage educ) // scatter plot of `wage` by `educ`
twoway (scatter wage educ) (lfit wage educ) // scatter plot with fitted line
graph box wage, by(nonwhite) // boxplot of wage by `nonwhite`
```



```
hist(wage1$wage) # histogram of `wage`
```



```
plot(y = wage$1wage, x = wage1$educ) # scatter plot
abline(lm(wage1$wage~wage1$educ), col="red") # add fitted line to scatterplot
```



```
boxplot(wage1$wage~wage1$nonwhite) # boxplot of `wage` by `nonwhite`
```

Estimate Models, 1/2

OLS

example data: `wage1`

```
reg wage educ // simple regression of `wage` by `educ` (Results printed automatically).

reg wage educ if nonwhite==1 // add condition with if statement

reg wage educ exper, robust // multiple regression using HC1 robust standard errors
reg wage educ exper, cluster(numdep) // use clustered standard errors
```

Tip: An alternate way to compute robust standard errors in R for any models not covered by {estimatr} package is load the {AER} package and run:

```
coeftest(mod1, vcov. = vcovHC, type = "HC1")
```

```
mod1 <- lm(wage ~ educ, data = wage1) # simple regression of `wage` by `educ`, store results in `mod1`
summary(mod1) # print summary of `mod1` results

mod2 <- lm(wage ~ educ, data = wage1[wage1$nonwhite==1, ]) # add condition with if statement`
mod3 <- estimatr::lm_robust(wage ~ educ + exper, data = wage1, se_type = "stata") # multiple regression with HC1 (Stata default) robust standard errors, use {estimatr} package
mod4 <- estimatr::lm_robust(wage ~ educ + exper, data = wage1, clusters = numdep) # use clustered standard errors.
```

MLE (Logit/Probit/Tobit)

example data: `mroz`

```
logit inlf nwifeinc educ // estimate logistic regression

probit inlf nwifeinc educ // estimate logistic regression

tobit hours nwifeinc educ, ll(0) // estimate tobit regression, lower-limit of y censored at zero
```

```
mod_log <- glm(inlf~nwifeinc + educ + family=binomial(link="logit"),
    data=mroz) # estimate logistic regression

mod_pro <- glm(inlf~nwifeinc + educ + family=binomial(link="probit"),
    data=mroz) # estimate logistic regression

mod_tob <- AER::tobit(hours ~ nwifeinc + educ, left = 0, data = mroz) # estimate tobit regression, lower-limit of y censored at zero, use {AER} package
```

Postestimation, 1/2

example data: `wage1`

Note: Postestimation commands in Stata apply to the most recently run estimation commands.

```
reg wage educ // estimation used for the following post-estimation commands
predict yhat // get predicted values from last estimation, store as `yhat`
predict e, res // get residuals from last estimation, store as `e`
```

```
mod1 <- lm(wage ~ educ, data = wage1) # estimation used for the following post-estimation commands
yhat <- predict(mod1) # get predicted values

e <- residuals(mod1) # get residual values
```

stata ⟷ R

Create/Edit Variables

example data: `wage1`

Note: where `Stata` only allows one to work with one data set at a time, multiple data sets can be loaded into the R environment simultaneously, hence the data set must be specified for each command.

```
gen exper2 = exper^2 // create `exper` squared variable
egen wage_avg = mean(wage) // create average wage variable
```

```
wage1$exper2 <- wage1$exper^2 # create `exper` squared variable
wage1$wage_avg <- mean(wage1$wage) # create average wage variable
```

```
drop tenursq // drop `tenursq` variable
```

```
wage1$tenursq <- NULL #drop `tenursq`
```

```
keep wage educ exper nonwhite // keep selected variables
```

```
wage1 <- wage1[ , c("wage", "educ", "exper", "nonwhite")] # keep selected variables
```

```
tab numdep, gen(numdep) // create dummy variables for `numdep`
```

```
wage1 <- fastDummies::dummy_cols(wage1, select_columns = "numdep") # create dummy variables for `numdep`, use {fastDummies} package
```

```
recode exper (1/20 = 1 "1 to 20 years") (21/40 = 2 "21 to 40 years") (41/max = 3 "41+ years"),
gen(experlvl) // recode `exper` and gen new variable
```

```
wage1$experlvl <- 3 # recode `exper`
wage1$experlvl[wage1$exper < 41] <- 2
wage1$experlvl[wage1$exper < 21] <- 1
```

Statistical tests / diagnostics

example data: `wage1`

```
reg lwage educ exper // estimation used for examples below
estat hettest // Breusch-Pagan / Cook-Weisberg test for heteroskedasticity
estat ovtest // Ramsey RESET test for omitted variables
ttest wage, by(nonwhite) // independent group t-test, compare means of same variable between groups
```

```
mod <-lm(lwage ~ educ exper, data = wage1) # estimate used for examples below
lmtest::bptest(mod) # Breusch-Pagan / Cook-Weisberg test for hetero-skedasticity using the {lmtest} package
lmtest::resettest(mod) # Ramsey RESET test
t.test(wage ~ nonwhite, data = wage1) # independent group t-test
```

Interactions, categorical/continuous variables

example data: `wage1`

In `Stata`, it is common to use special operators to specify the treatment of variables as continuous (`c.`) or categorical (`i.`). Similarly, the `#` operator denotes different ways to return the interaction of those variables. Here we show some common uses of these operators as well as their R equivalents.

```
reg lwage i.numdep // treat `numdep` as a factor variable
reg lwage c.educ#c.exper // return interaction term only
reg lwage c.educ##c.exper // return full factorial specification
reg lwage c.exper##i.numdep // return full, interact continuous and categorical
```

```
lm(lwage ~ as.factor(numdep), data = wage1) # treat `numdep` as factor
lm(lwage ~ educ:exper, data = wage1) # return interaction term only
lm(lwage ~ educ*exper, data = wage1) # return full factorial specification
lm(wage ~ exper*as.factor(numdep), data = wage1) # return full, interact continuous and categorical
```

Estimate Models, 2/2

Panel/Longitudinal

example data: `murder`

```
xtset id year // set `id` as entities (panel) and `year` as time variable
xtdescribe // describe pattern of xt data
xtsum // summarize xt data
xtreg mrdrte unem, fe // fixed effects regression
```

```
plm::is.pbalanced(murder$id, murder$year) # check panel balance with {plm} package
modfe <- plm::plm(mrdrte ~ unem, index = c("id", "year"),model = "within", data = murder) # estimate fixed effects ("within") model
summary(modfe) # display results
```

Instrumental Variables (2SLS)

example data: `mroz`

```
ivreg lwage (educ = fatheduc), first // show results of first stage regression
etest first // test IV and endogenous variable
ivreg lwage(educ = fatheduc) // show results of 2SLS directly
```

```
modiv <-AER::ivreg(lwage ~ educ | fatheduc, data = mroz) # estimate 2SLS with {AER} package
summary(modiv, diagnostics = TRUE) # get diagnostic tests of IV and endogenous variable
```

Post-estimation, 2/2

example data: `wage1`

Note: Postestimation commands in `Stata` apply to the most recently run estimation commands.

```
reg lwage educ exper##exper // estimation used for following post-estimation commands
estimates store mod1 // stores in memory the last estimation results to `mod1`
```

```
mod1 <- lm(lwage ~ educ + exper + I(exper^2), data = wage1) # Note: in R, mathematical expressions inside a formula call must be isolated with `I()`
```

```
margins // get average predictive margins
margins, dydx(*) // get average marginal effects for all variables
marginsplot // plot marginal effects
```

```
margins::prediction(mod1) # get average predictive margins with {margins} package
m1 <- margins::margins(mod1) # get average marginal effects for all variables
plot(m) # plot marginal effects
```

```
margins, dydx(exper) // average marginal effects of experience
margins, at(exper=(1(10)51)) // average predictive margins over `exper` range at 10-year increments
```

```
summary(m) # get detailed summary of marginal effects
margins::prediction(mod1, at = list(exper = seq(1,51,10))) # predictive margins over `exper` range at 10-year increments
```

```
estimates use mod1 // loads `mod1` back into working memory
estimates table mod1 mod2 // display table with stored estimation results
```

```
stargazer::stargazer(mod1, mod2, type = "text") # use {stargazer} package, with `type=text` to display results within R. Note: `type=` also can be changed for LaTex and HTML output.
```

String manipulation with stringr : : CHEAT SHEET

stringr

The **stringr** package provides a set of internally consistent tools for working with character strings, i.e. sequences of characters surrounded by quotation marks.

Detect Matches

str_detect(string, **pattern**, negate = FALSE**)** Detect the presence of a pattern match in a string. Also **str_like()**. str_detect(fruit, "a")

str_starts(string, **pattern**, negate = FALSE**)** Detect the presence of a pattern match at the beginning of a string. Also **str_ends()**. str_starts(fruit, "a")

str_which(string, **pattern**, negate = FALSE**)** Find the indexes of strings that contain a pattern match. str_which(fruit, "a")

str_locate(string, **pattern)** Locate the positions of pattern matches in a string. Also **str_locate_all()**. str_locate(fruit, "a")

str_count(string, **pattern)** Count the number of matches in a string. str_count(fruit, "a")

Subset Strings

str_sub(string, start = 1L, end = -1L**)** Extract substrings from a character vector. str_sub(fruit, 1, 3); str_sub(fruit, -2)

str_subset(string, **pattern**, negate = FALSE**)** Return only the strings that contain a pattern match. str_subset(fruit, "p")

str_extract(string, **pattern)** Return the first pattern match found in each string, as a vector. Also **str_extract_all()** to return every pattern match. str_extract(fruit, "[aeiou]")

str_match(string, **pattern)** Return the first pattern match found in each string, as a matrix with a column for each ( ) group in pattern. Also **str_match_all()**. str_match(sentences, "(a|the) ([^ +])")

Manage Lengths

str_length(string**)** The width of strings (i.e. number of code points, which generally equals the number of characters). str_length(fruit)

str_pad(string, width, side = c("left", "right", "both"), pad = " "**)** Pad strings to constant width. str_pad(fruit, 17)

str_trunc(string, width, side = c("right", "left", "center"), ellipsis = "..."**)** Truncate the width of strings, replacing content with ellipsis. str_trunc(sentences, 6)

str_trim(string, side = c("both", "left", "right")**)** Trim whitespace from the start and/or end of a string. str_trim(str_pad(fruit, 17))

str_squish(string**)** Trim whitespace from each end and collapse multiple spaces into single spaces. str_squish(str_pad(fruit, 17, "both"))

Mutate Strings

str_sub() <- value. Replace substrings by identifying the substrings with str_sub() and assigning into the results. str_sub(fruit, 1, 3) <- "str"

str_replace(string, **pattern**, replacement**)** Replace the first matched pattern in each string. Also **str_remove()**. str_replace(fruit, "p", "-")

str_replace_all(string, **pattern**, replacement**)** Replace all matched patterns in each string. Also **str_remove_all()**. str_replace_all(fruit, "p", "-")

A STRING → a string

str_to_lower(string, locale = "en"**)**[1] Convert strings to lower case. str_to_lower(sentences)

a string → A STRING

str_to_upper(string, locale = "en"**)**[1] Convert strings to upper case. str_to_upper(sentences)

a string → A String

str_to_title(string, locale = "en"**)**[1] Convert strings to title case. Also **str_to_sentence()**. str_to_title(sentences)

Join and Split

str_c(..., sep = "", collapse = NULL**)** Join multiple strings into a single string. str_c(letters, LETTERS)

str_flatten(string, collapse = ""**)** Combines into a single string, separated by collapse. str_flatten(fruit, ", ")

str_dup(string, times**)** Repeat strings times times. Also **str_unique()** to remove duplicates. str_dup(fruit, times = 2)

str_split_fixed(string, **pattern**, n**)** Split a vector of strings into a matrix of substrings (splitting at occurrences of a pattern match). Also **str_split()** to return a list of substrings and **str_split_n()** to return the nth substring. str_split_fixed(sentences, " ", n=3)

{xx} {yy}

str_glue(..., .sep = "", .envir = parent.frame()**)** Create a string from strings and {expressions} to evaluate. str_glue("Pi is {pi}")

str_glue_data(.x, ..., .sep = "", .envir = parent.frame(), .na = "NA"**)** Use a data frame, list, or environment to create a string from strings and {expressions} to evaluate. str_glue_data(mtcars, "{rownames(mtcars)} has {hp} hp")

Order Strings

str_order(x, decreasing = FALSE, na_last = TRUE, locale = "en", numeric = FALSE, ...**)**[1] Return the vector of indexes that sorts a character vector. fruit[str_order(fruit)]

str_sort(x, decreasing = FALSE, na_last = TRUE, locale = "en", numeric = FALSE, ...**)**[1] Sort a character vector. str_sort(fruit)

Helpers

str_conv(string, encoding**)** Override the encoding of a string. str_conv(fruit,"ISO-8859-1")

appl<e>
banana
p<e>ar

str_view_all(string, **pattern**, match = NA**)** View HTML rendering of all regex matches. Also **str_view()** to see only the first match. str_view_all(sentences, "[aeiou]")

str_equal(x, y, locale = "en", ignore_case = FALSE, ...**)**[1] Determine if two strings are equivalent. str_equal(c("a", "b"), c("a", "c"))

This is a long sentence. → This is a long sentence.

str_wrap(string, width = 80, indent = 0, exdent = 0**)** Wrap strings into nicely formatted paragraphs. str_wrap(sentences, 20)

[1] See **bit.ly/ISO639-1** for a complete list of locales.

RStudio

Need to Know

Pattern arguments in stringr are interpreted as regular expressions *after any special characters have been parsed.*

In R, you write regular expressions as *strings*, sequences of characters surrounded by quotes (**""**) or single quotes(**''**).

Some characters cannot be represented directly in an R string . These must be represented as **special characters**, sequences of characters that have a specific meaning., e.g.

Special Character	Represents
\\\\	\\
\\"	"
\n	new line

Run **?"'"** to see a complete list

Because of this, whenever a \ appears in a regular expression, you must write it as \\\\ in the string that represents the regular expression.

Use **writeLines()** to see how R views your string after all special characters have been parsed.

writeLines("\\\\.")
 # \\.

writeLines("\\\\ is a backslash")
 # \\ is a backslash

INTERPRETATION

Patterns in stringr are interpreted as regexs. To change this default, wrap the pattern in one of:

regex(pattern, ignore_case = FALSE, multiline = FALSE, comments = FALSE, dotall = FALSE, ...**)** Modifies a regex to ignore cases, match end of lines as well of end of strings, allow R comments within regex's , and/or to have . match everything including \n.
str_detect("I", regex("i", TRUE))

fixed() Matches raw bytes but will miss some characters that can be represented in multiple ways (fast). str_detect("\u0130", fixed("i"))

coll() Matches raw bytes and will use locale specific collation rules to recognize characters that can be represented in multiple ways (slow).
str_detect("\u0130", coll("i", TRUE, locale = "tr"))

boundary() Matches boundaries between characters, line_breaks, sentences, or words.
str_split(sentences, boundary("word"))

Regular Expressions -

Regular expressions, or *regexps*, are a concise language for describing patterns in strings.

MATCH CHARACTERS

see <- function(rx) str_view_all("abc ABC 123\t.!?\\\\(){}\n", rx)

string (type this)	regexp (to mean this)	matches (which matches this)	example	
	a (etc.)	a (etc.)	see("a")	abc ABC 123 .!?\\(){}
\\\\.	**\\.**	.	see("\\\\.")	abc ABC 123 .!?\\(){}
\\\\!	**\\!**	!	see("\\\\!")	abc ABC 123 .!?\\(){}
\\\\?	**\\?**	?	see("\\\\?")	abc ABC 123 .!?\\(){}
\\\\\\\\	****	\\	see("\\\\\\\\")	abc ABC 123 .!?\\(){}
\\\\(	**\\(**	(	see("\\\\(")	abc ABC 123 .!?\\(){}
\\\\)	**\\)**	)	see("\\\\)")	abc ABC 123 .!?\\(){}
\\\\{	**\\{**	{	see("\\\\{")	abc ABC 123 .!?\\(){}
\\\\}	**\\}**	}	see("\\\\}")	abc ABC 123 .!?\\(){}
\\\\n	**\\n**	new line (return)	see("\\\\n")	abc ABC 123 .!?\\(){}
\\\\t	**\\t**	tab	see("\\\\t")	abc ABC 123 .!?\\(){}
\\\\s	**\\s**	any whitespace (**\\S** *for non-whitespaces)*	see("\\\\s")	abc ABC 123 .!?\\(){}
\\\\d	**\\d**	any digit (**\\D** *for non-digits)*	see("\\\\d")	abc ABC 123 .!?\\(){}
\\\\w	**\\w**	any word character (**\\W** *for non-word chars)*	see("\\\\w")	abc ABC 123 .!?\\(){}
\\\\b	**\\b**	word boundaries	see("\\\\b")	abc ABC 123 .!?\\(){}
	[:digit:] [1]	digits	see("[:digit:]")	abc ABC 123 .!?\\(){}
	[:alpha:] [1]	letters	see("[:alpha:]")	abc ABC 123 .!?\\(){}
	[:lower:] [1]	lowercase letters	see("[:lower:]")	abc ABC 123 .!?\\(){}
	[:upper:] [1]	uppercase letters	see("[:upper:]")	abc ABC 123 .!?\\(){}
	[:alnum:] [1]	letters and numbers	see("[:alnum:]")	abc ABC 123 .!?\\(){}
	[:punct:] [1]	punctuation	see("[:punct:]")	abc ABC 123 .!?\\(){}
	[:graph:] [1]	letters, numbers, and punctuation	see("[:graph:]")	abc ABC 123 .!?\\(){}
	[:space:] [1]	space characters (i.e. \\s)	see("[:space:]")	abc ABC 123 .!?\\(){}
	[:blank:] [1]	space and tab (but not new line)	see("[:blank:]")	abc ABC 123 .!?\\(){}
	.	every character except a new line	see(".")	abc ABC 123 .!?\\(){}

[1] Many base R functions require classes to be wrapped in a second set of [ ], e.g. **[[:digit:]]**

[:space:]
new line

[:blank:]
space
tab

[:graph:]

[:punct:]
. , : ; ? ! / * @ #
- _ " ' [ ] { } ( )

[:symbol:]
| ` = + ^
~ < > $

[:alnum:]

[:digit:]
0 1 2 3 4 5 6 7 8 9

[:alpha:]

[:lower:]
a b c d e f
g h i j k l
m n o p q r
s t u v w x
y z

[:upper:]
A B C D E F
G H I J K L
M N O P Q R
S T U V W X
Y Z

stringr

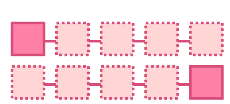
ALTERNATES

alt <- function(rx) str_view_all("abcde", rx)

regexp	matches	example	
ab|d	or	alt("ab|d")	abcde
[abe]	one of	alt("[abe]")	abcde
[^abe]	anything but	alt("[^abe]")	abcde
[a-c]	range	alt("[a-c]")	abcde

ANCHORS

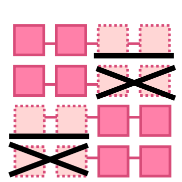
anchor <- function(rx) str_view_all("aaa", rx)



regexp	matches	example	
^a	start of string	anchor("^a")	aaa
a$	end of string	anchor("a$")	aaa

LOOK AROUNDS

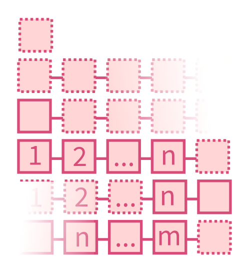
look <- function(rx) str_view_all("bacad", rx)



regexp	matches	example	
a(?=c)	followed by	look("a(?=c)")	bacad
a(?!c)	not followed by	look("a(?!c)")	bacad
(?<=b)a	preceded by	look("(?<=b)a")	bacad
(?<!b)a	not preceded by	look("(?<!b)a")	bacad

QUANTIFIERS

quant <- function(rx) str_view_all(".a.aa.aaa", rx)



regexp	matches	example	
a?	zero or one	quant("a?")	.a.aa.aaa
a*	zero or more	quant("a*")	.a.aa.aaa
a+	one or more	quant("a+")	.a.aa.aaa
a{n}	exactly **n**	quant("a{2}")	.a.aa.aaa
a{n, }	**n** or more	quant("a{2,}")	.a.aa.aaa
a{n, m}	between **n** and **m**	quant("a{2,4}")	.a.aa.aaa

GROUPS

ref <- function(rx) str_view_all("abbaab", rx)

Use parentheses to set precedent (order of evaluation) and create groups

regexp	matches	example	
(ab|d)e	sets precedence	alt("(ab|d)e")	abcde

Use an escaped number to refer to and duplicate parentheses groups that occur earlier in a pattern. Refer to each group by its order of appearance

string (type this)	regexp (to mean this)	matches (which matches this)	example (the result is the same as ref("abba"))	
\\\\1	**\\1** (etc.)	first () group, etc.	ref("(a)(b)\\\\2\\\\1")	abbaab

R Studio

Creating Survival Plots

Informative and Elegant with *survminer*

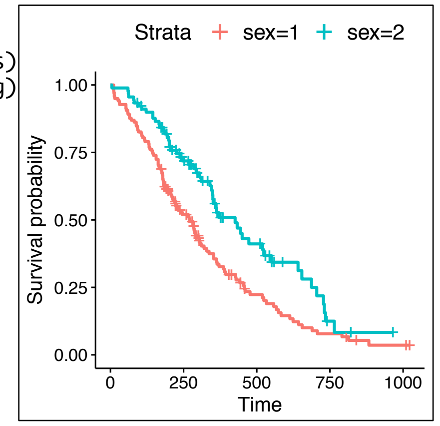
Survival Curves

The **ggsurvplot()** function creates **ggplot2** plots from **survfit** objects.

```
library("survival")
fit <- survfit(Surv(time,status)
        ~ sex, data = lung)

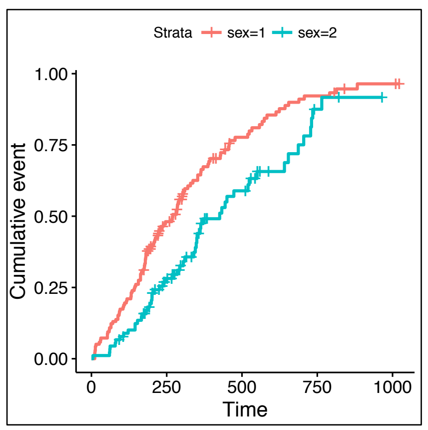
class(fit)
## [1] "survfit"

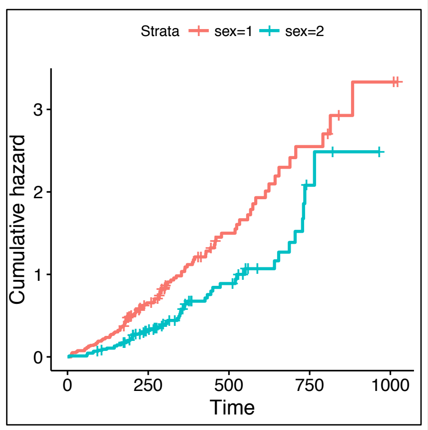
library("survminer")
ggsurvplot(fit, data = lung)
```



Use the **fun** argument to set the transformation of the survival curve. E.g. **"event"** for cumulative events, **"cumhaz"** for the cumulative hazard function or **"pct"** for survival probability in percentage.

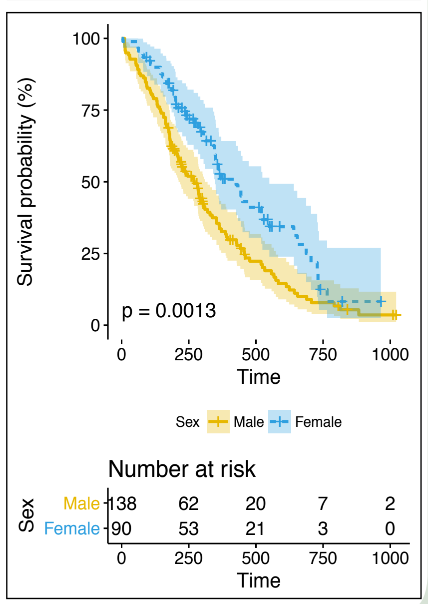
```
ggsurvplot(fit, data = lung, fun = "event")
ggsurvplot(fit, data = lung, fun = "cumhaz")
```





With lots of graphical parameters you have full control over look and feel of the survival plots; position and content of the legend; additional annotations like p-value, title, subtitle.

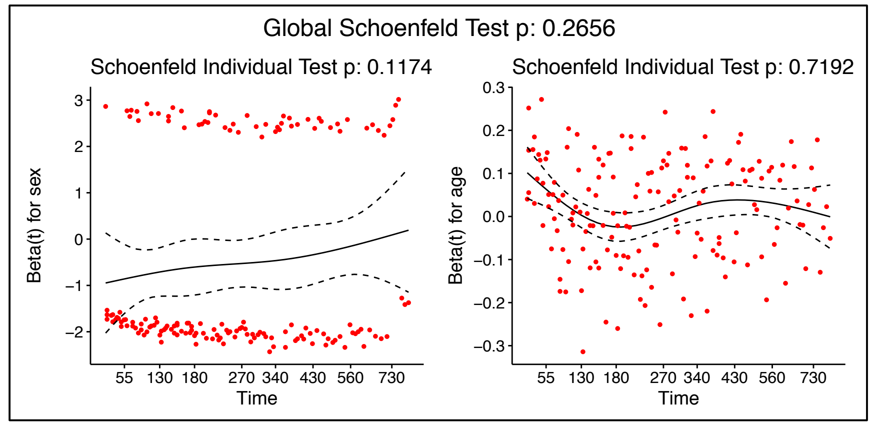
```
ggsurvplot(fit, data = lung,
    conf.int = TRUE,
    pval = TRUE,
    fun = "pct",
    risk.table = TRUE,
    size = 1,
    linetype = "strata",
    palette = c("#E7B800",
                "#2E9FDF"),
    legend = "bottom",
    legend.title = "Sex",
    legend.labs = c("Male",
                    "Female"))
```



Diagnostics of Cox Model

The function **cox.zph()** from **survival** package may be used to test the proportional hazards assumption for a Cox regression model fit. The graphical verification of this assumption may be performed with the function **ggcoxzph()** from the **survminer** package. For each covariate it produces plots with scaled Schoenfeld residuals against the time.

```
library("survival")
fit <- coxph(Surv(time, status) ~ sex + age, data = lung)
ftest <- cox.zph(fit)
ftest
##           rho chisq     p
## sex    0.1236 2.452 0.117
## age   -0.0275 0.129 0.719
## GLOBAL     NA 2.651 0.266
library("survminer")
ggcoxzph(ftest)
```

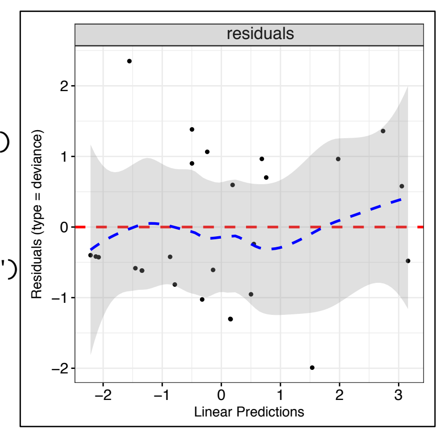


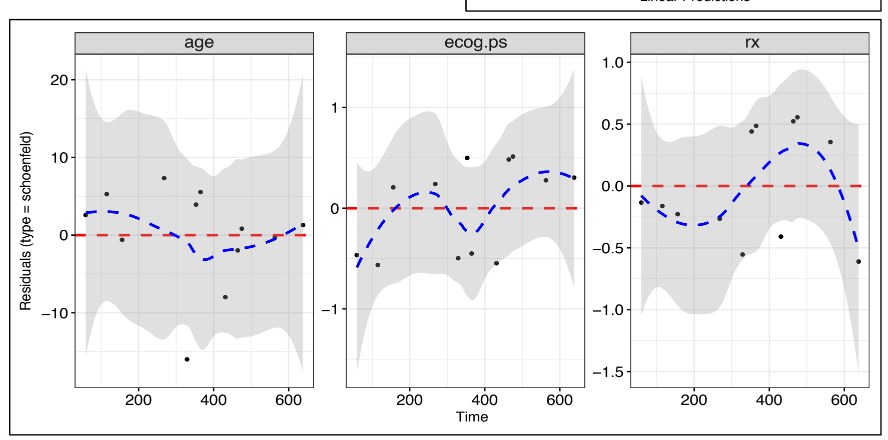
The function **ggcoxdiagnostics()** plots different types of residuals as a function of time, linear predictor or observation id. The type of residual is selected with **type** argument. Possible values are "martingale", "deviance", "score", "schoenfeld", "dfbeta"', "dfbetas", and "scaledsch".
The **ox.scale** argument defines what shall be plotted on the OX axis. Possible values are "linear.predictions", "observation.id", "time".
Logical arguments **hline** and **sline** may be used to add horizontal line or smooth line to the plot.

```
library("survival")
library("survminer")
fit <- coxph(Surv(time, status) ~
          sex + age, data = lung)


ggcoxdiagnostics(fit,
     type = "deviance",
     ox.scale = "linear.predictions")


ggcoxdiagnostics(fit,
     type = "schoenfeld",
     ox.scale = "time")
```





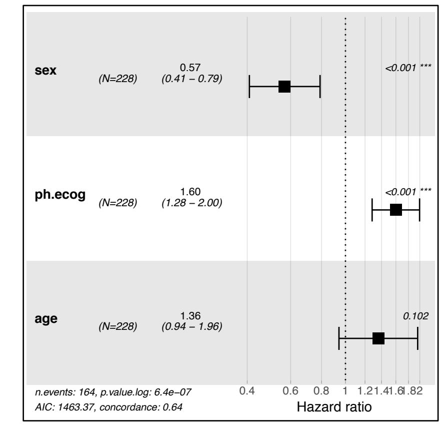
Summary of Cox Model

The function **ggforest()** from the **survminer** package creates a forest plot for a Cox regression model fit. Hazard ratio estimates along with confidence intervals and p-values are plotter for each variable.

```
library("survival")
library("survminer")
lung$age <- ifelse(lung$age > 70, ">70","<= 70")
fit <- coxph( Surv(time, status) ~ sex + ph.ecog + age, data = lung)
fit

## Call:
## coxph(formula = Surv(time, status) ~ sex+ph.ecog+age, data=lung)
##
##           coef exp(coef) se(coef)     z       p
## sex     -0.567     0.567    0.168 -3.37 0.00075
## ph.ecog  0.470     1.600    0.113  4.16 3.1e-05
## age>70   0.307     1.359    0.187  1.64 0.10175
##
## Likelihood ratio test=31.6  on
## n= 227, number of events= 164

ggforest(fit)
```



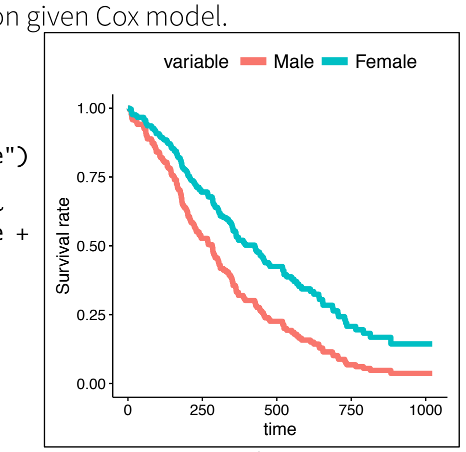
The function **ggadjustedcurves()** from the **survminer** package plots Adjusted Survival Curves for Cox Proportional Hazards Model. Adjusted Survival Curves show how a selected factor influences survival estimated from a Cox model.
Note that these curves differ from Kaplan Meier estimates since they present expected ssurvival based on given Cox model.

```
library("survival")
library("survminer")

lung$sex <- ifelse(lung$sex == 1,
                   "Male", "Female")

fit <- coxph(Surv(time, status) ~
                 sex + ph.ecog + age +
                 strata(sex),
                 data = lung)

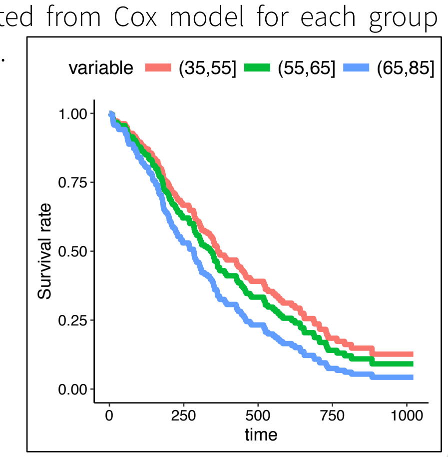
ggadjustedcurves(fit, data=lung)
```



Note that it is not necessary to include the grouping factor in the Cox model. Survival curves are estimated from Cox model for each group defined by the factor independently.

```
lung$age3 <- cut(lung$age,
                 c(35,55,65,85))

ggadjustedcurves(fit, data=lung,
                 variable="age3")
```



This onepager presents the **survminer** package [Alboukadel Kassambara, Marcin Kosinski, Przemyslaw Biecek, Scheipl Fabian 2021] in version 0.4.9
See *https://github.com/kassambara/survminer/* for more details.

R Syntax Comparison : : CHEAT SHEET

Dollar sign syntax

```
goal(data$x, data$y)
```

SUMMARY STATISTICS:

one continuous variable:
```
mean(mtcars$mpg)
```

one categorical variable:
```
table(mtcars$cyl)
```

two categorical variables:
```
table(mtcars$cyl, mtcars$am)
```

one continuous, one categorical:
```
mean(mtcars$mpg[mtcars$cyl==4])
mean(mtcars$mpg[mtcars$cyl==6])
mean(mtcars$mpg[mtcars$cyl==8])
```

PLOTTING:

one continuous variable:
```
hist(mtcars$disp)

boxplot(mtcars$disp)
```

one categorical variable:
```
barplot(table(mtcars$cyl))
```

two continuous variables:
```
plot(mtcars$disp, mtcars$mpg)
```

two categorical variables:
```
mosaicplot(table(mtcars$am, mtcars$cyl))
```

one continuous, one categorical:
```
histogram(mtcars$disp[mtcars$cyl==4])
histogram(mtcars$disp[mtcars$cyl==6])
histogram(mtcars$disp[mtcars$cyl==8])

boxplot(mtcars$disp[mtcars$cyl==4])
boxplot(mtcars$disp[mtcars$cyl==6])
boxplot(mtcars$disp[mtcars$cyl==8])
```

WRANGLING:

subsetting:
```
mtcars[mtcars$mpg>30, ]
```

making a new variable:
```
mtcars$efficient[mtcars$mpg>30] <- TRUE
mtcars$efficient[mtcars$mpg<30] <- FALSE
```

Formula syntax

```
goal(y~x|z, data=data, group=w)
```

SUMMARY STATISTICS:

one continuous variable:
```
mosaic::mean(~mpg, data=mtcars)
```

one categorical variable:
```
mosaic::tally(~cyl, data=mtcars)
```

two categorical variables:
```
mosaic::tally(cyl~am, data=mtcars)
```

one continuous, one categorical:
```
mosaic::mean(mpg~cyl, data=mtcars)
```

tilde

PLOTTING:

one continuous variable:
```
lattice::histogram(~disp, data=mtcars)

lattice::bwplot(~disp, data=mtcars)
```

one categorical variable:
```
mosaic::bargraph(~cyl, data=mtcars)
```

two continuous variables:
```
lattice::xyplot(mpg~disp, data=mtcars)
```

two categorical variables:
```
mosaic::bargraph(~am, data=mtcars, group=cyl)
```

one continuous, one categorical:
```
lattice::histogram(~disp|cyl, data=mtcars)

lattice::bwplot(cyl~disp, data=mtcars)
```

The variety of R syntaxes give you many ways to “say” the same thing

read **across** the cheatsheet to see how different syntaxes approach the same problem

Tidyverse syntax

```
data %>% goal(x)
```

SUMMARY STATISTICS:

one continuous variable:
```
mtcars %>% dplyr::summarize(mean(mpg))
```

one categorical variable:
```
mtcars %>% dplyr::group_by(cyl) %>%
dplyr::summarize(n())
```

the pipe

two categorical variables:
```
mtcars %>% dplyr::group_by(cyl, am) %>%
dplyr::summarize(n())
```

one continuous, one categorical:
```
mtcars %>%  dplyr::group_by(cyl) %>%
  dplyr::summarize(mean(mpg))
```

PLOTTING:

one continuous variable:
```
ggplot2::qplot(x=mpg, data=mtcars, geom = "histogram")

ggplot2::qplot(y=disp, x=1, data=mtcars, geom="boxplot")
```

one categorical variable:
```
ggplot2::qplot(x=cyl, data=mtcars, geom="bar")
```

two continuous variables:
```
ggplot2::qplot(x=disp, y=mpg, data=mtcars, geom="point")
```

two categorical variables:
```
ggplot2::qplot(x=factor(cyl), data=mtcars, geom="bar") +
      facet_grid(.~am)
```

one continuous, one categorical:
```
ggplot2::qplot(x=disp, data=mtcars, geom = "histogram") +
      facet_grid(.~cyl)

ggplot2::qplot(y=disp, x=factor(cyl), data=mtcars,
             geom="boxplot")
```

WRANGLING:

subsetting:
```
mtcars %>% dplyr::filter(mpg>30)
```

making a new variable:
```
mtcars <- mtcars %>%
dplyr::mutate(efficient = if_else(mpg>30,  TRUE, FALSE))
```

R Syntax Comparison : : CHEAT SHEET

Syntax is the set of rules that govern what code works and doesn't work in a programming language. Most programming languages offer one standardized syntax, but R allows package developers to specify their own syntax. As a result, there is a large variety of (equally valid) R syntaxes.

The three most prevalent R syntaxes are:

1. The **dollar sign syntax,** sometimes called **base R syntax**, expected by most `base` R functions. It is characterized by the use of `dataset$variablename`, and is also associated with square bracket subsetting, as in `dataset[1,2]`. Almost all R functions will accept things passed to them in dollar sign syntax.
2. The **formula syntax**, used by modeling functions like `lm()`, `lattice` graphics, and `mosaic` summary statistics. It uses the tilde (~) to connect a response variable and one (or many) predictors. Many base R functions will accept formula syntax.
3. The **tidyverse syntax** used by `dplyr`, `tidyr`, and more. These functions expect data to be the first argument, which allows them to work with the "pipe" (%>%) from the `magrittr` package. Typically, `ggplot2` is thought of as part of the tidyverse, although it has its own flavor of the syntax using plus signs (+) to string pieces together. `ggplot2` author Hadley Wickham has said the package would have had different syntax if he had written it after learning about the pipe.

Educators often try to teach within one unified syntax, but most R programmers use some combination of all the syntaxes.

Internet research tip:

If you are searching on google, StackOverflow, or another favorite online source and see code in a syntax you don't recognize:

- Check to see if the code is using one of the three common syntaxes listed on this cheatsheet
- Try your search again, using a keyword from the syntax name ("tidyverse") or a relevant package ("mosaic")

❗ Sometimes particular syntaxes work, but are considered dangerous to use, because they are so easy to get wrong. For example, passing variable names without assigning them to a named argument.

Even **more** ways to say the same thing

Even within one syntax, there are often variations that are equally valid. As a case study, let's look at the `ggplot2` syntax. `ggplot2` is the plotting package that lives within the tidyverse. If you read **down** this column, all the code here produces the same graphic.

read down this column for many pieces of code in one syntax that look different but produce the same graphic

quickplot

`qplot()` stands for quickplot, and allows you to make quick plots. It doesn't have the full power of `ggplot2`, and it uses a slightly different syntax than the rest of the package.

```
ggplot2::qplot(x=disp, y=mpg, data=mtcars, geom="point")
```

```
ggplot2::qplot(x=disp, y=mpg, data=mtcars)
```
❗

```
ggplot2::qplot(disp, mpg, data=mtcars)
```
❗ ❗

ggplot

To unlock the power of `ggplot2`, you need to use the `ggplot()` function (which sets up a plotting region) and add `geoms` to the plot.

```
ggplot2::ggplot(mtcars) +
    geom_point(aes(x=disp, y=mpg))
```

```
ggplot2::ggplot(data=mtcars) +
    geom_point(mapping=aes(x=disp, y=mpg))
```

plus adds layers

```
ggplot2::ggplot(mtcars, aes(x=disp, y=mpg)) +
    geom_point()
```

```
ggplot2::ggplot(mtcars, aes(x=disp)) +
    geom_point(aes(y=mpg))
```

ggformula

The "third and a half way" to use the formula syntax, but get ggplot2-style graphics

```
ggformula::gf_point(mpg~disp, data= mtcars)
```

formulas in base plots

Base R plots will also take the formula syntax, although it's not as commonly used

```
plot(mpg~disp, data=mtcars)
```

The teachR's : : CHEAT SHEET

Getting ready to teach some R? Use our cheat sheet to **prepare**, **teach** and **debrief**

DRAFT v0.1

Before the course (design)

Use these to prepare your lecture/course:

Who are your learners? (Persona Analysis)
(change according to requirements…[1])

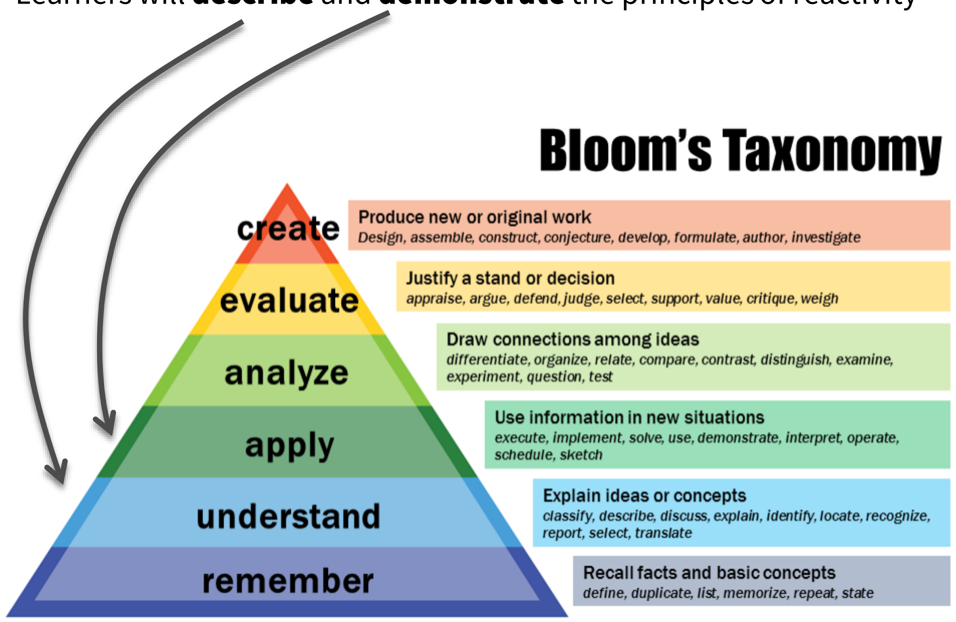
The R novice
Background: some statistics, some programming
Prior knowledge: basic R course, base R syntax
Goals: understand tidy concepts,
expose to tidyverse practices
Special needs: First successes, mitigate fears, encourage learning

The R "false expert"
Background: working with R for some time, but doesn't keep-up
Prior knowledge: been using base R syntax, loops, and functions
Goals: strengthen tidyverse familiarity, apply dplyr workflow
Special needs: switch from obsolete methods to state-of-the-art R

Define goals using Bloom's Taxonomy [2]

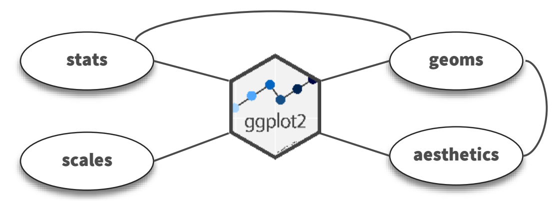
Design your classes to move your learners "up the pyramid"
Keep "realistic goals" for each persona

For example (R shiny – novice):
Learners will **describe** and **demonstrate** the principles of reactivity



Design your lecture using Conceptual maps

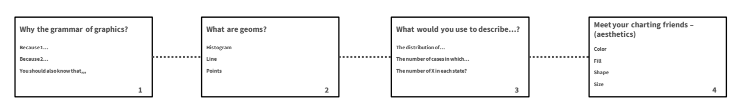
Keep the number of elements small (up to ~7 items), e.g.:



Write the "final exam"

How are you going to test knowledge after the lecture?
What should learners be able to answer?

Turn the concepts into slides



Add faded examples (exercises) and check-in slides

Check-ins, e.g.: multiple choice quick questions"
Faded examples = fill in the blanks, e.g.:
ggplot(data = ___, mapping = aes(x = ___, y = ___)) +
geom_*() +

During the course (implement)

Things you can implement to improve the lecture workflow

Learners use **sticky notes** to indicate status:
Green = everything is OK/Exercise completed.
Red = help me! I ran into a problem.
Blue = I need a break.

Engage with online mini-polls during lecture
Use regular check-ins during your lecture (3-4 check-ins per hour). No one "opts-out" (everyone answers once in a while – you choose)

After the course (learn/improve)

Make sure you make the most to improve your next lecture

Use feedback to understand what went well, and what you need to improve.

Measure the time each lecture takes you (or where did you get to), so that next time your time estimates will be better

Useful tips and tricks

Useful tips for preparations

Use github to upload course materials

RMarkdown for exercises

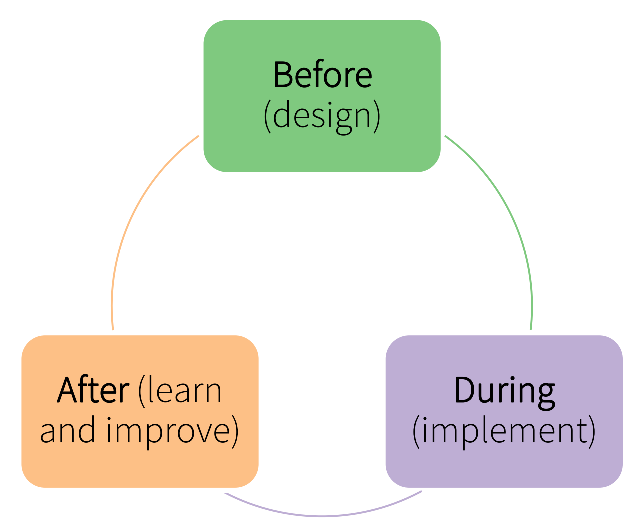
Recommended reading materials/references for R courses:

R for Data Science / Garrett Grolemund and Hadley Wickham (r4ds.had.co.nz)

Advanced R/ Hadley Wickham (adv-r.had.co.nz)

RStudio **Cheat sheets**:
https://www.rstudio.com/resources/cheatsheets/

Iterative work flow



Additional sources

[1] Dreyfus, Stuart E., and Hubert L. Dreyfus. *A five stage model of the mental activities involved in directed skill acquisition.* No. ORC-80-2. California Univ Berkeley Operations Research Center, 1980.

[2] Content downloaded from https://cft.vanderbilt.edu/guides-sub-pages/blooms-taxonomy/
(CC-BY-SA Vanderbilt University Center for Teaching)

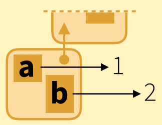
Sarid Research Services

Tidy evaluation with rlang : : CHEAT SHEET

Vocabulary

Tidy Evaluation (Tidy Eval) is not a package, but a framework for doing non-standard evaluation (i.e. delayed evaluation) that makes it easier to program with tidyverse functions.

pi — **Symbol** - a name that represents a value or object stored in R. *is_symbol(expr(pi))*



Environment - a list-like object that binds symbols (names) to objects stored in memory. Each env contains a link to a second, **parent** env, which creates a chain, or search path, of environments. *is_environment(current_env())*

rlang::**caller_env**(n = 1) Returns calling env of the function it is in.

rlang::**child_env**(.parent, ...) Creates new env as child of .parent. Also **env**.

rlang::**current_env**() Returns execution env of the function it is in.

1 — **Constant** - a bare value (i.e. an atomic vector of length 1). *is_bare_atomic(1)*

abs (1) — **Call object** - a vector of symbols/constants/calls that begins with a function name, possibly followed by arguments. *is_call(expr(abs(1)))*

pi — code, **3.14** — result — **Code** - a sequence of symbols/constants/calls that will return a result if evaluated. Code can be:

1. Evaluated immediately (**Standard Eval**)
2. Quoted to use later (**Non-Standard Eval**)

is_expression(expr(pi))

e / a + b — **Expression** - an object that stores quoted code without evaluating it. is_*expression(expr(a + b))*

q / a + b, — **Quosure**- an object that stores both quoted code (without evaluating it) and the code's environment. *is_quosure(quo(a + b))*

rlang::**quo_get_env**(quo) Return the environment of a quosure.

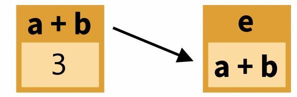
rlang::**quo_set_env**(quo, expr) Set the environment of a quosure.

a + b — rlang::**quo_get_expr**(quo) Return the expression of a quosure.

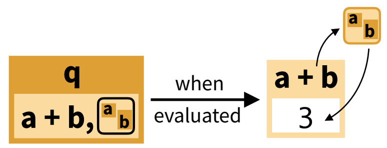
Expression Vector - a list of pieces of quoted code created by base R's *expression* and *parse* functions. Not to be confused with **expression**.

Quoting Code

Quote code in one of two ways (if in doubt use a quosure):



QUOSURES



Quosure- An expression that has been saved *with an environment* (aka a closure).

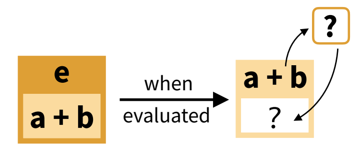
A quosure can be evaluated later in the stored environment to return a predictable result.

rlang::**quo**(expr) Quote contents as a quosure. Also **quos** to quote multiple expressions. *a <- 1; b <- 2; q <- quo(a + b); qs <- quos(a, b)*

rlang::**enquo**(arg) Call from within a function to quote what the user passed to an argument as a quosure. Also **enquos** for multiple args.
quote_this < - function(x) enquo(x)
quote_these < - function(…) enquos(…)

rlang::**new_quosure**(expr, env = caller_env()) Build a quosure from a quoted expression and an environment.
new_quosure(expr(a + b), current_env())

EXPRESSION



Quoted Expression - An expression that has been saved by itself.

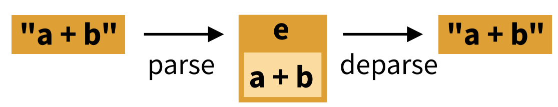
A quoted expression can be evaluated later to return a result that will depend on the environment it is evaluated in

rlang::**expr**(expr) Quote contents. Also **exprs** to quote multiple expressions. *a <- 1; b <- 2; e <- expr(a + b); es <- exprs(a, b, a + b)*

rlang::**enexpr**(arg) Call from within a function to quote what the user passed to an argument. Also **enexprs** to quote multiple arguments.
quote_that < - function(x) enexpr(x)
quote_those < - function(…) enexprs(…)

rlang::**ensym**(x) Call from within a function to quote what the user passed to an argument as a symbol, accepts strings. Also **ensyms**.
quote_name < - function(name) ensym(name)
quote_names < - function(…) ensyms(…)

Parsing and Deparsing



Parse - Convert a string to a saved expression.

rlang::**parse_expr**(x) Convert a string to an expression. Also **parse_exprs**, **sym**, **parse_quo**, **parse_quos**. e<-*parse_expr("a+b")*

Deparse - Convert a saved expression to a string.

rlang::**expr_text**(expr, width = 60L, nlines = Inf) Convert expr to a string. Also **quo_name**.
expr_text(e)

Building Calls

rlang::**call2**(.fn, ..., .ns = NULL) Create a call from a function and a list of args. Use **exec** to create and then evaluate the call. (See back page for **!!!**) *args <- list(x = 4, base = 2)*

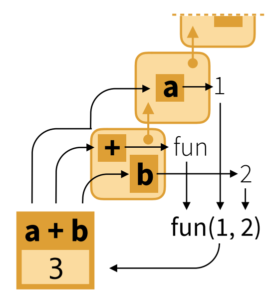
log (x = **4** , base = **2**)

2

call2("log", x = 4, base = 2)
call2("log", !!!args)

exec("log", x = 4, base = 2)
exec("log", !!!args)

Evaluation



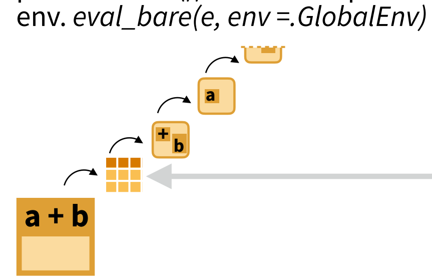
To evaluate an expression, R :

1. Looks up the symbols in the expression in the active environment (or a supplied one), followed by the environment's parents
2. Executes the calls in the expression

The result of an expression depends on which environment it is evaluated in.

QUOTED EXPRESSION

rlang::**eval_bare**(expr, env = parent.frame()) Evaluate expr in env. *eval_bare(e, env =.GlobalEnv)*



a <- 1; b <- 2
*p <- quo(**.data$**a + **!!**b)*
mask <- tibble(a = 5, b = 6)
eval_tidy(p, data = mask)

QUOSURES (and quoted exprs)

rlang::**eval_tidy**(expr, data = NULL, env = caller_env()) Evaluate expr in env, using data as a **data mask**. Will evaluate quosures in their stored environment. *eval_tidy(q)*

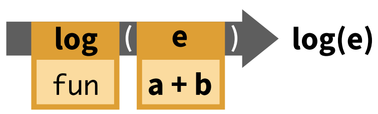
Data Mask - If data is non-NULL, eval_tidy inserts data into the search path before env, matching symbols to names in data.

Use the pronoun **.data$** to force a symbol to be matched in data, and **!!** (see back) to force a symbol to be matched in the environments.

Quasiquotation (!!, !!!, :=)

QUOTATION

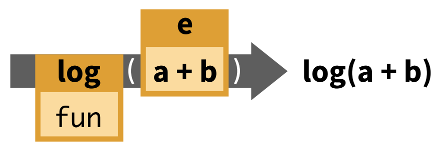
Storing an expression without evaluating it.
e <- expr(a + b)



expr(log(e))

QUASIQUOTATION

Quoting *some* parts of an expression while evaluating and then inserting the results of others (**unquoting** others).
e <- expr(a + b)



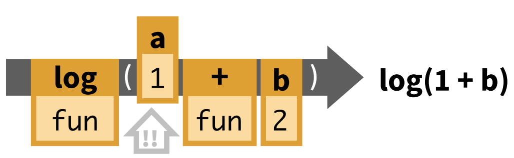
expr(log(!!e))

rlang provides **!!**, **!!!**, and **:=** for doing quasiquotation.

!!, **!!!**, and **:=** are not functions but syntax (symbols recognized by the functions they are passed to). Compare this to how

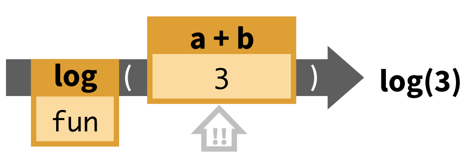
. is used by magrittr::**%>%()**
. is used by stats::**lm()**
.x is used by purrr::**map()**, and so on.

!!, **!!!**, and **:=** are only recognized by some rlang functions and functions that use those functions (such as tidyverse functions).



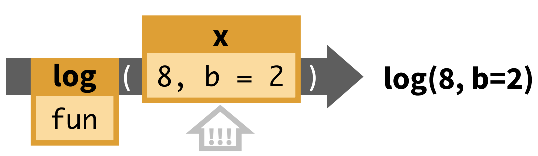
expr(log(!!a + b))

!! Unquotes the symbol or call that follows. Pronounced "unquote" or "bang-bang." *a <- 1; b <- 2*
expr(log(!!a + b))



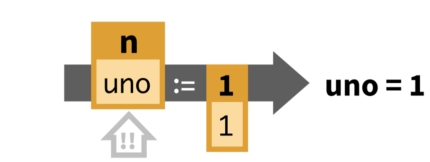
expr(log(!!(a + b)))

Combine **!!** with **()** to unquote a longer expression.
a <- 1; b <- 2
expr(log(!!(a + b)))



expr(log(!!!x))

!!! Unquotes a vector or list and splices the results as arguments into the surrounding call. Pronounced "unquote splice" or "bang-bang-bang."
x <- list(8, b = 2)
expr(log(!!!x))



tibble::tibble(!!n := 1)

:= Replaces an = to allow unquoting within the name that appears on the left hand side of the =. Use with **!!**
n <- expr(uno)
tibble::tibble(!!n := 1)

Programming Recipes

Quoting function- A function that quotes any of its arguments internally for delayed evaluation in a chosen environment. You must take **special steps to program safely** with a quoting function.

How to spot a quoting function?
A function quotes an argument if the argument returns an error when run on its own.

```
dplyr::filter(cars, speed = = 25)
   speed dist
1     25   85
```

Many tidyverse functions are quoting functions: e.g. **filter**, **select**, **mutate**, **summarise**, etc.

```
speed == 25
Error!
```

WRITE A FUNCTION THAT RECOGNIZES QUASIQUOTATION (!!,!!!,:=)

1. Capture the quasiquotation-aware argument with rlang::**enquo**.
2. Evaluate the arg with rlang::**eval_tidy**.

```
add1 <- function(x) {
  q <- rlang::enquo(x)            1
  rlang::eval_tidy(q) + 1         2
}
```

PROGRAM WITH A QUOTING FUNCTION

```
data_mean <- function(data, var) {
  require(dplyr)
  var <- rlang::enquo(var)                 1
  data %>%
    summarise(mean = mean(!!var))          2
}
```

1. Capture user argument that will be quoted with rlang::**enquo**.
2. Unquote the user argument into the quoting function with **!!**.

PASS MULTIPLE ARGUMENTS TO A QUOTING FUNCTION

```
group_mean <- function(data, var, ...) {
  require(dplyr)
  var <- rlang::enquo(var)
  group_vars <- rlang::enquos(...)         1
  data %>%
    group_by(!!!group_vars) %>%            2
    summarise(mean = mean(!!var))
}
```

1. Capture user arguments that will be quoted with rlang::**enquos**.
2. Unquote splice the user arguments into the quoting function with **!!!**.

PASS TO ARGUMENT NAMES OF A QUOTING FUNCTION

```
named_m <- function(data, var, name) {
  require(dplyr)
  var <- rlang::enquo(var)
  name <- rlang::ensym(name)               1
  data %>%
    summarise(!!name := mean(!!var))       2
}
```

1. Capture user argument that will be quoted with rlang::**ensym**.
2. Unquote the name into the quoting function with **!!** and **:=**.

MODIFY USER ARGUMENTS

```
my_do <- function(f, v, df) {
  f <- rlang::enquo(f)                     1
  v <- rlang::enquo(v)
  todo <- rlang::quo((!!f)(!!v))           2
  rlang::eval_tidy(todo, df)               3
}
```

1. Capture user arguments with rlang::**enquo**.
2. **Unquote** user arguments into a new expression or quosure to use
3. **Evaluate** the new expression/ quosure instead of the original argument

APPLY AN ARGUMENT TO A DATA FRAME

```
subset2 <- function(df, rows) {
  rows <- rlang::enquo(rows)                      1
  vals <- rlang::eval_tidy(rows, data = df)
  df[vals, , drop = FALSE]                        2
}
```

1. Capture user argument with rlang::**enquo**.
2. Evaluate the argument with rlang::**eval_tidy**. Pass the data frame to **data** to use as a data mask.
3. **Suggest** in your documentation that your users use the **.data** and **.env** pronouns.

PASS CRAN CHECK

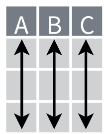
```
#' @importFrom rlang .data                  1
mutate_y <- function(df) {
  dplyr::mutate(df, y = .data$a +1)        2
}
```

Quoted arguments in tidyverse functions can trigger an **R CMD check** NOTE about undefined global variables. To avoid this:

1. Import rlang::**.data** to your package, perhaps with the roxygen2 tag **@importFrom rlang .data**
2. Use the **.data$** pronoun in front of variable names in tidyverse functions

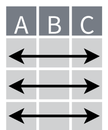
Data tidying with tidyr : : CHEAT SHEET

Tidy data is a way to organize tabular data in a consistent data structure across packages.
A table is tidy if:

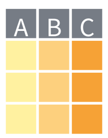


Each **variable** is in its own **column**

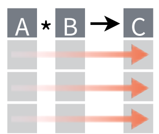
&



Each **observation**, or **case**, is in its own row



Access **variables** as **vectors**



Preserve **cases** in vectorized operations

Tibbles

AN ENHANCED DATA FRAME

Tibbles are a table format provided by the **tibble** package. They inherit the data frame class, but have improved behaviors:

- **Subset** a new tibble with], a vector with [[and $.
- **No partial matching** when subsetting columns.
- **Display** concise views of the data on one screen.

options(tibble.print_max = n, tibble.print_min = m, tibble.width = Inf**)** Control default display settings.

View() or **glimpse()** View the entire data set.

CONSTRUCT A TIBBLE

tibble(…**)** Construct by columns.
tibble(x = 1:3, y = c("a", "b", "c"))

tribble(…**)** Construct by rows.
tribble(~x, ~y,
 1, "a",
 2, "b",
 3, "c")

Both make this tibble

```
A tibble: 3 × 2
     x     y
  <int> <chr>
1     1     a
2     2     b
3     3     c
```

as_tibble(x, …**)** Convert a data frame to a tibble.

enframe(x, name = "name", value = "value"**)** Convert a named vector to a tibble. Also **deframe()**.

is_tibble(x**)** Test whether x is a tibble.

Reshape Data

- Pivot data to reorganize values into a new layout.

table4a

country	1999	2000
A	0.7K	2K
B	37K	80K
C	212K	213K

→

country	year	cases
A	1999	0.7K
B	1999	37K
C	1999	212K
A	2000	2K
B	2000	80K
C	2000	213K

pivot_longer(data, cols, names_to = "name", values_to = "value", values_drop_na = FALSE**)**

"Lengthen" data by collapsing several columns into two. Column names move to a new names_to column and values to a new values_to column.

pivot_longer(table4a, cols = 2:3, names_to ="year", values_to = "cases")

table2

country	year	type	count
A	1999	cases	0.7K
A	1999	pop	19M
A	2000	cases	2K
A	2000	pop	20M
B	1999	cases	37K
B	1999	pop	172M
B	2000	cases	80K
B	2000	pop	174M
C	1999	cases	212K
C	1999	pop	1T
C	2000	cases	213K
C	2000	pop	1T

→

country	year	cases	pop
A	1999	0.7K	19M
A	2000	2K	20M
B	1999	37K	172M
B	2000	80K	174M
C	1999	212K	1T
C	2000	213K	1T

pivot_wider(data, names_from = "name", values_from = "value"**)**

The inverse of pivot_longer(). "Widen" data by expanding two columns into several. One column provides the new column names, the other the values.

pivot_wider(table2, names_from = type, values_from = count)

Split Cells

- Use these functions to split or combine cells into individual, isolated values.

table5

country	century	year
A	19	99
A	20	00
B	19	99
B	20	00

→

country	year
A	1999
A	2000
B	1999
B	2000

unite(data, col, …, sep = "_", remove = TRUE, na.rm = FALSE**)** Collapse cells across several columns into a single column.

unite(table5, century, year, col = "year", sep = "")

table3

country	year	rate
A	1999	0.7K/19M
A	2000	2K/20M
B	1999	37K/172M
B	2000	80K/174M

→

country	year	cases	pop
A	1999	0.7K	19M
A	2000	2K	20M
B	1999	37K	172
B	2000	80K	174

separate(data, col, into, sep = "[^[:alnum:]]+", remove = TRUE, convert = FALSE, extra = "warn", fill = "warn", …**)** Separate each cell in a column into several columns. Also **extract()**.

separate(table3, rate, sep = "/", into = c("cases", "pop"))

table3

country	year	rate
A	1999	0.7K/19M
A	2000	2K/20M
B	1999	37K/172M
B	2000	80K/174M

→

country	year	rate
A	1999	0.7K
A	1999	19M
A	2000	2K
A	2000	20M
B	1999	37K
B	1999	172M
B	2000	80K
B	2000	174M

separate_rows(data, …, sep = "[^[:alnum:].]+", convert = FALSE**)** Separate each cell in a column into several rows.

separate_rows(table3, rate, sep = "/")

Expand Tables

Create new combinations of variables or identify implicit missing values (combinations of variables not present in the data).

x

x1	x2	x3
A	1	3
B	1	4
B	2	3

→

x1	x2
A	1
A	2
B	1
B	2

expand(data, …**)** Create a new tibble with all possible combinations of the values of the variables listed in … Drop other variables.
expand(mtcars, cyl, gear, carb)

x

x1	x2	x3
A	1	3
B	1	4
B	2	3

→

x1	x2	x3
A	1	3
A	2	NA
B	1	4
B	2	3

complete(data, …, fill = list()**)** Add missing possible combinations of values of variables listed in … Fill remaining variables with NA.
complete(mtcars, cyl, gear, carb)

Handle Missing Values

Drop or replace explicit missing values (NA).

x

x1	x2
A	1
B	NA
C	NA
D	3
E	NA

→

x1	x2
A	1
D	3

drop_na(data, …**)** Drop rows containing NA's in … columns.
drop_na(x, x2)

x

x1	x2
A	1
B	NA
C	NA
D	3
E	NA

→

x1	x2
A	1
B	1
C	1
D	3
E	3

fill(data, …, .direction = "down"**)** Fill in NA's in … columns using the next or previous value.
fill(x, x2)

x

x1	x2
A	1
B	NA
C	NA
D	3
E	NA

→

x1	x2
A	1
B	2
C	2
D	3
E	2

replace_na(data, replace**)** Specify a value to replace NA in selected columns.
replace_na(x, list(x2 = 2))

RStudio

Nested Data

A **nested data frame** stores individual tables as a list-column of data frames within a larger organizing data frame. List-columns can also be lists of vectors or lists of varying data types.
Use a nested data frame to:

- Preserve relationships between observations and subsets of data. Preserve the type of the variables being nested (factors and datetimes aren't coerced to character).
- Manipulate many sub-tables at once with **purrr** functions like map(), map2(), or pmap() or with **dplyr** rowwise() grouping.

CREATE NESTED DATA

nest(data, ...**)** Moves groups of cells into a list-column of a data frame. Use alone or with dplyr::**group_by()**:

1. Group the data frame with **group_by()** and use **nest()** to move the groups into a list-column.

```
n_storms <- storms %>%
  group_by(name) %>%
  nest()
```

2. Use **nest(new_col = c(x, y))** to specify the columns to group using dplyr::**select()** syntax.

```
n_storms <- storms %>%
  nest(data = c(year:long))
```

name	yr	lat	long
Amy	1975	27.5	-79.0
Amy	1975	28.5	-79.0
Amy	1975	29.5	-79.0
Bob	1979	22.0	-96.0
Bob	1979	22.5	-95.3
Bob	1979	23.0	-94.6
Zeta	2005	23.9	-35.6
Zeta	2005	24.2	-36.1
Zeta	2005	24.7	-36.6

→

name	yr	lat	long
Amy	1975	27.5	-79.0
Amy	1975	28.5	-79.0
Amy	1975	29.5	-79.0
Bob	1979	22.0	-96.0
Bob	1979	22.5	-95.3
Bob	1979	23.0	-94.6
Zeta	2005	23.9	-35.6
Zeta	2005	24.2	-36.1
Zeta	2005	24.7	-36.6

→ nested data frame

name	data
Amy	<tibble [50x3]>
Bob	<tibble [50x3]>
Zeta	<tibble [50x3]>

"cell" contents

yr	lat	long
1975	27.5	-79.0
1975	28.5	-79.0
1975	29.5	-79.0

yr	lat	long
1979	22.0	-96.0
1979	22.5	-95.3
1979	23.0	-94.6

yr	lat	long
2005	23.9	-35.6
2005	24.2	-36.1
2005	24.7	-36.6

Index list-columns with [[]]. `n_storms$data[[1]]`

CREATE TIBBLES WITH LIST-COLUMNS

tibble::**tribble(**...**)** Makes list-columns when needed.

```
tribble( ~max, ~seq,
          3,   1:3,
          4,   1:4,
          5,   1:5)
```

max	seq
3	<int [3]>
4	<int [4]>
5	<int [5]>

tibble::**tibble(**...**)** Saves list input as list-columns.
`tibble(max = c(3, 4, 5), seq = list(1:3, 1:4, 1:5))`

tibble::**enframe(**x, name="name", value="value"**)** Converts multi-level list to a tibble with list-cols.
`enframe(list('3'=1:3, '4'=1:4, '5'=1:5), 'max', 'seq')`

OUTPUT LIST-COLUMNS FROM OTHER FUNCTIONS

dplyr::**mutate()**, **transmute()**, and **summarise()** will output list-columns if they return a list.

```
mtcars %>%
  group_by(cyl) %>%
  summarise(q = list(quantile(mpg)))
```

RESHAPE NESTED DATA

unnest(data, cols, ..., keep_empty = FALSE**)** Flatten nested columns back to regular columns. The inverse of nest().
`n_storms %>% unnest(data)`

unnest_longer(data, col, values_to = NULL, indices_to = NULL**)** Turn each element of a list-column into a row.

```
starwars %>%
  select(name, films) %>%
  unnest_longer(films)
```

name	films
Luke	<chr [5]>
C-3PO	<chr [6]>
R2-D2	<chr[7]>

→

name	films
Luke	The Empire Strik...
Luke	Revenge of the S...
Luke	Return of the Jed...
C-3PO	The Empire Strik...
C-3PO	Attack of the Cl...
C-3PO	The Phantom M...
R2-D2	The Empire Strik...
R2-D2	Attack of the Cl...
R2-D2	The Phantom M...

unnest_wider(data, col**)** Turn each element of a list-column into a regular column.

```
starwars %>%
  select(name, films) %>%
  unnest_wider(films)
```

name	films
Luke	<chr [5]>
C-3PO	<chr [6]>
R2-D2	<chr[7]>

→

name	..1	..2	..3
Luke	The Empire...	Revenge of...	Return of...
C-3PO	The Empire...	Attack of...	The Phantom...
R2-D2	The Empire...	Attack of...	The Phantom...

hoist(.data, .col, ..., .remove = TRUE**)** Selectively pull list components out into their own top-level columns. Uses purrr::pluck() syntax for selecting from lists.

```
starwars %>%
  select(name, films) %>%
  hoist(films, first_film = 1, second_film = 2)
```

name	films
Luke	<chr [5]>
C-3PO	<chr [6]>
R2-D2	<chr[7]>

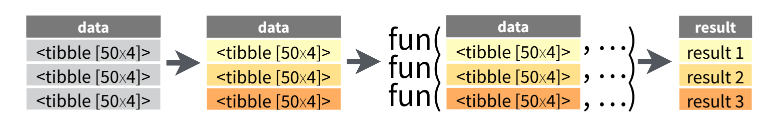
→

name	first_film	second_film	films
Luke	The Empire...	Revenge of...	<chr [3]>
C-3PO	The Empire...	Attack of...	<chr [4]>
R2-D2	The Empire...	Attack of...	<chr [5]>

TRANSFORM NESTED DATA

A vectorized function takes a vector, transforms each element in parallel, and returns a vector of the same length. By themselves vectorized functions cannot work with lists, such as list-columns.

dplyr::**rowwise(**.data, ...**)** Group data so that each row is one group, and within the groups, elements of list-columns appear directly (accessed with [[ ), not as lists of length one. **When you use rowwise(), dplyr functions will seem to apply functions to list-columns in a vectorized fashion.**



Apply a function to a list-column and **create a new list-column.**

```
n_storms %>%
  rowwise() %>%
  mutate(n = list(dim(data)))
```

dim() returns two values per row

wrap with list to tell mutate to create a list-column

Apply a function to a list-column and **create a regular column.**

```
n_storms %>%
  rowwise() %>%
  mutate(n = nrow(data))
```

nrow() returns one integer per row

Collapse **multiple list-columns** into a single list-column.

```
starwars %>%
  rowwise() %>%
  mutate(transport = list(append(vehicles, starships)))
```

append() returns a list for each row, so col type must be list

Apply a function to **multiple list-columns.**

```
starwars %>%
  rowwise() %>%
  mutate(n_transports = length(c(vehicles, starships)))
```

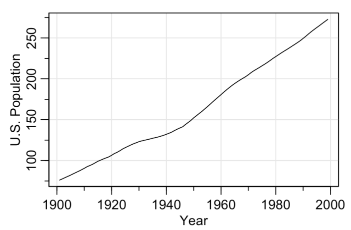
length() returns one integer per row

See **purrr** package for more list functions.

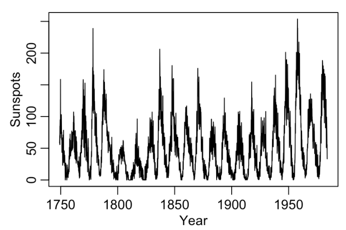
Time Series Cheat Sheet

Plot Time Series

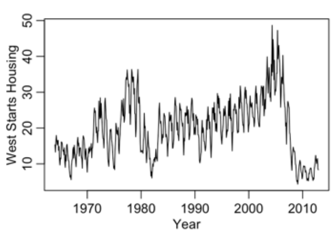
1. tsplot(x=time, y=data)



2. plot(ts(data, start=start_time, frequency=gap))



3. ts.plot(ts(data, start=start_time, frequency=gap))



Simulation

Autoregression of Order p

$$\mathbf{X_t} = \phi_1\mathbf{X_{t-1}} + \phi_2\mathbf{X_{t-2}} + \ldots + \phi_p\mathbf{X_{t-p}} + \mathbf{W_t}$$

Moving Average of Order q

$$\mathbf{X_t} = \mathbf{Z_t} + \theta_1\mathbf{Z_{t-1}} + \theta_2\mathbf{Z_{t-2}} + \ldots + \theta_q\mathbf{Z_{t-p}}$$

ARMA (p, q)

$$\mathbf{X_t} = \phi_1\mathbf{X_{t-1}} + \phi_2\mathbf{X_{t-2}} + \ldots + \phi_p\mathbf{X_{t-p}} + \mathbf{Z_t} + \theta_1\mathbf{Z_{t-1}} + \theta_2\mathbf{Z_{t-2}} + \ldots + \theta_q\mathbf{Z_{t-p}}$$

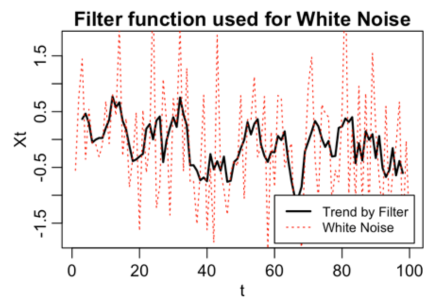
Simulation of ARMA (p, q)

arima.sim(model=list(ar=c($\phi_1, \ldots, \phi_p$), ma=c($\theta_1, \ldots, \theta_q$)), n=n)

Filters

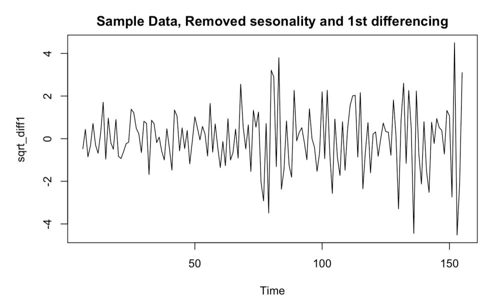
Linear Filter: filter()

filter(data, filter=filter_coefficients, sides=2, method="convolution", circular=F)



Differencing Filter: diff()

diff(data, lag=4, differences=1)

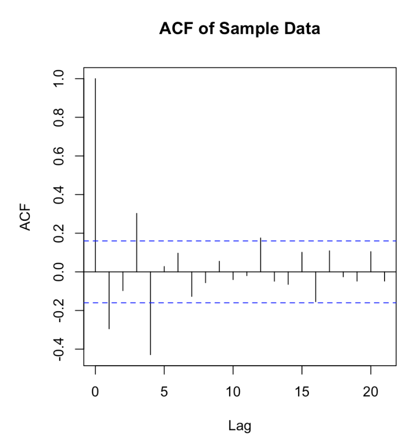


Auto-correlation

Use ACF and PACF to detect model

(Complete) Auto-correlation function: acf()

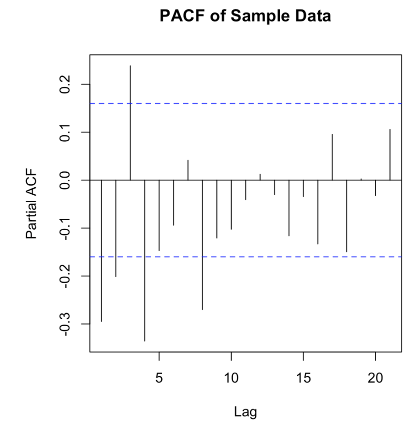
acf(data, type='correlation', na.action=na.pass)



Partial Auto-correlation function: pacf()

pacf(data, na.action=na.pass)

OR: acf(data, type='partial', na.action=na.pass)



Parameter Estimation

Fit an ARMA time series model to the data

ar(): To estimate parameters of an AR model

ar(x=data, aic=T, order.max = NULL, c("yule-walker", "burg", "ols", "mle", "yw"))

```
Call:
ar(x = sqrt1, aic = TRUE, order.max = NULL, method = c("yule-walker",     "burg", "ols", "mle", "yw"))

Coefficients:
      1        2        3        4        5        6        7        8        9
-0.3066  -0.1903   0.0793  -0.5065  -0.1873  -0.1149  -0.0580  -0.3031  -0.1207

Order selected 9  sigma^2 estimated as  1.52
```

arima(): To estimate parameters of an AM or ARMA model, and build model

arima(data, order=c(p, 0, q),method=c('ML'))

```
Call:
arima(x = sqrt1, order = c(2, 0, 6), method = c("ML"))

Coefficients:
          ar1      ar2      ma1     ma2      ma3      ma4     ma5      ma6  intercept
      -0.1658  -0.7951  -0.1536  0.7524  -0.2101  -0.7680  0.0605  -0.6812    -0.0048
s.e.   0.0918   0.0754   0.0916  0.1047   0.0794   0.0743  0.0812   0.0895     0.0062

sigma^2 estimated as 1.193:  log likelihood = -230.78,  aic = 481.55
```

AICc(): Compare models using AICC

AICc(fittedModel)

Forecasting

Forecasting future observations given a fitted ARMA model

predict(): Predict future observations given a fitted ARMA model

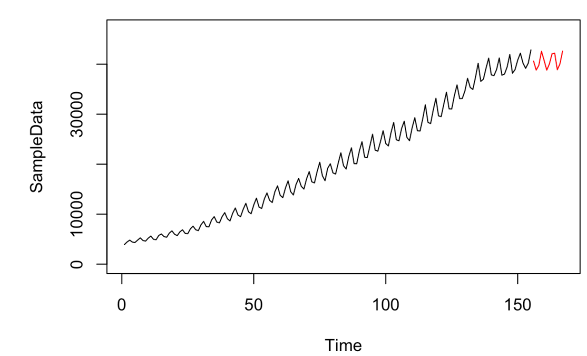
predict(arima_model, number_to_predict)

Plot Predicted values and Confidence Interval:

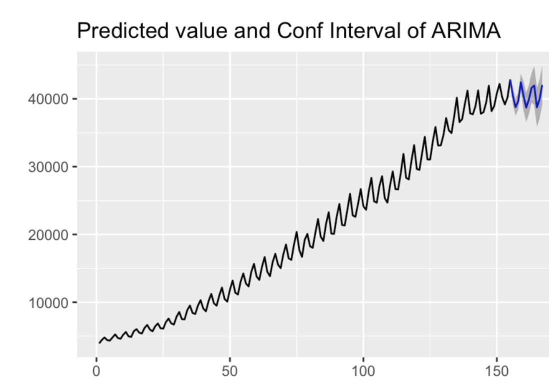
fit<-predict(arima_model, number_to_predict)

ts.plot(data,
    xlim=c(1, length(data)+number_to_predict),
    ylim=c(0, max(fit$pred+1.96*fit$se)))

lines(length(data)+1:length(data)+
    number_to_predict, fit$pred)



OR: autoplot(forecast(arima_model, level=c(95), h=number_to_predict))



Class Agnostic Time Series with tsbox : : CHEAT SHEET

Basics

IDEA

tsbox provides a time series toolkit which:

1. works identically with most time series **classes**
2. handles regular and irregular **frequencies**
3. **converts** between classes and frequencies

Most functions in tsbox have the same structure:

function starts with ts_

first argument is any ts-boxable object

```
a <- ts_pc(AirPassengers)
```

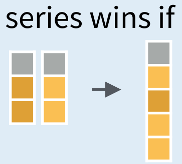
returns a ts-boxable obect of the same class as input

COMBINE TIME SERIES

collect time series of **all classes** and **frequencies** as multiple time series

```
ts_c(mdeaths, austres)
```

combine time series to a new, single time series (first series wins if overlapping)



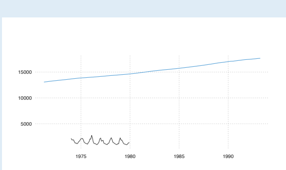
```
ts_bind(mdeaths, austres)
```

like ts_bind, but extra- and retropolate, using growth rates

```
ts_chain(mdeaths, austres)
```

PLOT AND SUMMARIZE

Plot time series of **all classes** and **frequencies**



```
ts_plot(mdeaths, austres)
ts_ggplot(mdeaths, austres)
```

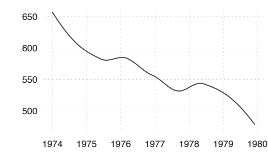
```
ts_summary(ts_c(mdeaths, austres))
```

```
       id obs    diff freq      start        end
1 mdeaths  72 1 month    12 1974-01-01 1979-12-01
2 austres  89 3 month     4 1971-04-01 1993-04-01
```

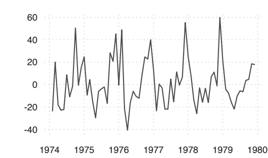
Helper Functions

Transform time series of **all classes** and **frequencies**

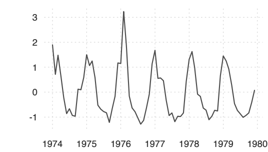
TRANSFORM



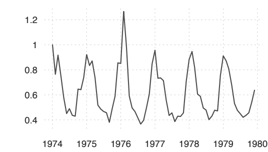
ts_trend(): Trend estimation based on loess
`ts_trend(fdeaths)`



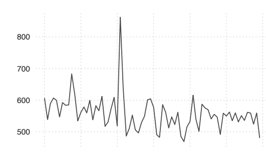
ts_pc(), ts_pcy(), ts_pca(), ts_diff(), ts_diffy(): (annualized) Percentage change rates or differences to previous period, year
`ts_pc(fdeaths)`



ts_scale(): normalize mean and variance
`ts_scale(fdeaths)`

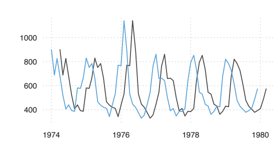


ts_index():Index, based on levels
ts_compound(): Index, based on growth rates
`ts_index(fdeaths, base = 1976)`

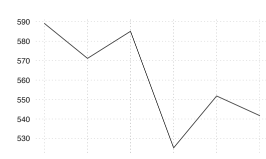


ts_seas(): seasonal adjustment using X-13
`ts_seas(fdeaths)`

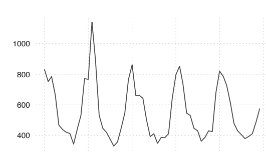
SPAN AND FREQUENCY



ts_lag(): Lag or lead of time series
`ts_lag(fdeaths, 4)`



ts_frequency(): convert to frequency
`ts_frequency(fdeaths, "year")`



ts_span(): filter time series for a time span.
```
ts_span(fdeaths, "1976-01-01")
ts_span(fdeaths, "-5 year")
```

Class Conversion

tsbox is built around a set of converters, which convert time series of the following **supported classes** to each other:

converter function	ts-boxable class
ts_ts()	ts, mts
ts_data.frame(), ts_df()	data.frame
ts_data.table(), ts_dt()	data.table
ts_tbl()	df_tbl, "tibble"
ts_xts()	xts
ts_zoo()	zoo
ts_tibbletime()	tibbletime
ts_timeSeries()	timeSeries
ts_tsibble()	tsibble
ts_tslist()	a list with ts objects

Time Series in data frames

LONG STRUCTURE

Default structure to store multiple time series in long data frames (or data tables, or tibbles)

`ts_df(ts_c(fdeaths, mdeaths))`

id	time	value
fdeaths	1974-01-01	901
fdeaths	1974-02-01	689
fdeaths	1974-03-01	827
...	...	...

AUTO-DETECT COLUMN NAMES

tsbox auto-detects a *value*-, a *time*- and zero, one or several *id*-columns. Alternatively, the *time*- and the *value*-column can be explicitly named **time** and **value**.

ts_default(): standardize column names in data frames

RESHAPE

ts_wide(): convert default long structure to wide
ts_long(): convert wide structure to default long

USE WITH PIPE

tsbox plays well with tibbles and with `%>%`, so it can be easily integrated into a dplyr/pipe workflow

```
library(dplyr)
ts_c(fdeaths, mdeaths) %>%
  ts_tbl() %>%
  ts_trend() %>%
  ts_pc()
```

pass return value as first argument to the next function

cynkra

Cheat Sheet : : VEGAN

What is VEGAN?

The **vegan** package provides tools for descriptive community ecology. It has basic functions of **community ordination**, **diversity analysis** and **dissimilarity analysis**. Most of its multivariate tools can be used for other data types as well.

Examples using : **data**(dune)

Unconstrained Ordination

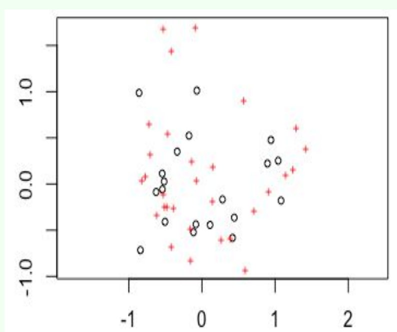
metaMDS(data, ...) `Nonmetric Multidimensional Scaling`

All ordination results can be displayed with

plot(data, type = "")

type = "p" results with points of black circles to indicate sites and red pluses to show species

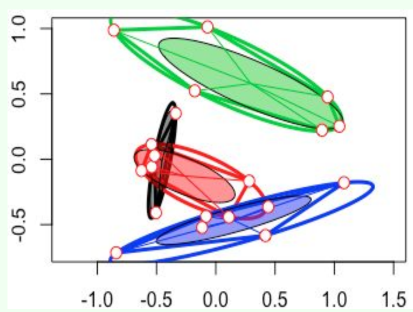
type = "t" results with text



ordihull() adds convex hulls

ordiellipse() adds ellipses of standard deviation, standard error or confidence areas

ordispider() draws items to their center



Constrained Ordination

cca(formula, data, ...) `Constrained Correspondence Analysis Displays only the variation that can be explained by used constraints`

rda(formula, data, scale=FALSE, ...) `Redundancy Analysis`

capscale(formula, data, distance = "", ...) `Distance based Redundancy Analysis`

formula( ) Model formula must be either community data matrix or dissimilarity matrix

OR

distance = "name of dissimilarity index**"** if formula is not specified

Analysis of constraints

anova.cca(object, permutations = "", ...) `Permutation Test for CCA & RDA to assess the significance of constraints`

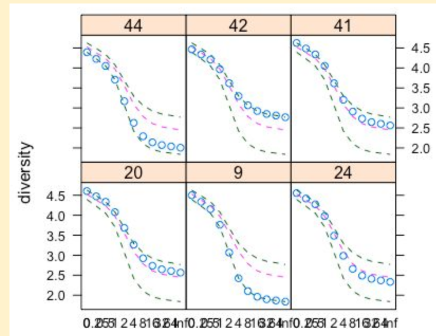
object specifies one or several result objects from cca, rda, or capscale

permutations = control values, or permutation index

Diversity Analysis of Eco Communities

diversity(data, index = " ", MARGIN = 1, base = exp(1), ...) `Shannon, Simpson, and Fisher diversity indices and species richness.`

renyi(data, scale = c(), raw = FALSE, ...) `Rényi Diversity index`



scale = c() Scales of Rényi diversity

raw = FALSE summary stats of permutations

raw = TRUE individual permutations

rarefy(data, sample, ...) `Rarefied Species Richness results in expected species richness of subsample`

Taxonomic Diversity

taxondive(data, distance, match.force = FALSE) `Taxonomic diversity indices`

taxa2dist(data, varstep = FALSE, check = TRUE, ...) `Converts class tables to taxonomic distances`

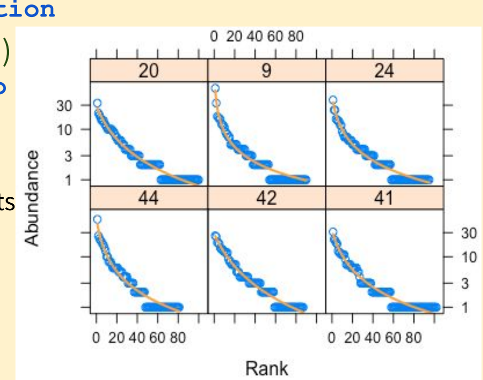
Ranked Abundance Distribution

radfit(data, ...) `Fits the most popular model to data using maximum likelihood estimation`

rad.null(data, family = poisson) `Fits broken stick model to expected abundance of species`

type = "b" Plots both observed points and fitted lines

family = Error distribution; poisson default is used for counts, gaussian may be appropriate for abundance



Beta Diversity

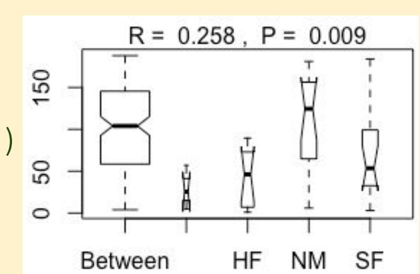
betadiver(data, method = NA, ...) `Estimates beta diversity`

method = "" can specify which beta index to use (24 options)

betadiver(help=TRUE) list all 24 indices available

Analysis of Diversity in Groups

anosim(data, grouping, permutations = "", distance = " ", ...) `Analysis of similarities between two or more groups`



Dissimilarity Analysis

vegdist(data, method=" ", na.rm = FALSE, ...) `Dissimilarity indices`

method = "dissimilarity index "

- "manhattan", "euclidean", "canberra", "clark", "bray", "kulczynski", "jaccard", "gower", "altGower", "morisita", "horn", "mountford", "raup", "binomial", "chao", "cao" or "mahalanobis".

Other Fun Features

vegemite(data, use, scale, sp.ind = "", site.ind = "", select , ...) `Creates a compact ordered community tree in text format`

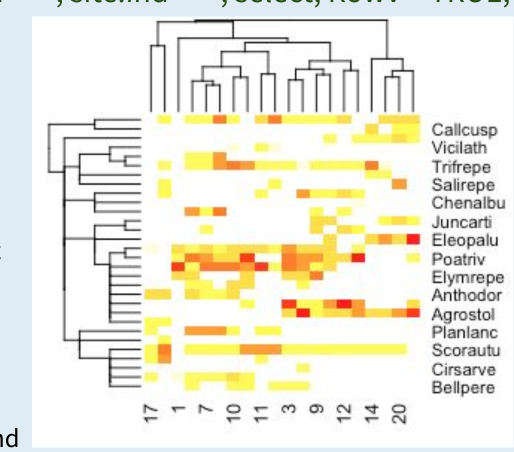
tabasco(data, use, sp.ind = "", site.ind = "", select, Rowv = TRUE, Colv = TRUE, scale, col = heat.colors(12), ...) `Creates a community table using heat map, abundances are coded by color`

use is either a vector or object

sp.ind / site.ind species and site indices

select a subset of plots

Rowv / Colv = reorder rows and columns, if TRUE it is ordered by correspondence analysis



beals(data, species = NA, reference = data, include = TRUE) `Beals Smoothing and Degree of Absence Analysis determines probability of a species occurring in a site based on joint occurrences with other species`

species = NA will compute for all species, or can specify single

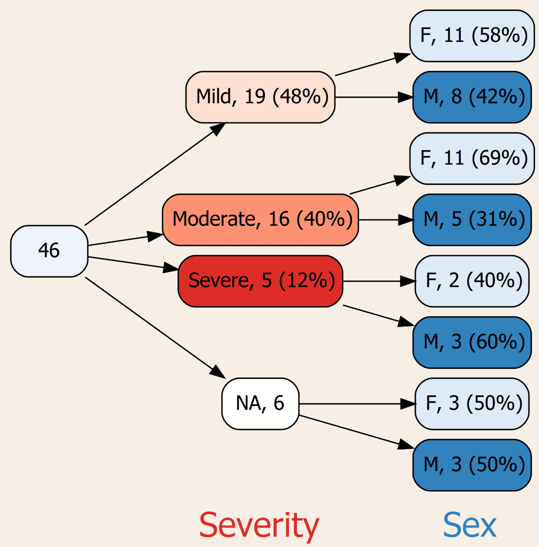
reference = data to be used to compare for joint analysis

include = TRUE to include target species in computations

****VEGAN** uses quantitative data but setting **binary = TRUE** will make data presence/absence**

Examining nested subsets with vtree: *cheat sheet*

```
vtree(FakeData,"Severity Sex",sameline=T)
```



Pruning

Parameter	Effect
`prune`	Remove identified nodes and their descendants.
`keep`	*Only* retain identified nodes and their descendants.
`prunebelow`	Remove descendants of identified nodes.
`follow`	*Only* retain descendants of identified nodes.

Example: `prune=list(Severity=c("Moderate","Severe"))`

Labels

Parameter setting	
`labelvar=c(variable="label")`	Assign *label* to *variable*
`labelnode= list(variable=c(New="Old"))`	In *variable*, replace *Old* with *New*
`tlabelnode=list(c(Group="A", Sex="F",label="girl")`	Change the label of a specific node
`varnamepointsize=30`	Set font size for variable names
`shownodelabels=FALSE`	Do not show node labels
`showvarnames=FALSE`	Do not show variable names
`showlegend=TRUE`	Show a legend
`title="All businesses"`	Show a title for the root node

Summaries

Type	Parameter setting
Simple	`summary="variable"`
Custom	`summary="variable format"`

Code	Produces
`%mean%`	mean
`%SD%`	standard deviation
`%sum%`	sum
`%range%`	range
`%median%`	median
`%IQR%`	inter-quartile range
`%freqpct%`	frequency and %
`%freq%`	just frequency
`%npct%`	frequency and %
`%pct%`	%
`%list%`	list values
`%trunc=n%`	truncation at ***n*** characters

Control code	summary restricted to:
`%noroot%`	all nodes except the root
`%leafonly%`	leaf nodes
`%var=v%`	nodes of variable *v*
`%node=n%`	nodes named *n*

Image settings

Parameter setting	Effect
`imagewidth="3in"`	3 inches wide
`imageheight="4in"`	4 inches tall
`pxwidth=800`	800 pixels wide
`pxheight=2000`	200 pixels high

Frequencies and percentages

Parameter setting	Effect
`vp=FALSE`	Full denominator
`showpct=FALSE`	Do not show %
`showcount=FALSE`	Do not show counts

Variable specification

Suffix	Effect
`#`	Variable names ending in numeric digits
`*`	Variable names ending in any character
`@`	REDCap checklist variable names

Prefix	Effect
`is.na:`	Missing value?
`r:`	REDCap checklist variable
`i:`	Intersection of group of variables
`any:`	Are any of a group of variables affirmative?
`all:`	Are all of a group of variables affirmative?

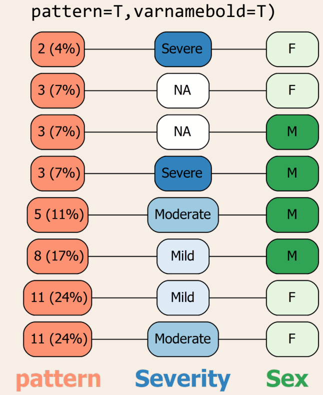
Text

Parameter setting	
`text=list(Category=c(triple="*"))`	Add * to all nodes of this type
`ttext=list(c(Group="A", Category="triple",text="*"))`	Add * to a specific node

Formatting			
`\n` line break	`*italics*`	`**bold**`	`%%red ...%%`

Pattern trees and tables

```
vtree(FakeData,"Severity Sex",
  pattern=T,varnamebold=T)
```




```
vtree(FakeData,"Severity Sex",
  ptable=T)
```

```
 n pct Severity Sex
 2   4   Severe   F
 3   7     <NA>   F
 3   7     <NA>   M
 3   7   Severe   M
 5  11 Moderate   M
 8  17     Mild   M
11  24     Mild   F
11  24 Moderate   F
```

Splitting text across lines

Parameter setting	Effect
`splitwidth=50`	Split text in nodes after 50 characters
`vsplitwidth=5`	Split text in variable names after 5 characters

xplain Cheat Sheet

Important Links

xplain package on CRAN	https://cran.r-project.org/web/packages/xplain/index.html
xplain web tutorial	http://www.zuckarelli.de/xplain/index.html
xplain cheat sheet	http://www.zuckarelli.de/xplain/xplain_cheatsheet.pdf
xplain on GitHub	https://www.github.com/jsugarelli/xplain

Purpose & Application

- xplain allows to **write interpretation/explanation texts** for statistical functions in the form of XML files.
- The user of the functions can read these explanations **while working on his/her specific problems**.
- xplain explanations **can react to the user's results** and provide meaningful insights related to the user's problem.
- For this, the xplain **XML files can contain R code** and can **work with the return object** of the user's function call.

```
> xplain("lm(education ~ young + income + urban)")
> Your R^2 is 0.11 which is quite low. There is a serious
risk your model is misspecified. You should reconsider the
selection of variables included in your model.
```

xplain XML files

<xplain>

1 Any valid xplain XML must be enclosed in an `<xplain>` block. Multiple `<xplain>` blocks per XML file are possible.

<package>

2 A `<package>` block combines all functions from the same package.

<function>

3 Within a `<function>` block, explanations/interpretations for the function as such or for specific elements of the return object can be provided.

<result>

4 Packages explanations/ interpretations related to one element of the function's return object.

```
<xml>
① <xplain>
  ② <package name = "stats">
    ③ <function name = "lm">
      ④ <title>This is about lm</title>
      ⑤ <text>…</text>
      ⑥ <result name = "coefficients">
        ④ <title>…<title>
        ⑤ <text>…</text>
      </result>
    </function>
  </package>
</xplain>
</xml>
```

Not case-sensitive

<title>

5 Structures explanations with headers.

<text>

6 The actual explanations/interpretations. Can include R code with references to the function's return object.

Main attributes: Overview

name	Name of the element (package, function, result).
lang	Language (ISO code) of the explanation (e.g. `"EN"`).
level	Complexity level; integer number; cumulative, i.e. `level=1` explanations will also be presented when `level=2` or `level=3` are called.

Attributes: Inheritance and necessity

- Elements **inherit attributes from higher-level** elements; e.g., if only one language, definition on `<xplain>` level suffices. Lower-level attributes overrule higher-level.
- **name** attribute required for `<package>`, `<function>` and `<result>` elements.
- All levels shown, if no `level` is given to `xplain()`.

Including R code

R code can be easily integrated into `<text></text>` elements:

```
<text> !%% R code %%! </text>
```

R code delimiter tags

Access the explained function's (`<function name="…">`) return object:

- Access the full return object with `@`. Example: `summary(@)`.
- Access the current `<result name="…">` item of the return object with `##`. Example: `mean(##)`.

Using placeholders

```
<define name= "placeholder" > !%% R code %%! </define>

</text> Text… !** "placeholder" **! Text… </text>
```

Placeholder name delimiter tags

Example: `<define name="s">!%% summary(@) %%!</define>`
`<text>And here is the summary !**s**! for your model</text>`

Iterating through (items of) the return object

- To apply a `<text>` element to a whole matrix, data frame, vector or list, use the **`foreach`** attribute.
- Value of `foreach` defines what is iterated over and (for 2D structures) in which sequence; `items` is for lists.
- `$` is a placeholder for the index of the current element.
- **Example** (shows all 1st column elements of the coefficient matrix):
`<text foreach="rows">!%% @$coefficients[$,1] %%!</text>`

foreach =
"rows"
"columns"
"rows, columns"
"columns, rows"
"items"

Calling xplain()

1 Direct call of `xplain()`

call	Call of the explained function as string
xml	Path of the XML file providing the explanations
lang	Language of the explanations to be shown (default means English)
level	Complexity level of the explanations (cumulative! Default means "all")

2 Wrapper function with `xplain.getcall()`

Example: lm

```
lm.xplain <- function(formula, data, subset, weights, na.action,
method = "qr", model = TRUE, x = FALSE, y = FALSE, qr = TRUE,
singular.ok = TRUE, contrasts = NULL, offset, ...) {
  call<-xplain.getcall("lm")
  xplain(call, xml="http://www.zuckarelli.de/example_lm.xml")
}
```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