Executive Summary of Data Science and Artificial Intelligence

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Part II

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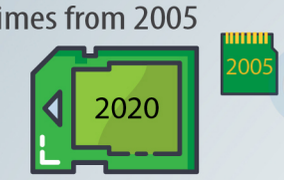
1. Overview

Data Flair

BIG DATA

Volume
SCALE OF DATA

40 ZETTABYTES
[43 TRILLION GIGABYTES]
of data will be created by 2020, an increase of 300 times from 2005



It's esimated that
2.5 QUINTILLION BYTES
[2.3 TRILLION GIGABYTES]
of data is created each day

6 BILLION PEOPLE
have cell phones

WORLD POPULATION: 7 BILLION

Most companies in the U.S. have at least
100 TERABYTES
[1,00,000 GIGABYTES]
of data stored

Variety
DIFFERENT FROMS OF DATA

400 MILLION TWEETS
are sent per day by about 200 million monthly active users

As of 2011, the global size of data in healthcare was estimated to be
150 EXABYTES
[161 BILLION GIGABYTES]

30 BILLION PIECES OF CONTENT
are shared on Facebook every month

facebook

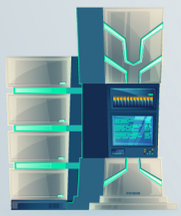
4 BILLION+ HOURS OF VIDEO
are watched on YouTube each month

YouTube YouTube

1 IN 3 BUSINESS
don't trust the information they use to make decisions

Velocity
ANALYSIS OF STREAMING DATA

Morden cars have close to
100 SENSORS
that monitor items such as fuel level and tire pressure

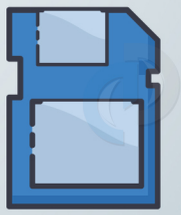


The New York Stock Exchange capture
1 TB OF TRADE INFORMATION
during each trading session

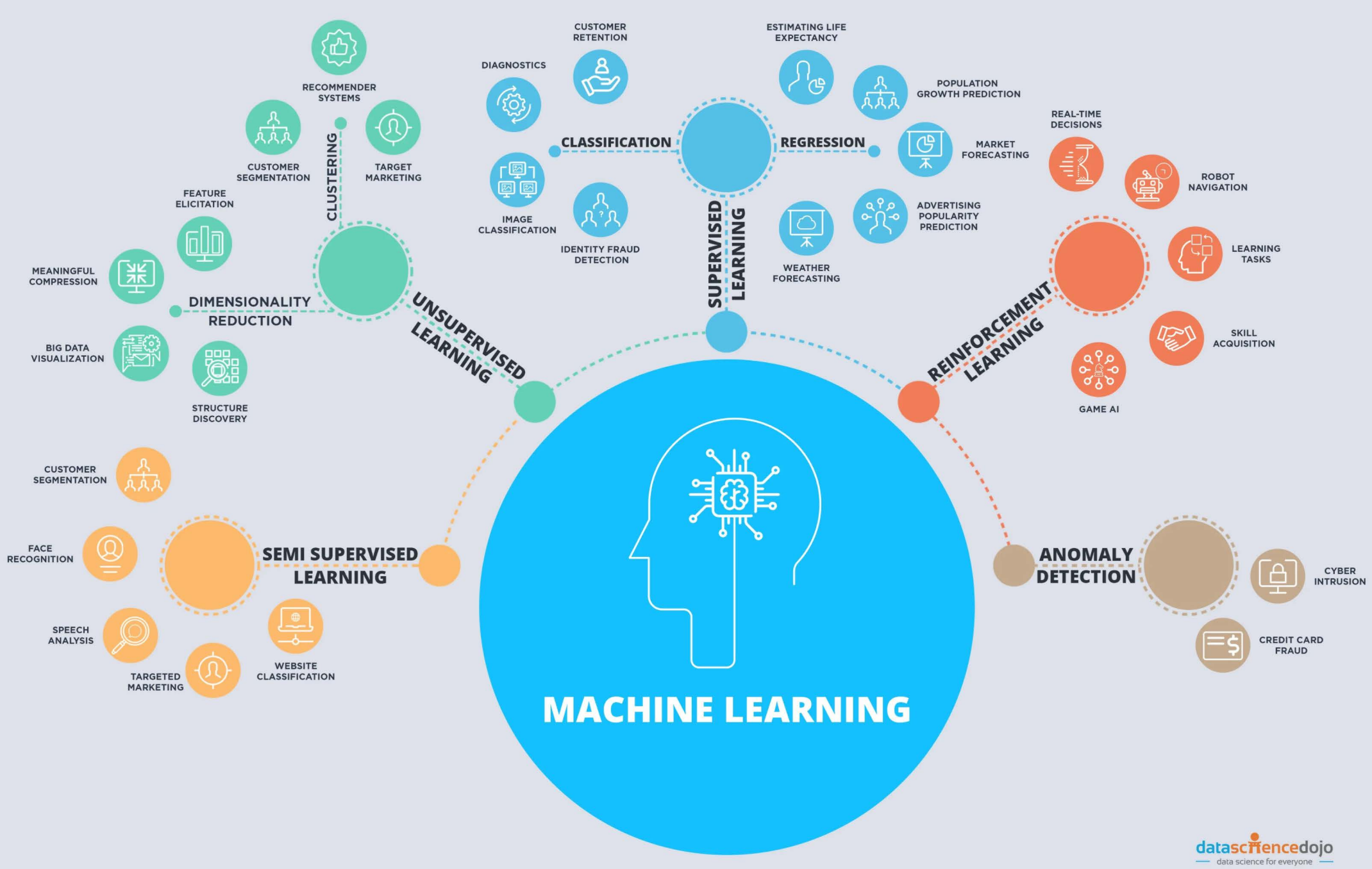
By 2016, it is projected there will be
18.9 BILLION NETWORK CONNECTIONS - almost 2.5 connections per person on earth

Veracity
UNCERTAINTY OF DATA

in one survey were unsure of how much of their data was inaccurate



Poor data quality costs the US economy around
$3.1 TRILLION A YEAR


MACHINE LEARNING
UNSUPERVISED LEARNING
CLUSTERING
RECOMMENDER SYSTEMS
CUSTOMER SEGMENTATION
TARGET MARKETING
DIMENSIONALITY REDUCTION
FEATURE ELICITATION
MEANINGFUL COMPRESSION
BIG DATA VISUALIZATION
STRUCTURE DISCOVERY
SUPERVISED LEARNING
CLASSIFICATION
DIAGNOSTICS
CUSTOMER RETENTION
IMAGE CLASSIFICATION
IDENTITY FRAUD DETECTION
REGRESSION
ESTIMATING LIFE EXPECTANCY
POPULATION GROWTH PREDICTION
MARKET FORECASTING
ADVERTISING POPULARITY PREDICTION
WEATHER FORECASTING
REINFORCEMENT LEARNING
REAL-TIME DECISIONS
ROBOT NAVIGATION
LEARNING TASKS
SKILL ACQUISITION
GAME AI
SEMI SUPERVISED LEARNING
CUSTOMER SEGMENTATION
FACE RECOGNITION
SPEECH ANALYSIS
TARGETED MARKETING
WEBSITE CLASSIFICATION
ANOMALY DETECTION
CYBER INTRUSION
CREDIT CARD FRAUD
datasciencedojo
data science for everyone

TOP PREDICTION ALGORITHMS

TYPE	NAME	DESCRIPTION	ADVANTAGES	DISADVANTAGES
Linear	Linear regression	**The "best fit" line** through all data points. Predictions are numerical.	Easy to understand -- you clearly see what the biggest drivers of the model are.	X **Sometimes too simple to capture complex relationships between variables.** X **Does poorly with correlated features.**
Linear	Logistic regression	The adaptation of **linear regression** to problems of classification (e.g., yes/no questions, groups, etc.)	Also easy to understand.	X **Sometimes too simple to capture complex relationships between variables.** X **Does poorly with correlated features.**
Tree-based	Decision tree	**A series of yes/no rules based on the features,** forming a tree, to match all possible outcomes of a decision.	Easy to understand.	X **Not often used on its own for prediction because it's also often too simple and not powerful enough for complex data.**
Tree-based	Random Forest	Takes advantage of many decision trees, with rules created from subsamples of features. Each tree is weaker than a full decision tree, but **by combining them we get better overall performance.**	A sort of "wisdom of the crowd". Tends to result in very high quality models. Fast to train.	X **Models can get very large.** X **Not easy to understand predictions.**
Tree-based	Gradient Boosting	Uses even weaker decision trees, that are increasingly **focused on "hard" examples.**	High-performing.	X **A small change in the feature set or training set can create radical changes in the model.** X **Not easy to understand predictions.**
Neural networks	Neural networks	Interconnected «neurons» that pass messages to each other. Deep learning uses several **layers of neural networks stacked on top of one another.**	Can handle extremely complex tasks - no other algorithm comes close in image recognition.	X **Very slow to train, because they often have a very complex architecture.** X **Almost impossible to understand predictions.**

A mostly complete chart of

Neural Networks

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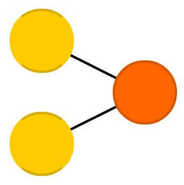
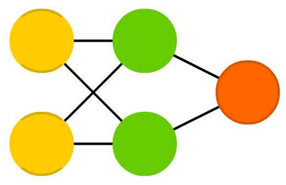
- Input Cell
- Backfed Input Cell
- Noisy Input Cell
- Hidden Cell
- Probablistic Hidden Cell
- Spiking Hidden Cell
- Capsule Cell
- Output Cell
- Match Input Output Cell
- Recurrent Cell
- Memory Cell
- Gated Memory Cell
- Kernel
- Convolution or Pool

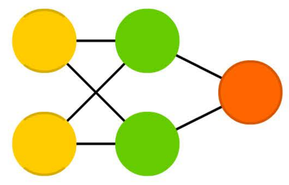
Perceptron (P)



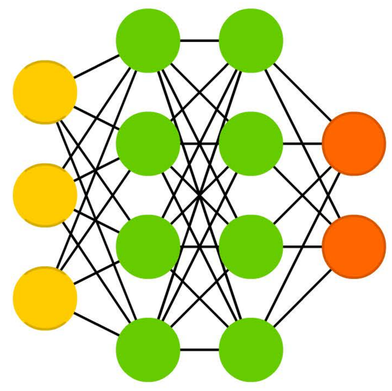
Feed Forward (FF)



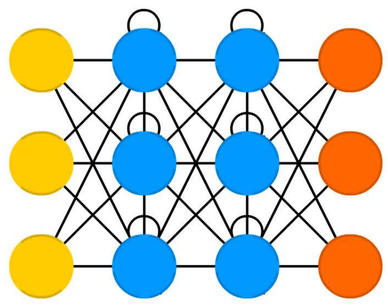
Radial Basis Network (RBF)



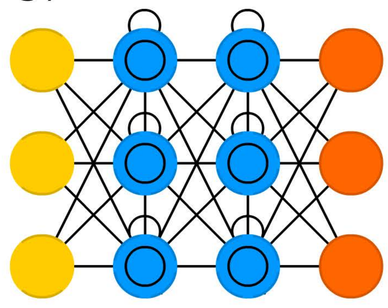
Deep Feed Forward (DFF)



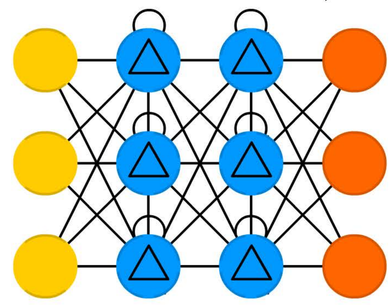
Recurrent Neural Network (RNN)



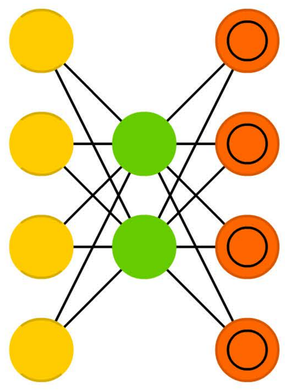
Long / Short Term Memory (LSTM)



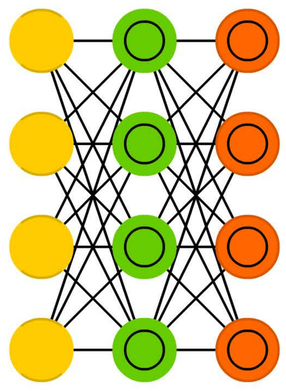
Gated Recurrent Unit (GRU)



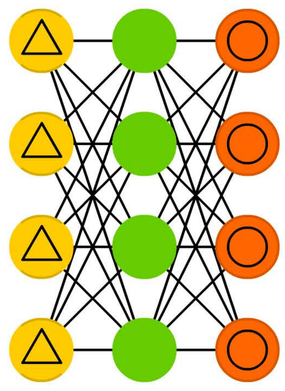
Auto Encoder (AE)



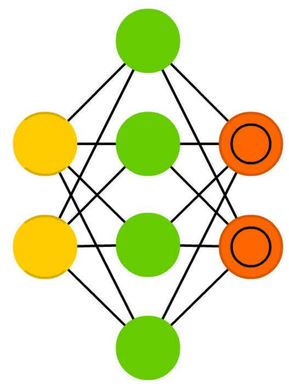
Variational AE (VAE)



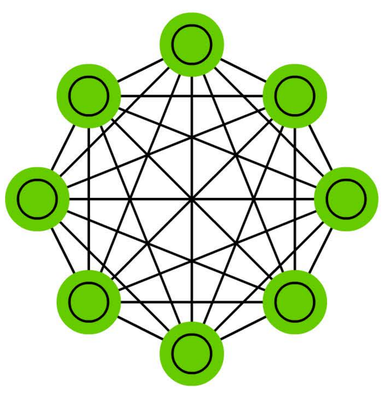
Denoising AE (DAE)



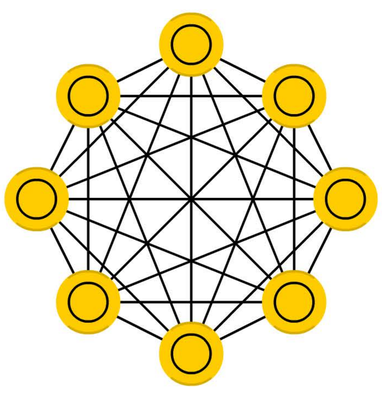
Sparse AE (SAE)



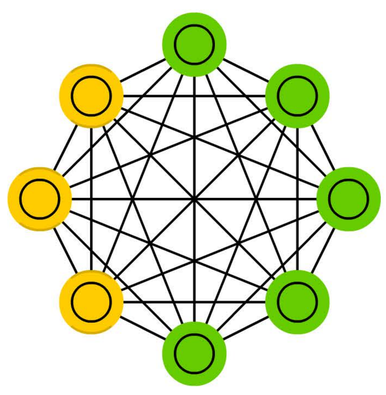
Markov Chain (MC)



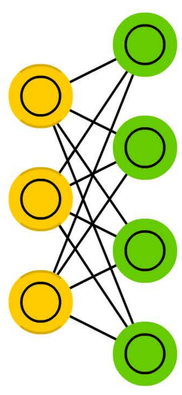
Hopfield Network (HN)



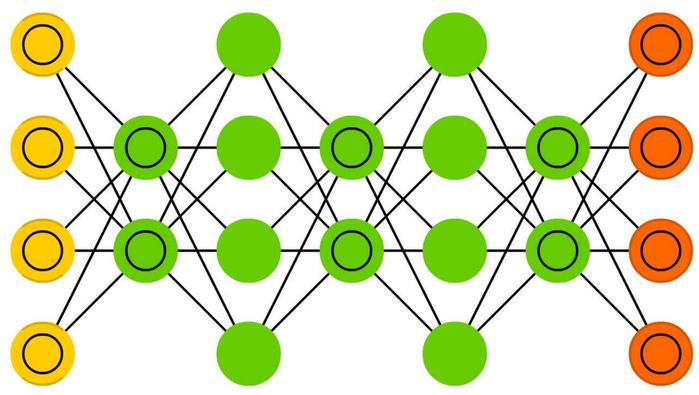
Boltzmann Machine (BM)



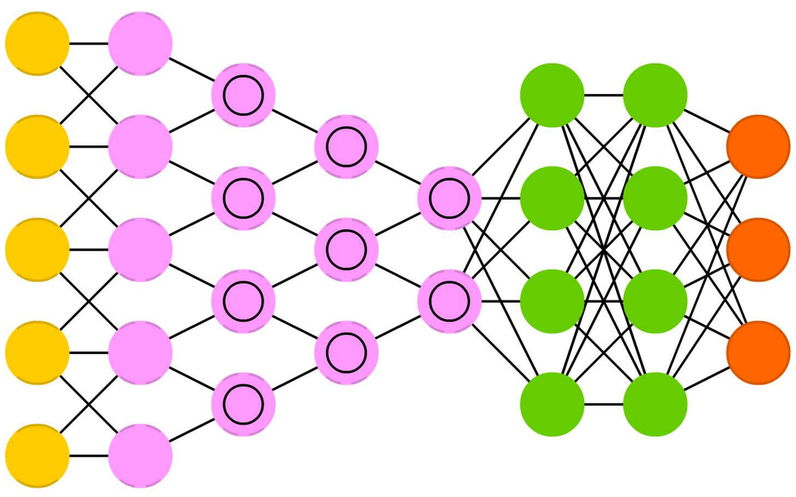
Restricted BM (RBM)



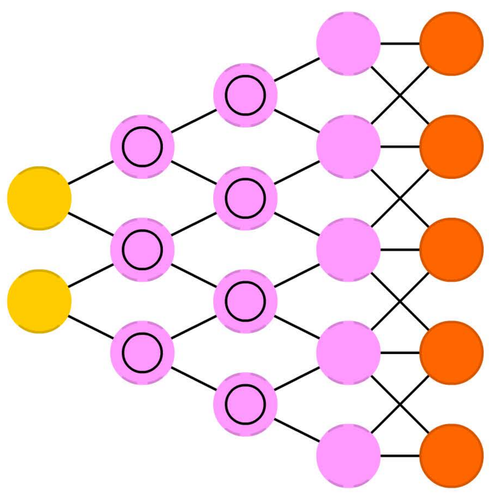
Deep Belief Network (DBN)



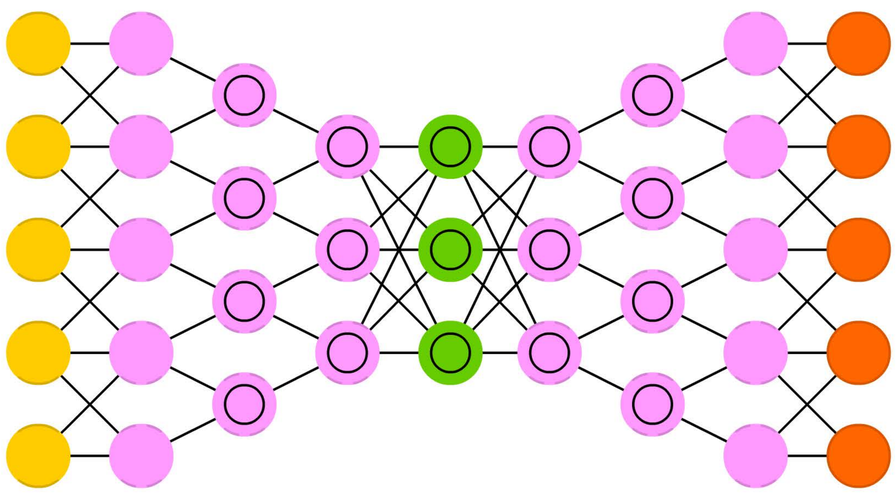
Deep Convolutional Network (DCN)



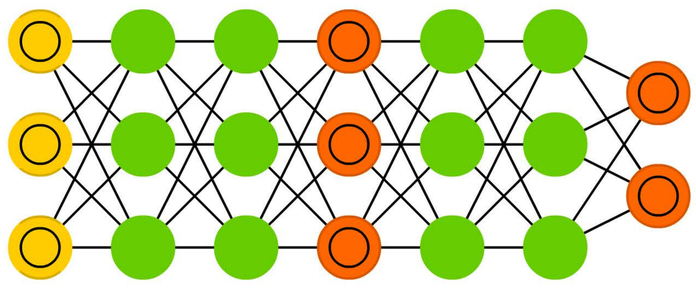
Deconvolutional Network (DN)



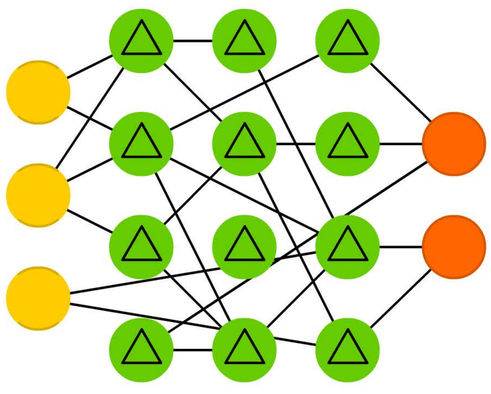
Deep Convolutional Inverse Graphics Network (DCIGN)



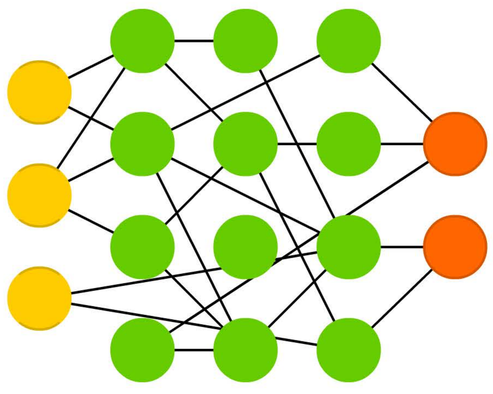
Generative Adversarial Network (GAN)



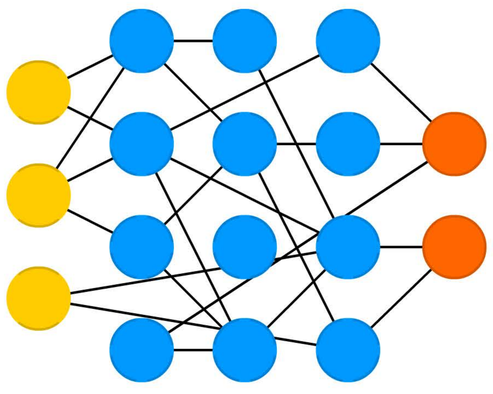
Liquid State Machine (LSM)



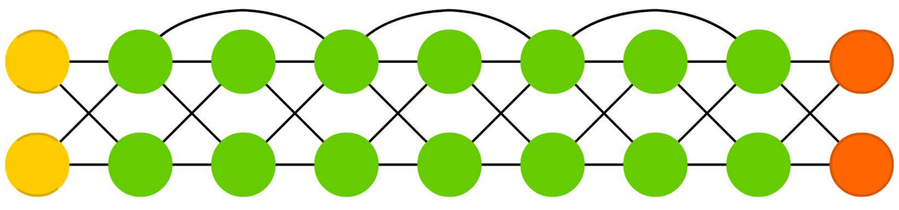
Extreme Learning Machine (ELM)



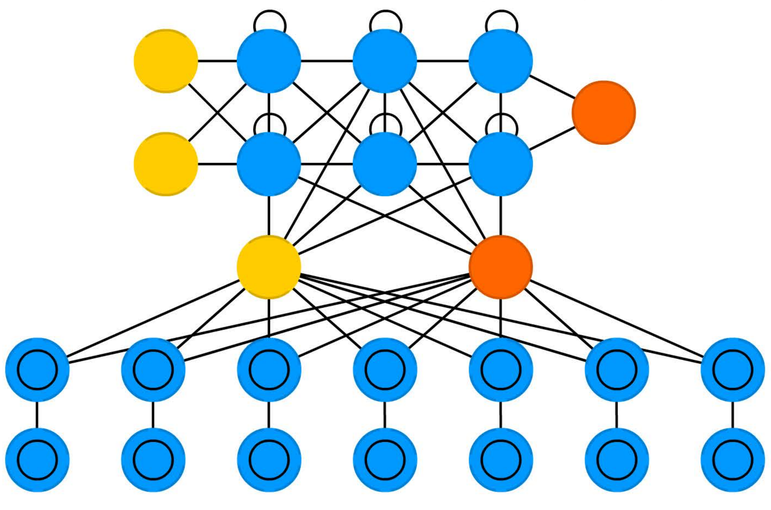
Echo State Network (ESN)



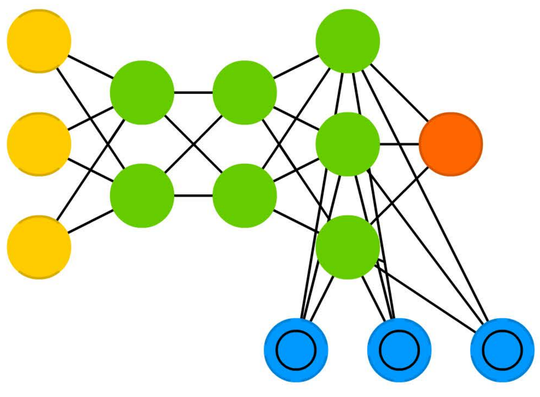
Deep Residual Network (DRN)



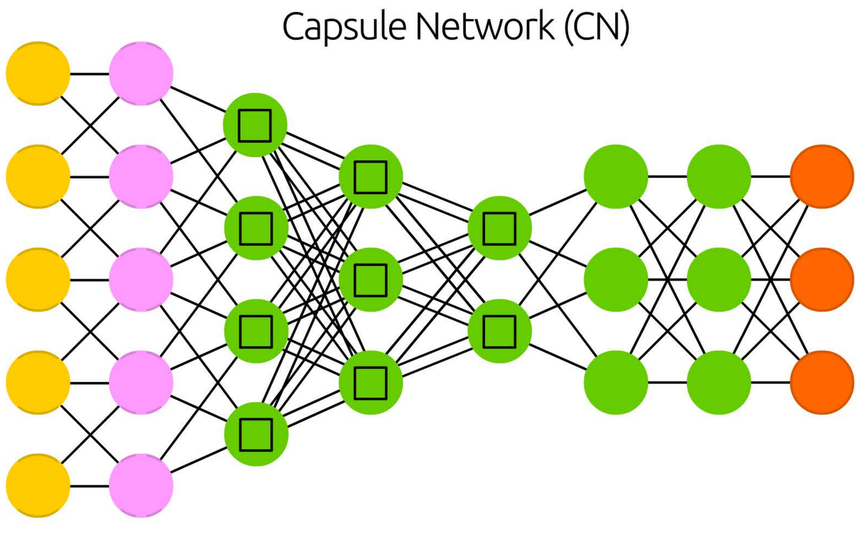
Differentiable Neural Computer (DNC)



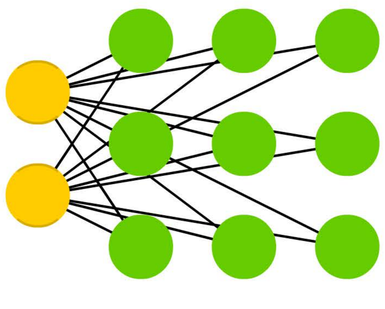
Neural Turing Machine (NTM)



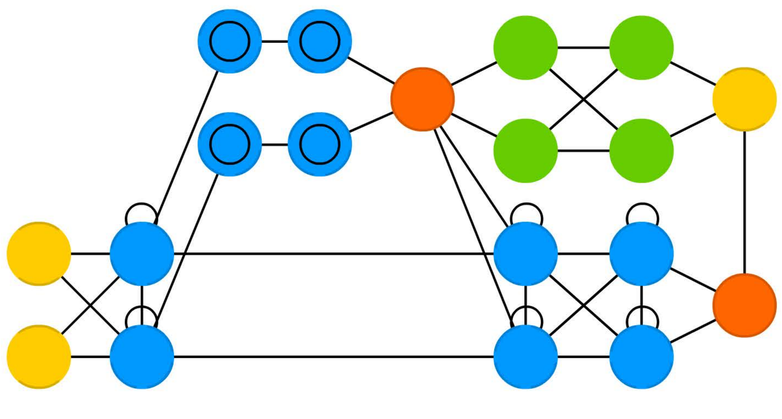
Capsule Network (CN)



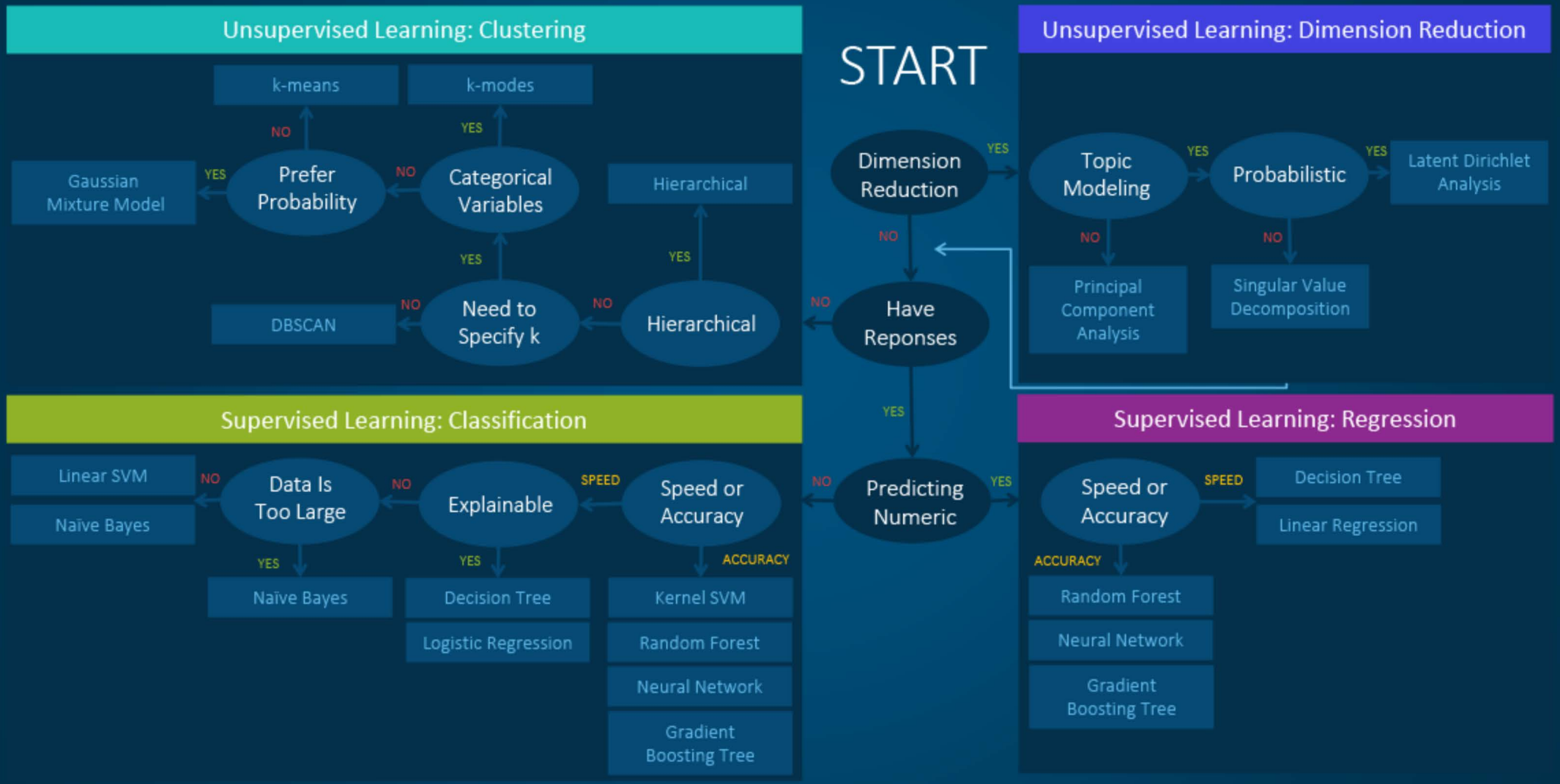
Kohonen Network (KN)



Attention Network (AN)



Machine Learning Algorithms Cheat Sheet



Microsoft Azure Machine Learning: Algorithm Cheat Sheet

This cheat sheet helps you choose the best Azure Machine Learning Studio algorithm for your predictive analytics solution. Your decision is driven by both the nature of your data and the question you're trying to answer.

START

Finding unusual data points

ANOMALY DETECTION

- **One-class SVM** — >100 features, aggressive boundary
- **PCA-based anomaly detection** — Fast training

Discovering structure

CLUSTERING

- **K-means**

Three or more

MULTI-CLASS CLASSIFICATION

- Fast training, linear model — **Multiclass logistic regression**
- Accuracy, long training times — **Multiclass neural network**
- Accuracy, fast training — **Multiclass decision forest**
- Accuracy, small memory footprint — **Multiclass decision jungle**
- Depends on the two-class classifier, see notes below — **One-v-all multiclass**

Predicting categories

Predicting values

REGRESSION

- **Ordinal regression** — Data in rank ordered categories
- **Poisson regression** — Predicting event counts
- **Fast forest quantile regression** — Predicting a distribution
- **Linear regression** — Fast training, linear model
- **Bayesian linear regression** — Linear model, small data sets
- **Neural network regression** — Accuracy, long training time
- **Decision forest regression** — Accuracy, fast training
- **Boosted decision tree regression** — Accuracy, fast training, large memory footprint

Two

TWO-CLASS CLASSIFICATION

- **Two-class SVM** — >100 features, linear model
- **Two-class averaged perceptron** — Fast training, linear model
- **Two-class logistic regression** — Fast training, linear model
- **Two-class Bayes point machine** — Fast training, linear model

- Accuracy, fast training — **Two-class decision forest**
- Accuracy, fast training, large memory footprint — **Two-class boosted decision tree**
- Accuracy, small memory footprint — **Two-class decision jungle**
- >100 features — **Two-class locally deep SVM**
- Accuracy, long training times — **Two-class neural network**

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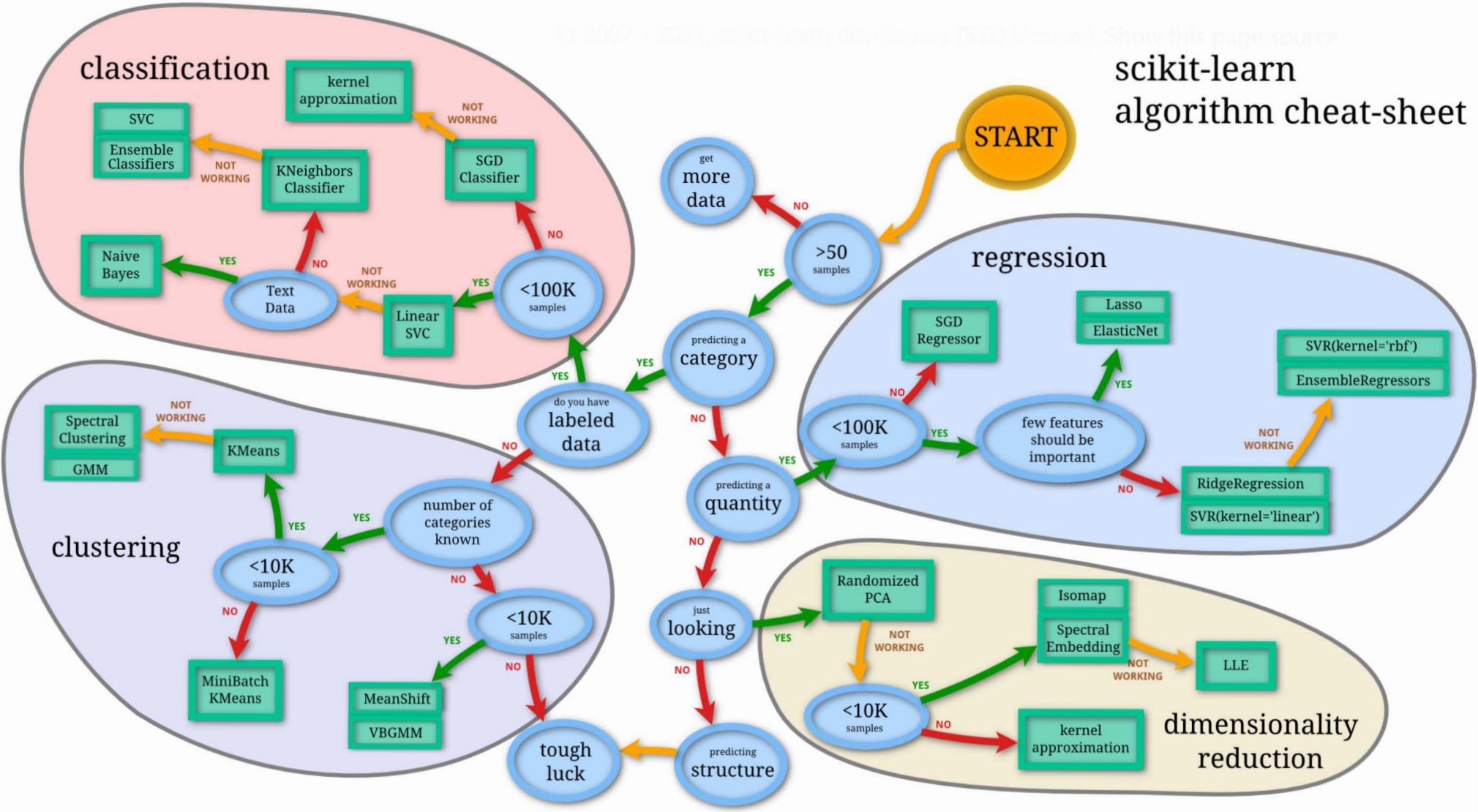
scikit-learn algorithm cheat-sheet



2. Python

matplotlib Cheat sheet

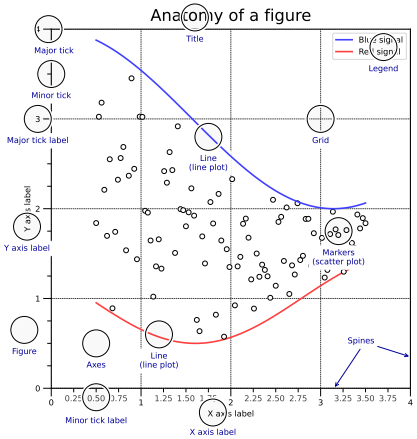
Version 3.5.0

Quick start

API

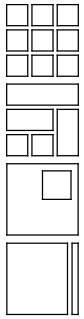
```
import numpy as np
import matplotlib as mpl
import matplotlib.pyplot as plt


X = np.linspace(0, 2*np.pi, 100)
Y = np.cos(X)

fig, ax = plt.subplots()
ax.plot(X, Y, color='green')

fig.savefig("figure.pdf")
fig.show()
```

Anatomy of a figure



Subplots layout

API



```
subplot[s](rows,cols,…)
fig, axs = plt.subplots(3, 3)

G = gridspec(rows,cols,…)
ax = G[0,:]

ax.inset_axes(extent)

d=make_axes_locatable(ax)
ax = d.new_horizontal('10%')
```

Getting help

- matplotlib.org
- github.com/matplotlib/matplotlib/issues
- discourse.matplotlib.org
- stackoverflow.com/questions/tagged/matplotlib
- gitter.im/matplotlib
- twitter.com/matplotlib
- Matplotlib users mailing list

Basic plots

`plot([X],Y,[fmt],…)` API
X, **Y**, fmt, color, marker, linestyle

`scatter(X,Y,…)` API
X, **Y**, [s]izes, [c]olors, marker, cmap

`bar[h](x,height,…)` API
x, **height**, width, bottom, align, color

`imshow(Z,…)` API
Z, cmap, interpolation, extent, origin

`contour[f]([X],[Y],Z,…)` API
X, Y, **Z**, levels, colors, extent, origin

`pcolormesh([X],[Y],Z,…)` API
X, Y, **Z**, vmin, vmax, cmap

`quiver([X],[Y],U,V,…)` API
X, Y, **U**, **V**, C, units, angles

`pie(X,…)` API
Z, explode, labels, colors, radius

`text(x,y,text,…)` API
x, y, **text**, va, ha, size, weight, transform

`fill[_between][x](…)` API
X, Y1, Y2, color, where

Advanced plots

`step(X,Y,[fmt],…)` API
X, **Y**, fmt, color, marker, where

`boxplot(X,…)` API
X, notch, sym, bootstrap, widths

`errorbar(X,Y,xerr,yerr,…)` API
X, Y, xerr, yerr, fmt

`hist(X, bins, …)` API
X, bins, range, density, weights

`violinplot(D,…)` API
D, positions, widths, vert

`barbs([X],[Y], U, V, …)` API
X, Y, **U**, **V**, C, length, pivot, sizes

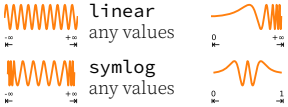
`eventplot(positions,…)` API
positions, orientation, lineoffsets

`hexbin(X,Y,C,…)` API
X, Y, C, gridsize, bins

Scales

API

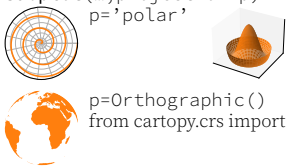
`ax.set_[xy]scale(scale,…)`



Projections

API

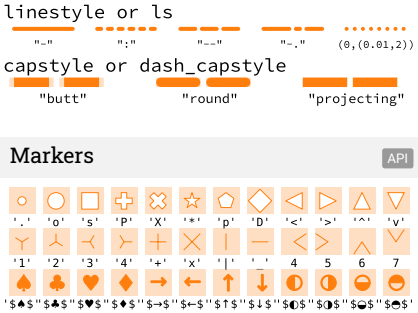
`subplot(…,projection=p)`



API

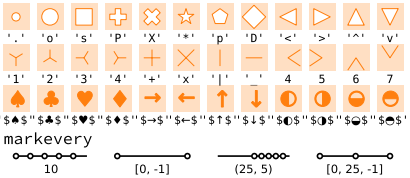
Lines

API



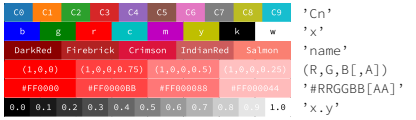
Markers

API



Colors

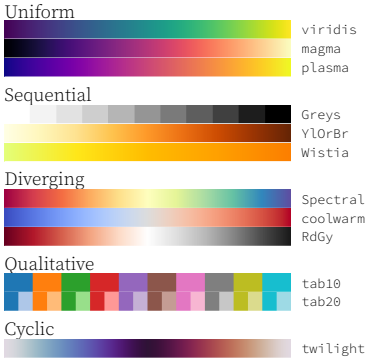
API



Colormaps

API

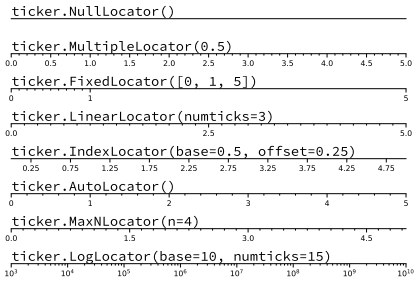
`plt.get_cmap(name)`



Tick locators

API

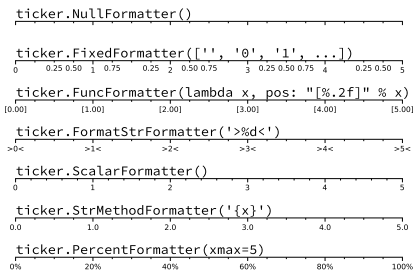
```
from matplotlib import ticker
ax.[xy]axis.set_[minor|major]_locator(locator)
```



Tick formatters

API

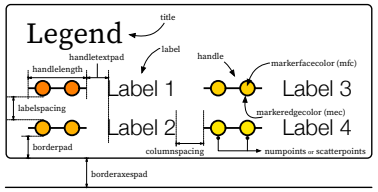
```
from matplotlib import ticker
ax.[xy]axis.set_[minor|major]_formatter(formatter)
```



Ornaments

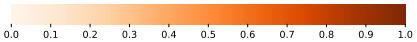
API

`ax.legend(…)`
handles, labels, loc, title, frameon



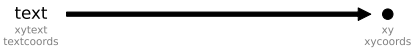
API

`ax.colorbar(…)`
mappable, ax, cax, orientation



API

`ax.annotate(…)`
text, **xy**, **xytext**, xycoords, textcoords, arrowprops



Event handling

API

```
fig, ax = plt.subplots()
def on_click(event):
  print(event)
fig.canvas.mpl_connect(
  'button_press_event', on_click)
```

Animation

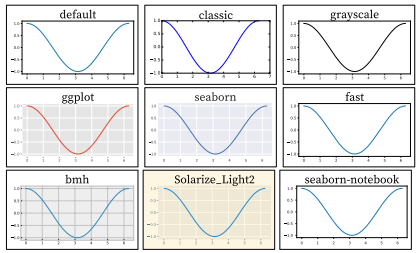
API

```
import matplotlib.animation as mpla

T = np.linspace(0, 2*np.pi, 100)
S = np.sin(T)
line, = plt.plot(T, S)
def animate(i):
    line.set_ydata(np.sin(T+i/50))
anim = mpla.FuncAnimation(
    plt.gcf(), animate, interval=5)
plt.show()
```

Styles

API

`plt.style.use(style)`



Quick reminder

```
ax.grid()
ax.patch.set_alpha(0)
ax.set_[xy]lim(vmin, vmax)
ax.set_[xy]label(label)
ax.set_[xy]ticks(list)
ax.set_[xy]ticklabels(list)
ax.set_[sup]title(title)
ax.tick_params(width=10, …)
ax.set_axis_[on|off]()

fig.tight_layout()
plt.gcf(), plt.gca()
mpl.rc('axes', linewidth=1, …)
fig.patch.set_alpha(0)
text=r'$\frac{-e^{i\pi}}{2^n}$'
```

Keyboard shortcuts

API

ctrl + s	Save	ctrl + w	Close plot
r	Reset view	f	Fullscreen 0/1
f	View forward	b	View back
p	Pan view	o	Zoom to rect
x	X pan/zoom	y	Y pan/zoom
g	Minor grid 0/1	G	Major grid 0/1
l	X axis log/linear	L	Y axis log/linear

Ten simple rules

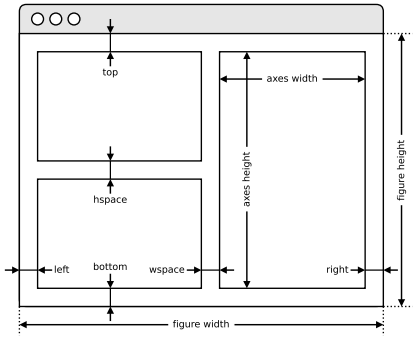
READ

1. Know Your Audience
2. Identify Your Message
3. Adapt the Figure
4. Captions Are Not Optional
5. Do Not Trust the Defaults
6. Use Color Effectively
7. Do Not Mislead the Reader
8. Avoid "Chartjunk"
9. Message Trumps Beauty
10. Get the Right Tool

Axes adjustments

API

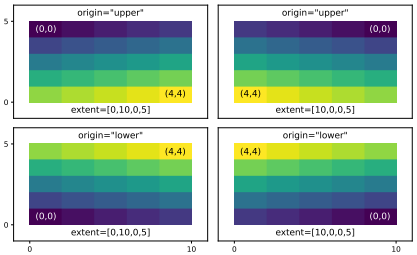
plt.**subplots_adjust**(...)



Extent & origin

API

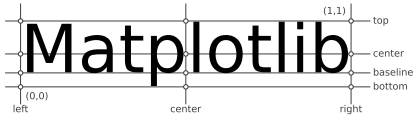
ax.**imshow**(extent=..., origin=...)



Text alignments

API

ax.**text**(..., ha=... , va=..., ...)



Text parameters

API

ax.**text**(..., family=..., size=..., weight=...)
ax.**text**(..., fontproperties=...)

The quick brown fox — xx-large (1.73)
The quick brown fox — x-large (1.44)
The quick brown fox — large (1.20)
The quick brown fox — medium (1.00)
The quick brown fox — small (0.83)
The quick brown fox — x-small (0.69)
The quick brown fox — xx-small (0.58)

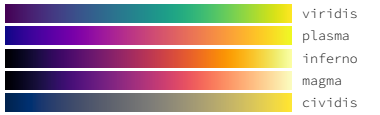
The quick brown fox jumps over the lazy dog — black (900)
The quick brown fox jumps over the lazy dog — bold (700)
The quick brown fox jumps over the lazy dog — semibold (600)
The quick brown fox jumps over the lazy dog — normal (400)
The quick brown fox jumps over the lazy dog — ultralight (100)

The quick brown fox jumps over the lazy dog — monospace
The quick brown fox jumps over the lazy dog — serif
The quick brown fox jumps over the lazy dog — sans
The quick brown fox jumps over the lazy dog — cursive

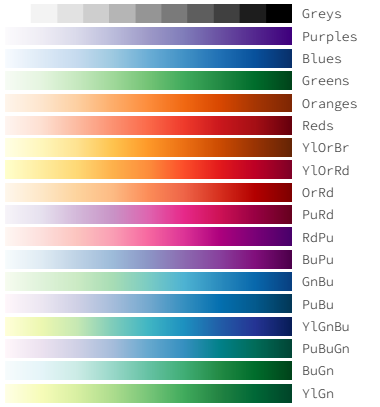
The quick brown fox jumps over the lazy dog — italic
The quick brown fox jumps over the lazy dog — normal

THE QUICK BROWN FOX JUMPS OVER THE LAZY DOG — small-caps
The quick brown fox jumps over the lazy dog — normal

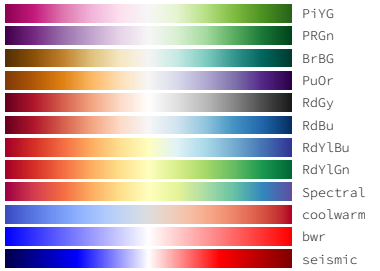
Uniform colormaps



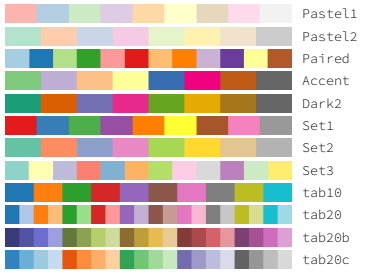
Sequential colormaps



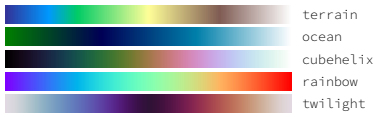
Diverging colormaps



Qualitative colormaps



Miscellaneous colormaps



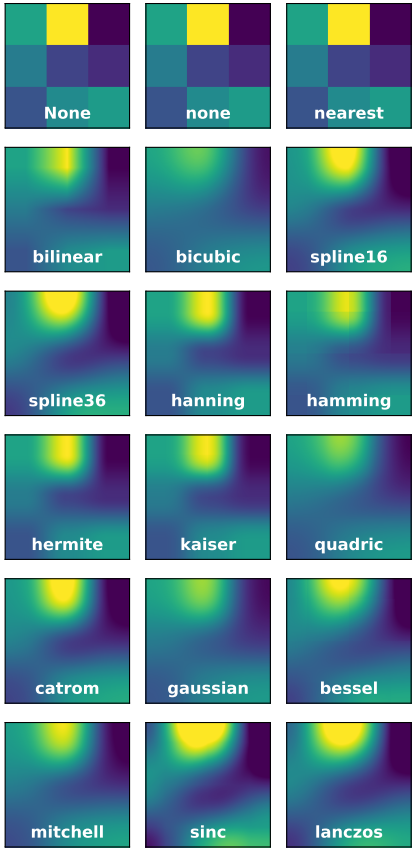
Color names

API

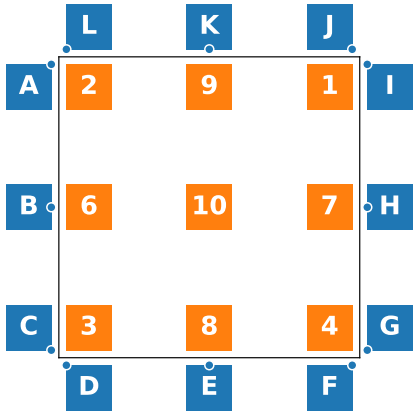
black, k, dimgray, dimgrey, gray, grey, darkgray, darkgrey, silver, lightgray, lightgrey, gainsboro, whitesmoke, w, white, snow, rosybrown, lightcoral, indianred, brown, firebrick, maroon, darkred, r, red, mistyrose, salmon, tomato, darksalmon, coral, orangered, lightsalmon, sienna, seashell, chocolate, saddlebrown, sandybrown, peachpuff, peru, linen, bisque, darkorange, burlywood, antiquewhite, tan, navajowhite, blanchedalmond, papayawhip, moccasin, orange, wheat, oldlace, floralwhite, darkgoldenrod, goldenrod, cornsilk, gold, lemonchiffon, khaki, palegoldenrod, darkkhaki, ivory, beige, lightyellow, lightgoldenrodyellow, olive, y, yellow, olivedrab, yellowgreen, darkolivegreen, greenyellow, chartreuse, lawngreen, honeydew, darkseagreen, palegreen, lightgreen, forestgreen, limegreen, darkgreen, g, green, lime, seagreen, mediumseagreen, springgreen, mintcream, mediumspringgreen, mediumaquamarine, aquamarine, turquoise, lightseagreen, mediumturquoise, azure, lightcyan, paleturquoise, darkslategray, darkslategrey, teal, darkcyan, c, aqua, cyan, darkturquoise, cadetblue, powderblue, lightblue, deepskyblue, skyblue, lightskyblue, steelblue, aliceblue, dodgerblue, lightslategray, lightslategrey, slategray, slategrey, lightsteelblue, cornflowerblue, royalblue, ghostwhite, lavender, midnightblue, navy, darkblue, mediumblue, b, blue, slateblue, darkslateblue, mediumslateblue, mediumpurple, rebeccapurple, blueviolet, indigo, darkorchid, darkviolet, mediumorchid, thistle, plum, violet, purple, darkmagenta, m, fuchsia, magenta, orchid, mediumvioletred, deeppink, hotpink, lavenderblush, palevioletred, crimson, pink, lightpink

Image interpolation

API



Legend placement



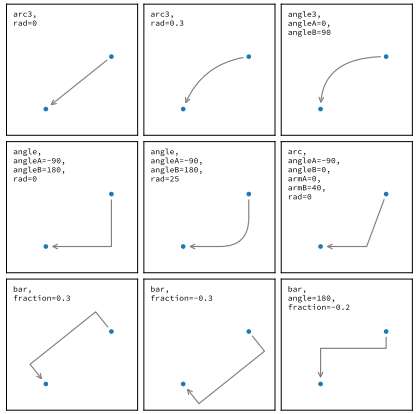
ax.**legend**(loc="string", bbox_to_anchor=(x,y))

2: upper left — 9: upper center — 1: upper right
6: center left — 10: center — 7: center right
3: lower left — 8: lower center — 4: lower right

A: upper right / (-0.1,0.9)
B: center right / (-0.1,0.5)
C: lower right / (-0.1,0.1)
D: upper left / (0.1,-0.1)
E: upper center / (0.5,-0.1)
F: upper right / (0.9,-0.1)
G: lower left / (1.1,0.1)
H: center left / (1.1,0.5)
I: upper left / (1.1,0.9)
J: lower right / (0.9,1.1)
K: lower center / (0.5,1.1)
L: lower left / (0.1,1.1)

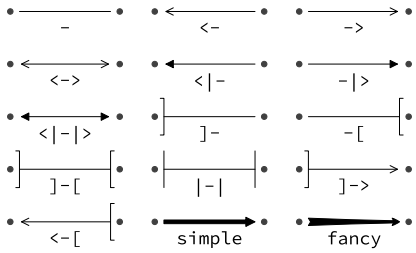
Annotation connection styles

API



Annotation arrow styles

API



How do I ...

... **resize a figure?**
→ fig.set_size_inches(w, h)
... **save a figure?**
→ fig.savefig("figure.pdf")
... **save a transparent figure?**
→ fig.savefig("figure.pdf", transparent=True)
... **clear a figure/an axes?**
→ fig.clear() → ax.clear()
... **close all figures?**
→ plt.close("all")
... **remove ticks?**
→ ax.set_[xy]ticks([])
... **remove tick labels ?**
→ ax.set_[xy]ticklabels([])
... **rotate tick labels ?**
→ ax.set_[xy]ticks(rotation=90)
... **hide top spine?**
→ ax.spines['top'].set_visible(False)
... **hide legend border?**
→ ax.legend(frameon=False)
... **show error as shaded region?**
→ ax.fill_between(X, Y+error, Y-error)
... **draw a rectangle?**
→ ax.add_patch(plt.Rectangle((0, 0), 1, 1)
... **draw a vertical line?**
→ ax.axvline(x=0.5)
... **draw outside frame?**
→ ax.plot(..., clip_on=False)
... **use transparency?**
→ ax.plot(..., alpha=0.25)
... **convert an RGB image into a gray image?**
→ gray = 0.2989*R + 0.5870*G + 0.1140*B
... **set figure background color?**
→ fig.patch.set_facecolor("grey")
... **get a reversed colormap?**
→ plt.get_cmap("viridis_r")
... **get a discrete colormap?**
→ plt.get_cmap("viridis", 10)
... **show a figure for one second?**
→ fig.show(block=False), time.sleep(1)

Performance tips

`scatter(X, Y)`	slow
`plot(X, Y, marker="o", ls="")`	fast
`for i in range(n): plot(X[i])`	slow
`plot(sum([x+[None] for x in X],[]))`	fast
`cla(), imshow(…), canvas.draw()`	slow
`im.set_data(…), canvas.draw()`	fast

Beyond Matplotlib

Seaborn: Statistical Data Visualization
Cartopy: Geospatial Data Processing
yt: Volumetric data Visualization
mpld3: Bringing Matplotlib to the browser
Datashader: Large data processing pipeline
plotnine: A Grammar of Graphics for Python

Matplotlib Cheatsheets
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NUMFOCUS
OPEN CODE = BETTER SCIENCE

Matplotlib for beginners

Matplotlib is a library for making 2D plots in Python. It is designed with the philosophy that you should be able to create simple plots with just a few commands:

1 Initialize

```
import numpy as np
import matplotlib.pyplot as plt
```

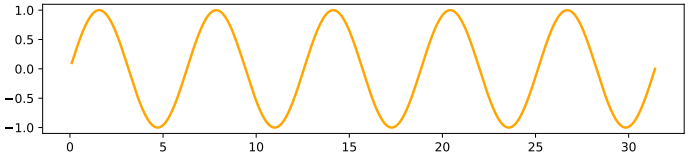
2 Prepare

```
X = np.linspace(0, 4*np.pi, 1000)
Y = np.sin(X)
```

3 Render

```
fig, ax = plt.subplots()
ax.plot(X, Y)
fig.show()
```

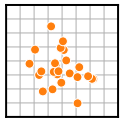
4 Observe



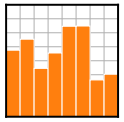
Choose

Matplotlib offers several kind of plots (see Gallery):

```
X = np.random.uniform(0, 1, 100)
Y = np.random.uniform(0, 1, 100)
ax.scatter(X, Y)
```



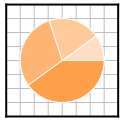
```
X = np.arange(10)
Y = np.random.uniform(1, 10, 10)
ax.bar(X, Y)
```



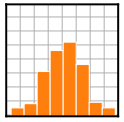
```
Z = np.random.uniform(0, 1, (8,8))

ax.imshow(Z)
```

```
Z = np.random.uniform(0, 1, (8,8))

ax.contourf(Z)
```

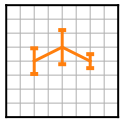
```
Z = np.random.uniform(0, 1, 4)

ax.pie(Z)
```



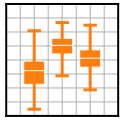
```
Z = np.random.normal(0, 1, 100)

ax.hist(Z)
```



```
X = np.arange(5)
Y = np.random.uniform(0, 1, 5)
ax.errorbar(X, Y, Y/4)
```



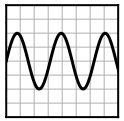
```
Z = np.random.normal(0, 1, (100,3))

ax.boxplot(Z)
```



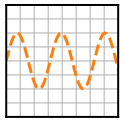
Tweak

You can modify pretty much anything in a plot, including limits, colors, markers, line width and styles, ticks and ticks labels, titles, etc.

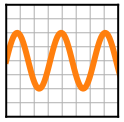
```
X = np.linspace(0, 10, 100)
Y = np.sin(X)
ax.plot(X, Y, color="black")
```



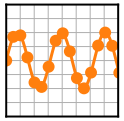
```
X = np.linspace(0, 10, 100)
Y = np.sin(X)
ax.plot(X, Y, linestyle="--")
```



```
X = np.linspace(0, 10, 100)
Y = np.sin(X)
ax.plot(X, Y, linewidth=5)
```



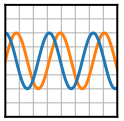
```
X = np.linspace(0, 10, 100)
Y = np.sin(X)
ax.plot(X, Y, marker="o")
```



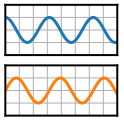
Organize

You can plot several data on the the same figure, but you can also split a figure in several subplots (named *Axes*):

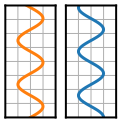
```
X = np.linspace(0, 10, 100)
Y1, Y2 = np.sin(X), np.cos(X)
ax.plot(X, Y1, X, Y2)
```



```
fig, (ax1, ax2) = plt.subplots((2,1))
ax1.plot(X, Y1, color="C1")
ax2.plot(X, Y2, color="C0")
```

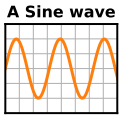


```
fig, (ax1, ax2) = plt.subplots((1,2))
ax1.plot(Y1, X, color="C1")
ax2.plot(Y2, X, color="C0")
```

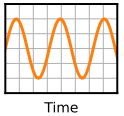


Label (everything)

```
ax.plot(X, Y)
fig.suptitle(None)
ax.set_title("A Sine wave")
```




```
ax.plot(X, Y)
ax.set_ylabel(None)
ax.set_xlabel("Time")
```



Explore

Figures are shown with a graphical user interface that allows to zoom and pan the figure, to navigate between the different views and to show the value under the mouse.

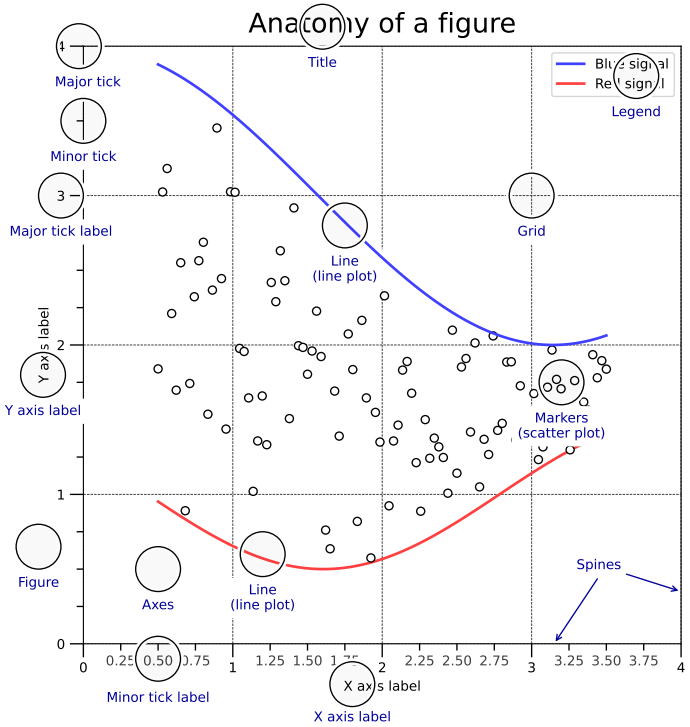
Save (bitmap or vector format)

```
fig.savefig("my-first-figure.png", dpi=300)
fig.savefig("my-first-figure.pdf")
```

Matplotlib 3.5.0 handout for beginners. Copyright (c) 2021 Matplotlib Development Team. Released under a CC-BY 4.0 International License. Supported by NumFOCUS.

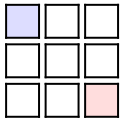
Matplotlib for intermediate users

A matplotlib figure is composed of a hierarchy of elements that forms the actual figure. Each element can be modified.

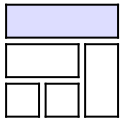


Figure, axes & spines

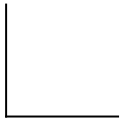
```
fig, axs = plt.subplots((3,3))
axs[0,0].set_facecolor("#ddddff")
axs[2,2].set_facecolor("#ffffdd")
```



```
gs = fig.add_gridspec(3, 3)
ax = fig.add_subplot(gs[0, :])
ax.set_facecolor("#ddddff")
```

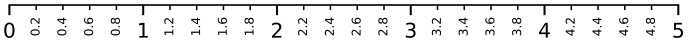


```
fig, ax = plt.subplots()
ax.spines["top"].set_color("None")
ax.spines["right"].set_color("None")
```



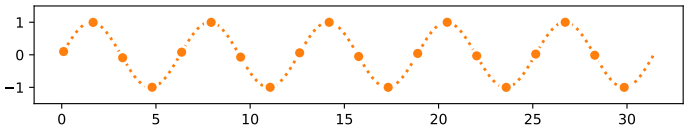
Ticks & labels

```
from mpl.ticker import MultipleLocator as ML
from mpl.ticker import ScalarFormatter as SF
ax.xaxis.set_minor_locator(ML(0.2))
ax.xaxis.set_minor_formatter(SF())
ax.tick_params(axis='x',which='minor',rotation=90)
```



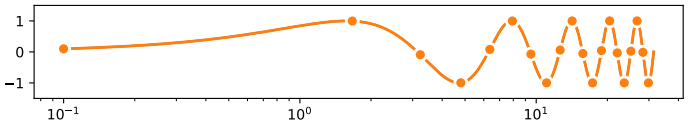
Lines & markers

```
X = np.linspace(0.1, 10*np.pi, 1000)
Y = np.sin(X)
ax.plot(X, Y, "C1o:", markevery=25, mec="1.0")
```



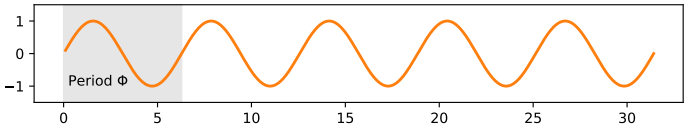
Scales & projections

```
fig, ax = plt.subplots()
ax.set_xscale("log")
ax.plot(X, Y, "C1o-", markevery=25, mec="1.0")
```



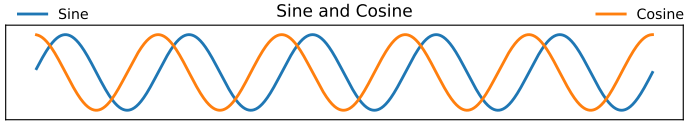
Text & ornaments

```
ax.fill_betweenx([-1,1],[0],[2*np.pi])
ax.text(0, -1, r" Period $\Phi$")
```



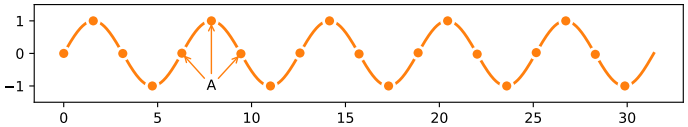
Legend

```
ax.plot(X, np.sin(X), "C0", label="Sine")
ax.plot(X, np.cos(X), "C1", label="Cosine")
ax.legend(bbox_to_anchor=(0,1,1,.1),ncol=2,
          mode="expand",  loc="lower left")
```



Annotation

```
ax.annotate("A", (X[250],Y[250]),(X[250],-1),
  ha="center", va="center",arrowprops =
  {"arrowstyle" : "->", "color": "C1"})
```



Colors

Any color can be used, but Matplotlib offers sets of colors:

C0	C1	C2	C3	C4	C5	C6	C7	C8	C9
0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0

Size & DPI

Consider a square figure to be included in a two-columns A4 paper with 2cm margins on each side and a column separation of 1cm. The width of a figure is (21 - 2*2 - 1)/2 = 8cm. One inch being 2.54cm, figure size should be 3.15×3.15 in.

```
fig = plt.figure(figsize=(3.15,3.15), dpi=50)
plt.savefig("figure.pdf", dpi=600)
```

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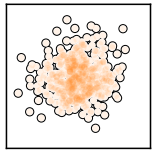
Matplotlib tips & tricks

Transparency

Scatter plots can be enhanced by using transparency (alpha) in order to show area with higher density. Multiple scatter plots can be used to delineate a frontier.

```
X = np.random.normal(-1, 1, 500)
Y = np.random.normal(-1, 1, 500)
ax.scatter(X, Y, 50, "0.0", lw=2) # optional
ax.scatter(X, Y, 50, "1.0", lw=0) # optional
ax.scatter(X, Y, 40, "C1",  lw=0, alpha=0.1)
```



Rasterization

If your figure has many graphical elements, such as a huge scatter, you can rasterize them to save memory and keep other elements in vector format.

```
X = np.random.normal(-1, 1, 10_000)
Y = np.random.normal(-1, 1, 10_000)
ax.scatter(X, Y, rasterized=True)
fig.savefig("rasterized-figure.pdf", dpi=600)
```

Offline rendering

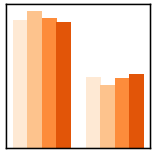
Use the Agg backend to render a figure directly in an array.

```
from matplotlib.backends.backend_agg import FigureCanvas
canvas = FigureCanvas(Figure()))
... # draw som stuff
canvas.draw()
Z = np.array(canvas.renderer.buffer_rgba())
```

Range of continuous colors

You can use colormap to pick from a range of continuous colors.

```
X = np.random.randn(1000, 4)
cmap = plt.get_cmap("Oranges")
colors = cmap([0.2, 0.4, 0.6, 0.8])

ax.hist(X, 2, histtype='bar', color=colors)
```



Text outline

Use text outline to make text more visible.

```
import matplotlib.patheffects as fx
text = ax.text(0.5, 0.1, "Label")
text.set_path_effects([
  fx.Stroke(linewidth=3, foreground='1.0'),
  fx.Normal()])
```

Multiline plot

You can plot several lines at once using None as separator.

```
X,Y = [], []
for x in np.linspace(0, 10*np.pi, 100):
  X.extend([x, x, None]), Y.extend([0, sin(x), None])
ax.plot(X, Y, "black")
```

Dotted lines

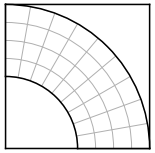
To have rounded dotted lines, use a custom `linestyle` and modify `dash_capstyle`.

```
ax.plot([0,1], [0,0], "C1",
        linestyle = (0, (0.01, 1)), dash_capstyle="round")
ax.plot([0,1], [1,1], "C1",
        linestyle = (0, (0.01, 2)), dash_capstyle="round")
```

Combining axes

You can use overlaid axes with different projections.

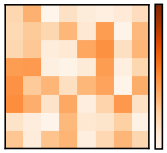
```
ax1 = fig.add_axes([0,0,1,1],
                   label="cartesian")
ax2 = fig.add_axes([0,0,1,1],
                   label="polar",
                   projection="polar")
```



Colorbar adjustment

You can adjust a colorbar's size when adding it.

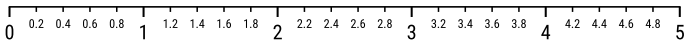
```
im = ax.imshow(Z)

cb = plt.colorbar(im,
        fraction=0.046, pad=0.04)
cb.set_ticks([])
```



Taking advantage of typography

You can use a condensed font such as Roboto Condensed to save space on tick labels.

```
for tick in ax.get_xticklabels(which='both'):
    tick.set_fontname("Roboto Condensed")
```



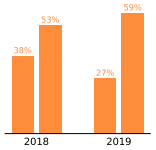
Getting rid of margins

Once your figure is finished, you can call `tight_layout()` to remove white margins. If there are remaining margins, you can use the `pdfcrop` utility (comes with TeX live).

Hatching

You can achieve a nice visual effect with thick hatch patterns.

```
cmap = plt.get_cmap("Oranges")
plt.rcParams['hatch.color'] = cmap(0.2)
plt.rcParams['hatch.linewidth'] = 8
ax.bar(X, Y, color=cmap(0.6), hatch="/" )
```



Read the documentation

Matplotlib comes with an extensive documentation explaining the details of each command and is generally accompanied by examples. Together with the huge online gallery, this documentation is a gold-mine.

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3. R language

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

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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.

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Data Import

with readr, tibble, and tidyr

Cheat Sheet

RStudio

R's **tidyverse** is built around **tidy data** stored in **tibbles**, an enhanced version of a data frame.

readr

The front side of this sheet shows how to read text files into R with **readr**.

tidyr

The reverse side shows how to create tibbles with **tibble** and to layout tidy data with **tidyr**.

Other types of data

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

- **haven** - SPSS, Stata, and SAS files
- **readxl** - excel files (.xls and .xlsx)
- **DBI** - databases
- **jsonlite** - json
- **xml2** - XML
- **httr** - Web APIs
- **rvest** - HTML (Web Scraping)

Write functions

Save **x**, an R object, to **path**, a file path, with:

write_csv(x, path, na = "NA", append = FALSE, col_names = !append**)**
Tibble/df to comma delimited file.

write_delim(x, path, delim = " ", na = "NA", append = FALSE, col_names = !append**)**
Tibble/df to file with any delimiter.

write_excel_csv(x, path, na = "NA", append = FALSE, col_names = !append**)**
Tibble/df to a CSV for excel

write_file(x, path, append = FALSE**)**
String to file.

write_lines(x, path, na = "NA", append = FALSE**)**
String vector to file, one element per line.

write_rds(x, path, compress = c("none", "gz", "bz2", "xz"), ...**)**
Object to RDS file.

write_tsv(x, path, na = "NA", append = FALSE, col_names = !append**)**
Tibble/df to tab delimited files.

Read functions

Read tabular data to tibbles

These functions share the common arguments:

read_*(file, col_names = TRUE, col_types = NULL, locale = default_locale(), na = c("", "NA"), quoted_na = TRUE, comment = "", trim_ws = TRUE, skip = 0, n_max = Inf, guess_max = min(1000, n_max), progress = interactive()**)**

```
a,b,c
1,2,3
4,5,NA
```

A	B	C
1	2	3
4	5	NA

read_csv()
Reads comma delimited files.
read_csv("file.csv")

```
a;b;c
1;2;3
4;5;NA
```

A	B	C
1	2	3
4	5	NA

read_csv2()
Reads Semi-colon delimited files.
read_csv2("file2.csv")

```
a|b|c
1|2|3
4|5|NA
```

A	B	C
1	2	3
4	5	NA

read_delim(delim, quote = "\"", escape_backslash = FALSE, escape_double = TRUE**)** Reads files with any delimiter.
read_delim("file.txt", delim = "|")

```
a b c
1 2 3
4 5 NA
```

A	B	C
1	2	3
4	5	NA

read_fwf(col_positions**)**
Reads fixed width files.
read_fwf("file.fwf", col_positions = c(1, 3, 5))

read_tsv()
Reads tab delimited files. Also **read_table().**
read_tsv("file.tsv")

Useful arguments

```
a,b,c
1,2,3
4,5,NA
```

Example file
write_csv (path = "file.csv",
x = read_csv("a,b,c\n1,2,3\n4,5,NA"))

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"))

1	2	3
4	5	NA

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

A	B	C
1	2	3

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

A	B	C
1	2	3
NA	NA	NA

Missing Values
read_csv("file.csv",
na = c("4", "5", ".")

Read non-tabular data

read_file(file, locale = default_locale()**)**
Read a file into a single string.

read_file_raw(file**)**
Read a file into a raw vector.

read_lines(file, skip = 0, n_max = -1L, locale = default_locale(), na = character(), progress = interactive()**)**
Read each line into its own string.

read_lines_raw(file, skip = 0, n_max = -1L, progress = interactive()**)**
Read each line into a raw vector.

read_log(file, col_names = FALSE, col_types = NULL, skip = 0, n_max = -1, progress = interactive()**)**
Apache style log files.

Parsing data types

readr functions guess the types of each column and convert types when appropriate (but will NOT convert strings to factors automatically).

A message shows the type of each column in the result.

```
## Parsed with column specification:
## cols(
##   age = col_integer(),
##   sex = col_character(),
##   earn = col_double()
## )
```

age is an integer

sex is a character

earn is a double (numeric)

1. Use **problems()** to diagnose problems
x <- read_csv("file.csv"); problems(x)

2. Use a col_ function to guide parsing
- **col_guess()** - the default
- **col_character()**
- **col_double()**
- **col_euro_double()**
- **col_datetime(**format = ""**)** Also **col_date(**format = ""**)** and **col_time(**format = ""**)**
- **col_factor(**levels, ordered = FALSE**)**
- **col_integer()**
- **col_logical()**
- **col_number()**
- **col_numeric()**
- **col_skip()**

x <- read_csv("file.csv", col_types = cols(
A = col_double(),
B = col_logical(),
C = col_factor()
))

3. Else, read in as character vectors then parse with a parse_ function.
- **parse_guess(**x, na = c("", "NA"), locale = default_locale()**)**
- **parse_character(**x, na = c("", "NA"), locale = default_locale()**)**
- **parse_datetime(**x, format = "", na = c("", "NA"), locale = default_locale()**)** Also **parse_date()** and **parse_time()**
- **parse_double(**x, na = c("", "NA"), locale = default_locale()**)**
- **parse_factor(**x, levels, ordered = FALSE, na = c("", "NA"), locale = default_locale()**)**
- **parse_integer(**x, na = c("", "NA"), locale = default_locale()**)**
- **parse_logical(**x, na = c("", "NA"), locale = default_locale()**)**
- **parse_number(**x, na = c("", "NA"), locale = default_locale()**)**

x$A <- parse_number(x$A)

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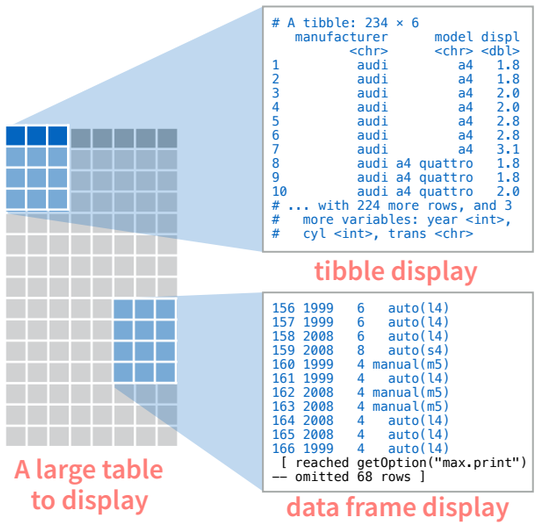
Tibbles - an enhanced data frame

The **tibble** package provides a new S3 class for storing tabular data, the tibble. Tibbles inherit the data frame class, but improve two behaviors:

- **Display** - When you print a tibble, R provides a concise view of the data that fits on one screen.
- **Subsetting** - [always returns a new tibble, [[and $ always return a vector.
- **No partial matching** - You must use full column names when subsetting



- Control the default appearance with options:
  options(tibble.print_max = n, tibble.print_min = m, tibble.width = Inf**)**
- View entire data set with **View(**x, title**)** or **glimpse(**x, width = NULL, …**)**
- Revert to data frame with **as.data.frame()** (required for some older packages)

Construct a tibble in two ways

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> <dbl>
1     1     a
2     2     b
3     3     c
```

as_tibble(x, …**)** Convert data frame to tibble.

enframe(x, name = "name", value = "value"**)** Converts named vector to a tibble with a names column and a values column.

is_tibble(x**)** Test whether x is a tibble.

Tidy Data with tidyr

Tidy data is a way to organize tabular data. It provides a consistent data structure across packages.

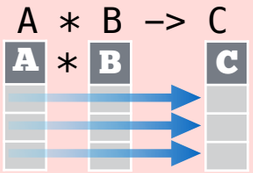
A table is tidy if:

Each **variable** is in its own **column**

Each **observation**, or **case**, is in its own **row**

Tidy data:

Makes variables easy to access as vectors



Preserves cases during vectorized operations

Reshape Data - change the layout of values in a table

Use **gather()** and **spread()** to reorganize the values of a table into a new layout. Each uses the idea of a key column: value column pair.

gather(data, key, value, …, na.rm = FALSE, convert = FALSE, factor_key = FALSE**)**

Gather moves column names into a key column, gathering the column values into a single value column.

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

key value

gather(table4a, `1999`, `2000`, key = "year", value = "cases")

spread(data, key, value, fill = NA, convert = FALSE, drop = TRUE, sep = NULL**)**

Spread moves the unique values of a key column into the column names, spreading the values of a value column across the new columns that result.

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

key value

→

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

spread(table2, type, count)

Handle Missing Values

drop_na(data, …**)**
Drop rows containing NA's in … columns.

x

x1	x2
A	1
B	NA
C	NA
D	3
E	NA

→

x1	x2
A	1
D	3

drop_na(x, x2)

fill(data, …, .direction = c("down", "up"))**
Fill in NA's in … columns with most recent non-NA values.

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(x, x2)

replace_na(data, replace = list(), …**)**
Replace NA's by column.

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(x,list(x2 = 2), x2)

Expand Tables - quickly create tables with combinations of values

complete(data, …, fill = list()**)**
Adds to the data missing combinations of the values of the variables listed in …
complete(mtcars, cyl, gear, carb)

expand(data, …**)**
Create new tibble with all possible combinations of the values of the variables listed in …
expand(mtcars, cyl, gear, carb)

Split and Combine Cells

Use these functions to split or combine cells into individual, isolated values.

separate(data, col, into, sep = "[^[:alnum:]]+", remove = TRUE, convert = FALSE, extra = "warn", fill = "warn", …**)**

Separate each cell in a column to make several columns.

table3

country	year	rate
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

→

country	year	cases	pop
A	1999	0.7K	19M
A	2000	2K	20M
B	1999	37K	172
B	2000	80K	174
C	1999	212K	1T
C	2000	213K	1T

separate_rows(table3, rate, into = c("cases", "pop"))

separate_rows(data, …, sep = "[^[:alnum:].]+", convert = FALSE**)**

Separate each cell in a column to make several rows. Also **separate_rows_()**.

table3

country	year	rate
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

→

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
C	1999	212K
C	1999	1T
C	2000	213K
C	2000	1T

separate_rows(table3, rate)

unite(data, col, …, sep = "_", remove = TRUE**)**

Collapse cells across several columns to make a single column.

table5

country	century	year
Afghan	19	99
Afghan	20	0
Brazil	19	99
Brazil	20	0
China	19	99
China	20	0

→

country	year
Afghan	1999
Afghan	2000
Brazil	1999
Brazil	2000
China	1999
China	2000

unite(table5, century, year, col = "year", sep = "")

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Learn more at browseVignettes(package = c("readr", "tibble", "tidyr")) • readr 1.1.0 • tibble 1.2.12 • tidyr 0.6.0 • Updated: 2017-01

Data Wrangling
with dplyr and tidyr
Cheat Sheet

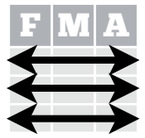
RStudio

Tidy Data - A foundation for wrangling in R

In a tidy data set:

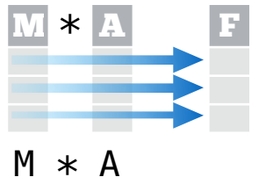
Each **variable** is saved in its own **column**

&



Each **observation** is saved in its own **row**

Tidy data complements R's **vectorized operations**. R will automatically preserve observations as you manipulate variables. No other format works as intuitively with R.



Syntax - Helpful conventions for wrangling

dplyr::**tbl_df(iris)**

Converts data to tbl class. tbl's are easier to examine than data frames. R displays only the data that fits onscreen:

```
Source: local data frame [150 x 5]

   Sepal.Length Sepal.Width Petal.Length
1           5.1         3.5          1.4
2           4.9         3.0          1.4
3           4.7         3.2          1.3
4           4.6         3.1          1.5
5           5.0         3.6          1.4
..          ...         ...          ...
Variables not shown: Petal.Width (dbl),
  Species (fctr)
```

dplyr::**glimpse(iris)**

Information dense summary of tbl data.

utils::**View(iris)**

View data set in spreadsheet-like display (note capital V).

iris × | Filter

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa
7	4.6	3.4	1.4	0.3	setosa
8	5.0	3.4	1.5	0.2	setosa

dplyr::**%>%**

Passes object on left hand side as first argument (or . argument) of function on righthand side.

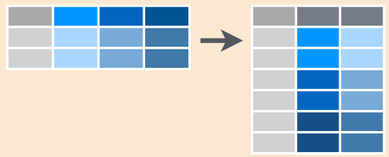
`x %>% f(y)` *is the same as* `f(x, y)`

`y %>% f(x, ., z)` *is the same as* `f(x, y, z )`

"Piping" with %>% makes code more readable, e.g.

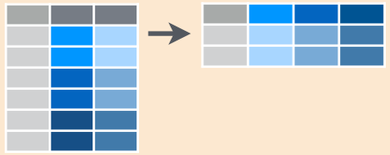
```
iris %>%
  group_by(Species) %>%
  summarise(avg = mean(Sepal.Width)) %>%
  arrange(avg)
```

Reshaping Data - Change the layout of a data set



tidyr::**gather(cases, "year", "n", 2:4)**

Gather columns into rows.



tidyr::**spread(pollution, size, amount)**

Spread rows into columns.

tidyr::**separate(storms, date, c("y", "m", "d"))**

Separate one column into several.

tidyr::**unite(data, col, ..., sep)**

Unite several columns into one.

dplyr::**data_frame(a = 1:3, b = 4:6)**

Combine vectors into data frame (optimized).

dplyr::**arrange(mtcars, mpg)**

Order rows by values of a column (low to high).

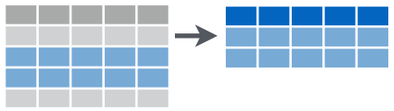
dplyr::**arrange(mtcars, desc(mpg))**

Order rows by values of a column (high to low).

dplyr::**rename(tb, y = year)**

Rename the columns of a data frame.

Subset Observations (Rows)



dplyr::**filter(iris, Sepal.Length > 7)**

Extract rows that meet logical criteria.

dplyr::**distinct(iris)**

Remove duplicate rows.

dplyr::**sample_frac(iris, 0.5, replace = TRUE)**

Randomly select fraction of rows.

dplyr::**sample_n(iris, 10, replace = TRUE)**

Randomly select n rows.

dplyr::**slice(iris, 10:15)**

Select rows by position.

dplyr::**top_n(storms, 2, date)**

Select and order top n entries (by group if grouped data).

Logic in R - ?Comparison, ?base::Logic

<	Less than	!=	Not equal to
>	Greater than	%in%	Group membership
==	Equal to	is.na	Is NA
<=	Less than or equal to	!is.na	Is not NA
>=	Greater than or equal to	&,|,!,xor,any,all	Boolean operators

Subset Variables (Columns)

dplyr::**select(iris, Sepal.Width, Petal.Length, Species)**

Select columns by name or helper function.

Helper functions for select - ?select

select(iris, contains(".")

Select columns whose name contains a character string.

select(iris, ends_with("Length"))

Select columns whose name ends with a character string.

select(iris, everything())

Select every column.

select(iris, matches(".t."))

Select columns whose name matches a regular expression.

select(iris, num_range("x", 1:5))

Select columns named x1, x2, x3, x4, x5.

select(iris, one_of(c("Species", "Genus")))

Select columns whose names are in a group of names.

select(iris, starts_with("Sepal"))

Select columns whose name starts with a character string.

select(iris, Sepal.Length:Petal.Width)

Select all columns between Sepal.Length and Petal.Width (inclusive).

select(iris, -Species)

Select all columns except Species.

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devtools::install_github("rstudio/EDAWR") for data sets

Learn more with browseVignettes(package = c("dplyr", "tidyr")) • dplyr 0.4.0• tidyr 0.2.0 • Updated: 1/15

Summarise Data

dplyr::**summarise(iris, avg = mean(Sepal.Length))**
Summarise data into single row of values.

dplyr::**summarise_each(iris, funs(mean))**
Apply summary function to each column.

dplyr::**count(iris, Species, wt = Sepal.Length)**
Count number of rows with each unique value of variable (with or without weights).

Summarise uses **summary functions**, functions that take a vector of values and return a single value, such as:

dplyr::**first**
First value of a vector.

dplyr::**last**
Last value of a vector.

dplyr::**nth**
Nth value of a vector.

dplyr::**n**
# of values in a vector.

dplyr::**n_distinct**
# of distinct values in a vector.

IQR
IQR of a vector.

min
Minimum value in a vector.

max
Maximum value in a vector.

mean
Mean value of a vector.

median
Median value of a vector.

var
Variance of a vector.

sd
Standard deviation of a vector.

Group Data

dplyr::**group_by(iris, Species)**
Group data into rows with the same value of Species.

dplyr::**ungroup(iris)**
Remove grouping information from data frame.

iris %>% group_by(Species) %>% summarise(…)
Compute separate summary row for each group.

Make New Variables

dplyr::**mutate(iris, sepal = Sepal.Length + Sepal. Width)**
Compute and append one or more new columns.

dplyr::**mutate_each(iris, funs(min_rank))**
Apply window function to each column.

dplyr::**transmute(iris, sepal = Sepal.Length + Sepal. Width)**
Compute one or more new columns. Drop original columns.

Mutate uses **window functions**, functions that take a vector of values and return another vector of values, such as:

dplyr::**lead**
Copy with values shifted by 1.

dplyr::**lag**
Copy with values lagged by 1.

dplyr::**dense_rank**
Ranks with no gaps.

dplyr::**min_rank**
Ranks. Ties get min rank.

dplyr::**percent_rank**
Ranks rescaled to [0, 1].

dplyr::**row_number**
Ranks. Ties got to first value.

dplyr::**ntile**
Bin vector into n buckets.

dplyr::**between**
Are values between a and b?

dplyr::**cume_dist**
Cumulative distribution.

dplyr::**cumall**
Cumulative `all`

dplyr::**cumany**
Cumulative `any`

dplyr::**cummean**
Cumulative `mean`

cumsum
Cumulative `sum`

cummax
Cumulative `max`

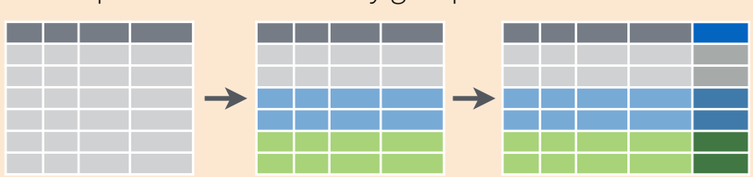
cummin
Cumulative `min`

cumprod
Cumulative `prod`

pmax
Element-wise `max`

pmin
Element-wise `min`

iris %>% group_by(Species) %>% mutate(…)
Compute new variables by group.



Combine Data Sets

a

x1	x2
A	1
B	2
C	3

+

b

x1	x3
A	T
B	F
D	T

=

Mutating Joins

x1	x2	x3
A	1	T
B	2	F
C	3	NA

dplyr::**left_join(a, b, by = "x1")**
Join matching rows from b to a.

x1	x3	x2
A	T	1
B	F	2
D	T	NA

dplyr::**right_join(a, b, by = "x1")**
Join matching rows from a to b.

x1	x2	x3
A	1	T
B	2	F

dplyr::**inner_join(a, b, by = "x1")**
Join data. Retain only rows in both sets.

x1	x2	x3
A	1	T
B	2	F
C	3	NA
D	NA	T

dplyr::**full_join(a, b, by = "x1")**
Join data. Retain all values, all rows.

Filtering Joins

x1	x2
A	1
B	2

dplyr::**semi_join(a, b, by = "x1")**
All rows in a that have a match in b.

x1	x2
C	3

dplyr::**anti_join(a, b, by = "x1")**
All rows in a that do not have a match in b.

y

x1	x2
A	1
B	2
C	3

+

z

x1	x2
B	2
C	3
D	4

=

Set Operations

x1	x2
B	2
C	3

dplyr::**intersect(y, z)**
Rows that appear in both y and z.

x1	x2
A	1
B	2
C	3
D	4

dplyr::**union(y, z)**
Rows that appear in either or both y and z.

x1	x2
A	1

dplyr::**setdiff(y, z)**
Rows that appear in y but not z.

Binding

x1	x2
A	1
B	2
C	3
B	2
C	3
D	4

dplyr::**bind_rows(y, z)**
Append z to y as new rows.

x1	x2	x1	x2
A	1	B	2
B	2	C	3
C	3	D	4

dplyr::**bind_cols(y, z)**
Append z to y as new columns.
Caution: matches rows by position.

R For Data Science *Cheat Sheet*

data.table

Learn R for data science Interactively at www.DataCamp.com

data.table

data.table is an R package that provides a high-performance version of base R's `data.frame` with syntax and feature enhancements for ease of use, convenience and programming speed.

Load the package:

```
> library(data.table)
```

Creating A `data.table`

```
> set.seed(45L)
> DT <- data.table(V1=c(1L,2L),
                   V2=LETTERS[1:3],
                   V3=round(rnorm(4),4),
                   V4=1:12)
```

Create a `data.table` and call it `DT`

Subsetting Rows Using `i`

```
> DT[3:5,]                    Select 3rd to 5th row
> DT[3:5]                     Select 3rd to 5th row
> DT[V2=="A"]                 Select all rows that have value A in column V2
> DT[V2 %in% c("A","C")]      Select all rows that have value A or C in column V2
```

Manipulating on Columns in `j`

```
> DT[,V2]                     Return V2 as a vector
[1] "A" "B" "C" "A" "B" "C" ...
> DT[,.(V2,V3)]               Return V2 and V3 as a data.table
> DT[,sum(V1)]                Return the sum of all elements of V1 in a vector
[1] 18
> DT[,.(sum(V1),sd(V3))]      Return the sum of all elements of V1 and the std. dev. of V3 in a data.table
   V1        V2
1: 18 0.4546055
> DT[,.(Aggregate=sum(V1),    The same as the above, with new names
        Sd.V3=sd(V3))]
   Aggregate      Sd.V3
1:        18 0.4546055
> DT[,.(V1,Sd.V3=sd(V3))]     Select column V2 and compute std. dev. of V3, which returns a single value and gets recycled
> DT[,.(print(V2),            Print column V2 and plot V3
        plot(V3),
        NULL)]
```

Doing `j` by Group

```
> DT[,.(V4.Sum=sum(V4)),by=V1]      Calculate sum of V4 for every group in V1
   V1 V4.Sum
1:  1     36
2:  2     42
> DT[,.(V4.Sum=sum(V4)),            Calculate sum of V4 for every group in V1 and V2
        by=.(V1,V2)]
> DT[,.(V4.Sum=sum(V4)),            Calculate sum of V4 for every group in sign(V1-1)
        by=sign(V1-1)]
   sign V4.Sum
1:    0     36
2:    1     42
> DT[,.(V4.Sum=sum(V4)),            The same as the above, with new name for the variable you're grouping by
        by=.(V1.01=sign(V1-1))]
> DT[1:5,.(V4.Sum=sum(V4)),         Calculate sum of V4 for every group in V1 after subsetting on the first 5 rows
        by=V1]
> DT[,.N,by=V1]                     Count number of rows for every group in V1
```

General form: `DT[i, j, by]`

"Take `DT`, subset rows using `i`, then calculate `j` grouped by `by`"

Adding/Updating Columns By Reference in `j` Using `:=`

```
> DT[,V1:=round(exp(V1),2)]         V1 is updated by what is after :=
> DT                                Return the result by calling DT
      V1 V2      V3 V4
1: 2.72  A -0.1107  1
2: 7.39  B -0.1427  2
3: 2.72  C -1.8893  3
4: 7.39  A -0.3571  4
...
> DT[,c("V1","V2"):=list(round(exp(V1),2),   Columns V1 and V2 are updated by what is after :=
                         LETTERS[4:6])]
> DT[,':='(V1=round(exp(V1),2),             Alternative to the above one. With [], you print the result to the screen
          V2=LETTERS[4:6])][]
        V1 V2      V3 V4
1:   15.18  D -0.1107  1
2: 1619.71  E -0.1427  2
3:   15.18  F -1.8893  3
4: 1619.71  D -0.3571  4
> DT[,V1:=NULL]                     Remove V1
> DT[,c("V1","V2"):=NULL]           Remove columns V1 and V2
> Cols.chosen=c("A","B")
> DT[,Cols.Chosen:=NULL]            Delete the column with column name Cols.chosen
> DT[,(Cols.Chosen):=NULL]          Delete the columns specified in the variable Cols.chosen
```

Indexing And Keys

```
> setkey(DT,V2)                     A key is set on V2; output is returned invisibly
> DT["A"]                           Return all rows where the key column (set to V2) has the value A
   V1 V2      V3 V4
1:  1  A -0.2392  1
2:  2  A -1.6148  4
3:  1  A  1.0498  7
4:  2  A  0.3262 10
> DT[c("A","C")]                    Return all rows where the key column (V2) has value A or C
> DT["A",mult="first"]              Return first row of all rows that match value A in key column V2
> DT["A",mult="last"]               Return last row of all rows that match value A in key column V2
> DT[c("A","D")]                    Return all rows where key column V2 has value A or D
   V1 V2      V3 V4
1:  1  A -0.2392  1
2:  2  A -1.6148  4
3:  1  A  1.0498  7
4:  2  A  0.3262 10
5: NA  D      NA NA
> DT[c("A","D"),nomatch=0]          Return all rows where key column V2 has value A or D
   V1 V2      V3 V4
1:  1  A -0.2392  1
2:  2  A -1.6148  4
3:  1  A  1.0498  7
4:  2  A  0.3262 10
> DT[c("A","C"),sum(V4)]            Return total sum of V4, for rows of key column V2 that have values A or C
> DT[c("A","C"),                    Return sum of column V4 for rows of V2 that have value A, and anohter sum for rows of V2 that have value C
     sum(V4),
     by=.EACHI]
   V2 V1
1:  A 22
2:  C 30
> setkey(DT,V1,V2)                  Sort by V1 and then by V2 within each group of V1 (invisible)
> DT[.(2,"C")]                      Select rows that have value 2 for the first key (V1) and the value C for the second key (V2)
   V1 V2      V3 V4
1:  2  C  0.3262  6
2:  2  C -1.6148 12
> DT[.(2,c("A","C"))]               Select rows that have value 2 for the first key (V1) and within those rows the value A or C for the second key (V2)
   V1 V2      V3 V4
1:  2  A -1.6148  4
2:  2  A  0.3262 10
3:  2  C  0.3262  6
4:  2  C -1.6148 12
```

Advanced Data Table Operations

```
> DT[.N-1]                          Return the penultimate row of the DT
> DT[,.N]                           Return the number of rows
> DT[,.(V2,V3)]                     Return V2 and V3 as a data.table
> DT[,list(V2,V3)]                  Return V2 and V3 as a data.table
> DT[,mean(V3),by=.(V1,V2)]         Return the result of j, grouped by all possible combinations of groups specified in by
   V1 V2      V1
1:  1  A  0.4053
2:  1  B  0.4053
3:  1  C  0.4053
4:  2  A -0.6443
5:  2  B -0.6443
6:  2  C -0.6443
```

`.SD` & `.SDcols`

```
> DT[,print(.SD),by=V2]             Look at what .SD contains
> DT[,.SD[c(1,.N)],by=V2]           Select the first and last row grouped by V2
> DT[,lapply(.SD,sum),by=V2]        Calculate sum of columns in .SD grouped by V2
> DT[,lapply(.SD,sum),by=V2,        Calculate sum of V3 and V4 in .SD grouped by V2
     .SDcols=c("V3","V4")]
   V2      V3 V4
1:  A -0.478 22
2:  B -0.478 26
3:  C -0.478 30
> DT[,lapply(.SD,sum),by=V2,        Calculate sum of V3 and V4 in .SD grouped by V2
     .SDcols=paste0("V",3:4)]
```

Chaining

```
> DT <- DT[,.(V4.Sum=sum(V4)),      Calculate sum of V4, grouped by V1
           by=V1]
   V1 V4.Sum
1:  1     36
2:  2     42
> DT[V4.Sum>40]                     Select that group of which the sum is >40
> DT[,.(V4.Sum=sum(V4)),            Select that group of which the sum is >40 (chaining)
        by=V1][V4.Sum>40]
   V1 V4.Sum
1:  2     42
> DT[,.(V4.Sum=sum(V4)),            Calculate sum of V4, grouped by V1, ordered on V1
        by=V1][order(-V1)]
   V1 V4.Sum
1:  2     42
2:  1     36
```

`set()`-Family

`set()`

Syntax: `for (i in from:to) set(DT, row, column, new value)`

```
> rows <- list(3:4,5:6)
> cols <- 1:2
> for(i in seq_along(rows))         Sequence along the values of rows, and for the values of cols, set the values of
    {set(DT,                        those elements equal to NA (invisible)
         i=rows[[i]],
         j=cols[i],
         value=NA)}
```

`setnames()`

Syntax: `setnames(DT,"old","new")[]`

```
> setnames(DT,"V2","Rating")        Set name of V2 to Rating (invisible)
> setnames(DT,                      Change 2 column names (invisible)
           c("V2","V3"),
           c("V2.rating","V3.DC"))
```

`setnames()`

Syntax: `setcolorder(DT,"neworder")`

```
> setcolorder(DT,                   Change column ordering to contents
              c("V2","V1","V4","V3"))  of the specified vector (invisible)
```

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**.

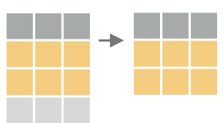
data.tables are also data frames – functions that work with data frames therefore also work with data.tables.

Create a data.table

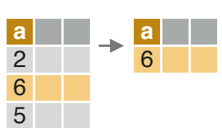
data.table(a = c(1, 2), b = c("a", "b")**)** – create a data.table from scratch. Analogous to data.frame().

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.

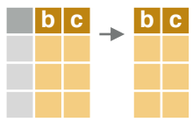
LOGICAL OPERATORS TO USE IN i

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

Manipulate columns with j

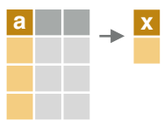
EXTRACT

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



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

SUMMARIZE

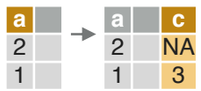


dt[, **.(x = sum(a))**] – create a data.table with new columns based on the summarized values of rows.

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

COMPUTE COLUMNS*

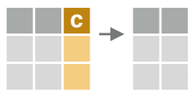
dt[, **c := 1 + 2**] – compute a column based on an expression.



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

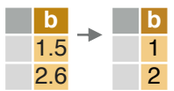
dt[, **`:=`(c = 1 , d = 2)**] – compute multiple columns based on separate expressions.

DELETE COLUMN



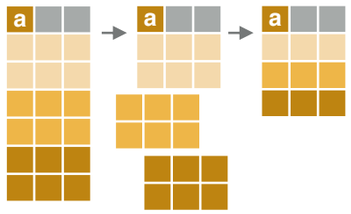
dt[, **c := NULL**] – delete a column.

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.

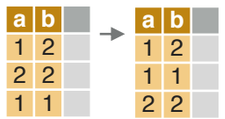
dt[, **.SD[.N]**, **by = a**] – extract last row of groups.

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)".

CC BY SA Erik Petrovski • www.petrovski.dk • Learn more with the data.table homepage or vignette • data.table version 1.11.8 • Updated: 2019-01

UNIQUE ROWS

a	b
1	2
2	2
1	2

→

a	b
1	2
2	2

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

a	b

→

x	y

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

a	b
1	c
2	a
3	b

+

x	y
3	b
2	c
1	a

=

a	b	x
3	b	3
1	c	2
2	a	1

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

a	b	c
1	c	7
2	a	5
3	b	6

+

x	y	z
3	b	4
2	c	5
1	a	8

=

a	b	c	x
3	b	4	3
1	c	5	2
NA	a	8	1

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

ROLLING JOIN

a	id	date
1	A	01-01-2010
2	A	01-01-2012
3	A	01-01-2014
1	B	01-01-2010
2	B	01-01-2012

+

b	id	date
1	A	01-01-2013
1	B	01-01-2013

=

a	id	date	b
2	A	01-01-2013	1
2	B	01-01-2013	1

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

a	b

+

a	b

=

a	b

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

a	b

+

x	y

=

a	b	x	y

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

Reshape a data.table

RESHAPE TO WIDE FORMAT

id	y	a	b
A	x	1	3
A	z	2	4
B	x	1	3
B	z	2	4

→

id	a_x	a_z	b_x	b_z
A	1	2	3	4
B	1	2	3	4

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

id	a_x	a_z	b_x	b_z
A	1	2	3	4
B	1	2	3	4

→

id	y	a	b
A	1	1	3
B	1	1	3
A	2	2	4
B	2	2	4

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

a	b
1	4
2	5
3	6

→

a	b
2	5

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.

a
1
2
3

→

a	a_m
1	2
2	2
3	2

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

a	b
1	a
2	a
3	b

→

a	b	c
1	a	1
2	a	2
3	b	1

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

LAG & LEAD

a	b
1	a
2	a
3	b
4	b
5	b

→

a	b	c
1	a	NA
2	a	1
3	b	NA
4	b	3
5	b	4

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.

Machine Learning Modelling in R : : CHEAT SHEET

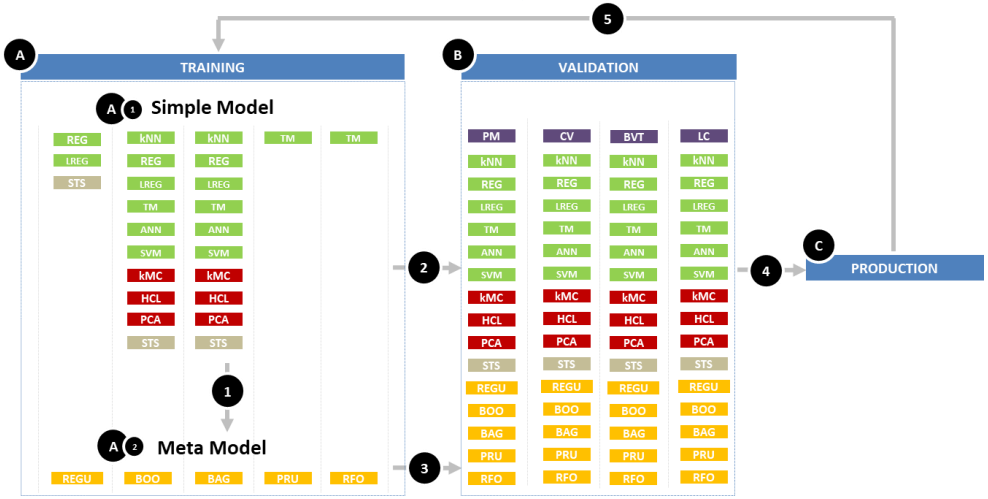
Supervised & Unsupervised Learning

	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)
	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)
	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)
	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)
	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)
	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)
	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)
	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)
	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)

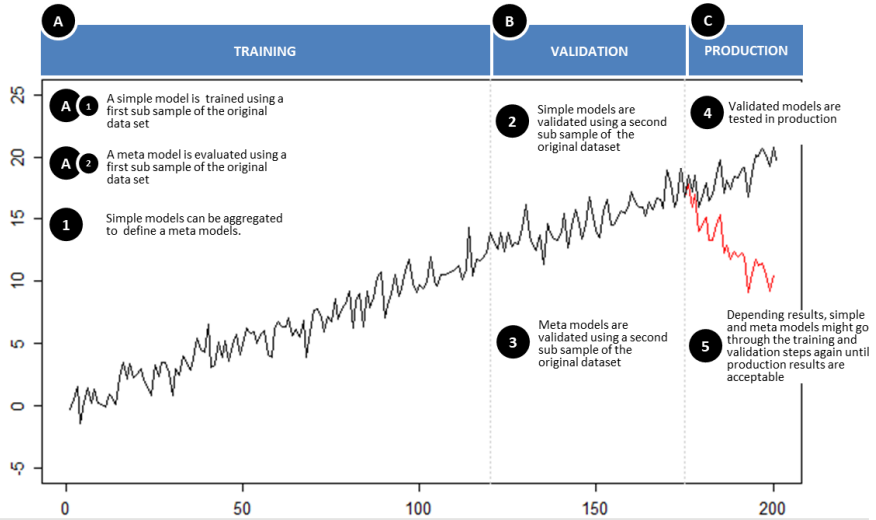
Meta-Algorithm, Time Series & Model Validation

	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)
	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.	**Parametric model** - mboost::glmboost	glmboost(Yen ~ ., data = curr1[trnidxs,])
	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)
	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)
	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	**Regression**: fit <- lm(Y~X,data=myData) outlierTest(fit) qqPlot(fit, main="QQ Plot")
	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
	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)
	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



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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.

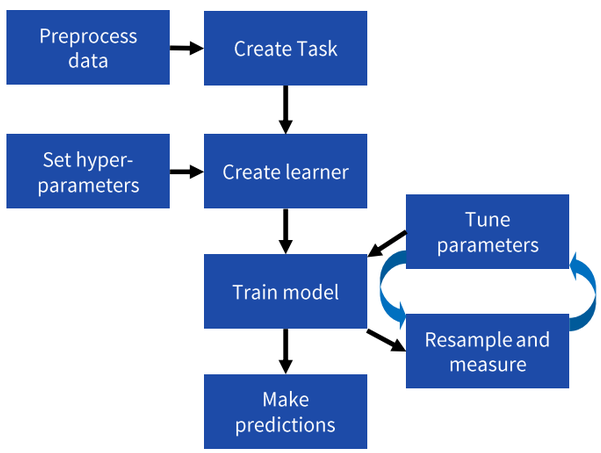
Predictions are the results of applying a model to either new data or the original training data.

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

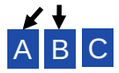
`summarizeColumns(obj=)` where `obj` is a data.frame or task. Provides type, NA, and distributional data about each column

See also `capLargeValues` `dropFeatures` `removeConstantFeatures` `summarizeLevels`

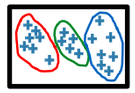
Creating a task

`makeClassifTask(data=,target=)`
Classification of a target variable, with optional positive class `positive`

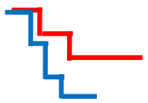
`makeRegrTask(data=,target=)`
Regression on a target variable



`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()`

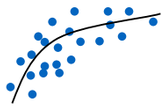
Training & Testing

Setting hyperparameters

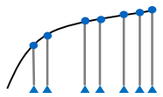
`setHyperPars(learner=,...)`
Set the hyperparameters (settings) for each learner, if you don't want to use the defaults. You can also specify hyperparameters in the `makeLearner()` call

`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 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:

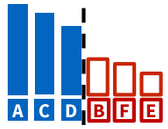
```
imputeConst(const=) imputeMedian() imputeMode()
imputeMin(multiplier=) imputeMax(multiplier=)
imputeNormal(mean=,sd=)
imputeHist(breaks=,use.mids=)
imputeLearner(learner=,features=)
```

`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.

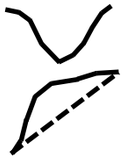
Benchmark results can be accessed with a variety of functions beginning with `getBMR<object>`: `AggrPerformance` `FeatSelResults` `FilteredFeatures` `LearnerIds` `LeanerShortNames` `Learners` `MeasureIds` `Measures` `Models` `Performances` `Predictions` `TaskDescs` `TaskIds` `TuneResults`

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

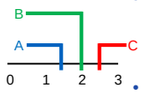
`generatePartialDependenceData(obj=,input=)` Get partial dependence of model (`obj`) prediction over each feature of data (`input`)

- `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

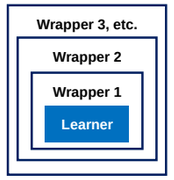
Other



- `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

R For Data Science *Cheat Sheet*

xts

Learn R for data science Interactively at www.DataCamp.com

xts

eXtensible Time Series (xts) is a powerful package that provides an extensible time series class, enabling uniform handling of many R time series classes by extending zoo.

Load the package as follows:

```
> library(xts)
```

xts Objects

xts objects have three main components:

- **coredata**: always a matrix for xts objects, while it could also be a vector for zoo objects
- **index**: vector of any `Date`, `POSIXct`, `chron`, `yearmon`, `yearqtr`, or `DateTime` classes
- **xtsAttributes**: arbitrary attributes

Creating xts Objects

```
> xts1 <- xts(x=1:10, order.by=Sys.Date()-1:10)
> data <- rnorm(5)
> dates <- seq(as.Date("2017-05-01"),length=5,by="days")
> xts2 <- xts(x=data, order.by=dates)
> xts3 <- xts(x=rnorm(10),
              order.by=as.POSIXct(Sys.Date()+1:10),
              born=as.POSIXct("1899-05-08"))
> xts4 <- xts(x=1:10, order.by=Sys.Date()+1:10)
```

Convert To And From xts

```
> data(AirPassengers)
> xts5 <- as.xts(AirPassengers)
```

Import From Files

```
> dat <- read.csv(tmp_file)
> xts(dat, order.by=as.Date(rownames(dat),"%m/%d/%Y"))
> dat_zoo <- read.zoo(tmp_file,
                      index.column=0,
                      sep=",",
                      format="%m/%d/%Y")
> dat_zoo <- read.zoo(tmp,sep=",",FUN=as.yearmon)
> dat_xts <- as.xts(dat_zoo)
```

Export xts Objects

```
> data_xts <- as.xts(matrix)
> tmp <- tempfile()
> write.zoo(data_xts,sep=",",file=tmp)
```

Replace & Update

`> xts2[dates] <- 0`	Replace values in `xts2` on `dates` with `0`
`> xts5["1961"] <- NA`	Replace dates from `1961` with `NA`
`> xts2["2016-05-02"] <- NA`	Replace the value at 1 specific index with `NA`

Applying Functions

`> ep1 <- endpoints(xts4,on="weeks",k=2)` `[1] 0 5 10`	Take index values by time
`> ep2 <- endpoints(xts5,on="years")` `[1] 0 12 24 36 48 60 72 84 96 108 120 132 144`	
`> period.apply(xts5,INDEX=ep2,FUN=mean)`	Calculate the yearly mean
`> xts5_yearly <- split(xts5,f="years")`	Split `xts5` by year
`> lapply(xts5_yearly,FUN=mean)`	Create a list of yearly means

`> do.call(rbind,`
`lapply(split(xts5,"years"),`
`function(w) last(w,n="1 month")))`
	Find the last observation in each year in `xts5`

`> do.call(rbind,`
`lapply(split(xts5,"years"),`
`cumsum))`
	Calculate cumulative annual passengers

`> rollapply(xts5, 3, sd)`	Apply sd to rolling margins of `xts5`

Selecting, Subsetting & Indexing

Select

`> mar55 <- xts5["1955-03"]`	Get value for March 1955

Subset

`> xts5_1954 <- xts5["1954"]`	Get all data from 1954
`> xts5_janmarch <- xts5["1954/1954-03"]`	Extract data from Jan to March '54
`> xts5_janmarch <- xts5["/1954-03"]`	Get all data until March '54
`> xts4[ep1]`	Subset `xts4` using `ep2`

`first()` and `last()`

`> first(xts4,'1 week')`	Extract first 1 week
`> first(last(xts4,'1 week'),'3 days')`	Get first 3 days of the last week of data

Indexing

`> xts2[index(xts3)]`	Extract rows with the index of `xts3`
`> days <- c("2017-05-03","2017-05-23")`	
`> xts3[days]`	Extract rows using the vector `days`
`> xts2[as.POSIXct(days,tz="UTC")]`	Extract rows using `days` as POSIXct
`> index <- which(.indexwday(xts1)==0|.indexwday(xts1)==6)`	Index of weekend days
`> xts1[index]`	Extract weekend days of `xts1`

Missing Values

`> na.omit(xts5)`	Omit NA values in `xts5`
`> xts_last <- na.locf(xts2)`	Fill missing values in `xts2` using last observation
`> xts_last <- na.locf(xts2, fromLast=TRUE)`	Fill missing values in `xts2` using next observation
`> na.approx(xts2)`	Interpolate NAs using linear approximation

Arithmetic Operations

`coredata()` or `as.numeric()`

`> xts3 + as.numeric(xts2)`	Addition
`> xts3 * as.numeric(xts4)`	Multiplication
`> coredata(xts4) - xts3`	Subtraction
`> coredata(xts4) / xts3`	Division

Shifting Index Values

`> xts5 - lag(xts5)`	Period-over-period differences
`> diff(xts5,lag=12,differences=1)`	Lagged differences

Reindexing

`> xts1 + merge(xts2,index(xts1),fill=0)`
`e1`
`2017-05-04 5.231538`
`2017-05-05 5.829257`
`2017-05-06 4.000000`
`2017-05-07 3.000000`
`2017-05-08 2.000000`
`2017-05-09 1.000000`
	Addition

`> xts1 - merge(xts2,index(xts1),fill=na.locf)`
`e1`
`2017-05-04 5.231538`
`2017-05-05 5.829257`
`2017-05-06 4.829257`
`2017-05-07 3.829257`
`2017-05-08 2.829257`
`2017-05-09 1.829257`
	Subtraction

Merging

`> merge(xts2,xts1,join='inner')`
`xts2 xts1`
`2017-05-05 -0.8382068 10`
	Inner join of `xts2` and `xts1`

`> merge(xts2,xts1,join='left',fill=0)`
`xts2 xts1`
`2017-05-01 1.7482704 0`
`2017-05-02 -0.2314678 0`
`2017-05-03 0.1685517 0`
`2017-05-04 1.1685649 0`
`2017-05-05 -0.8382068 10`
	Left join of `xts2` and `xts1`, fill empty spots with `0`

`> rbind(xts1, xts4)`	Combine `xts1` and `xts4` by rows

Inspect Your Data

`> core_data <- coredata(xts2)`	Extract core data of objects
`> index(xts1)`	Extract index of objects

Class Attributes

`> indexClass(xts2)`	Get index class
`> indexClass(convertIndex(xts,'POSIXct'))`	Replacing index class
`> indexTZ(xts5)`	Get index class
`> indexFormat(xts5) <- "%Y-%m-%d"`	Change format of time display

Time Zones

`> tzone(xts1) <- "Asia/Hong_Kong"`	Change the time zone
`> tzone(xts1)`	Extract the current time zone

Periods, Periodicity & Timestamps

`> periodicity(xts5)`	Estimate frequency of observations
`> to.yearly(xts5)`	Convert `xts5` to yearly OHLC
`> to.monthly(xts3)`	Convert `xts3` to monthly OHLC
`> to.quarterly(xts5)`	Convert `xts5` to quarterly OHLC
`> to.period(xts5,period="quarters")`	Convert to quarterly OHLC
`> to.period(xts5,period="years")`	Convert to yearly OHLC
`> nmonths(xts5)`	Count the months in `xts5`
`> nquarters(xts5)`	Count the quarters in `xts5`
`> nyears(xts5)`	Count the years in `xts5`
`> make.index.unique(xts3,eps=1e-4)`	Make index unique
`> make.index.unique(xts3,drop=TRUE)`	Remove duplicate times
`> align.time(xts3,n=3600)`	Round index time to the next `n` seconds

Other Useful Functions

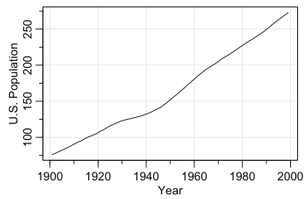
`> .index(xts4)`	Extract raw numeric index of `xts1`
`> .indexwday(xts3)`	Value of week(day), starting on Sunday, in index of `xts3`
`> .indexhour(xts3)`	Value of hour in index of `xts3`
`> start(xts3)`	Extract first observation of `xts3`
`> end(xts4)`	Extract last observation of `xts4`
`> str(xts3)`	Display structure of `xts3`
`> time(xts1)`	Extract raw numeric index of `xts1`
`> head(xts2)`	First part of `xts2`
`> tail(xts2)`	Last part of `xts2`

DataCamp
Learn R for Data Science Interactively

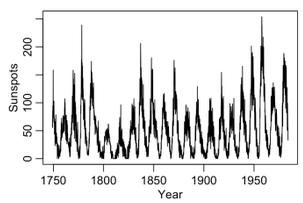
Time Series Cheat Sheet

Plot Time Series

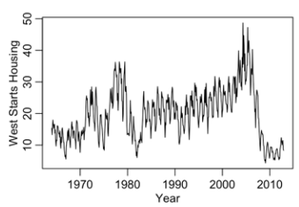
1. tsplot(x=time, y=data)



2. plot(ts(data, start=start_time, frequency=gap))



3. ts.plot(ts(data, start=start_time, frequency=gap))



Simulation

Autoregression of Order p

$$X_t = \phi_1 X_{t-1} + \phi_2 X_{t-2} + \ldots + \phi_p X_{t-p} + W_t$$

Moving Average of Order q

$$X_t = Z_t + \theta_1 Z_{t-1} + \theta_2 Z_{t-2} + \ldots + \theta_q Z_{t-p}$$

ARMA (p, q)

$$X_t = \phi_1 X_{t-1} + \phi_2 X_{t-2} + \ldots + \phi_p X_{t-p} + Z_t + \theta_1 Z_{t-1} + \theta_2 Z_{t-2} + \ldots + \theta_q Z_{t-p}$$

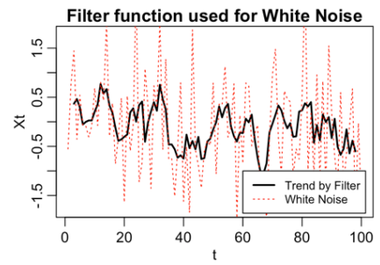
Simulation of ARMA (p, q)

arima.sim(model=list(ar=c($\phi_1, \ldots, \phi_p$), ma=c($\theta_1, \ldots, \theta_q$)), n=n)

Filters

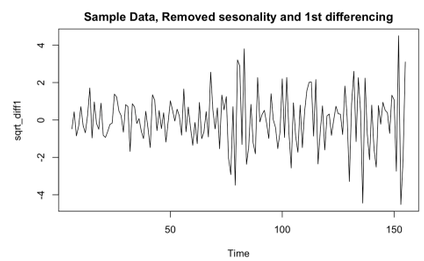
Linear Filter: filter()

filter(data, filter=filter_coefficients, sides=2, method="convolution", circular=F)



Differencing Filter: diff()

diff(data, lag=4, differences=1)

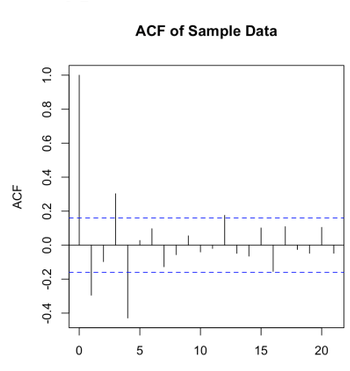


Auto-correlation

Use ACF and PACF to detect model

(Complete) Auto-correlation function: acf()

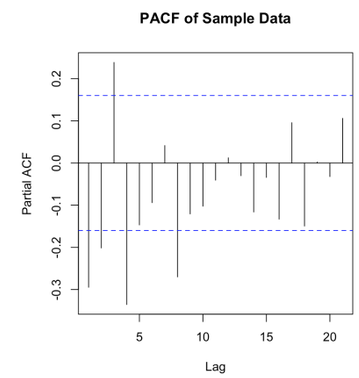
acf(data, type='correlation', na.action=na.pass)



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

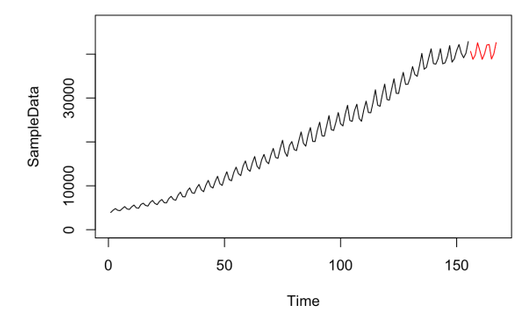
Forecasting future observations given a fitted ARMA model

predict(): Predict future observations given a fitted ARMA model

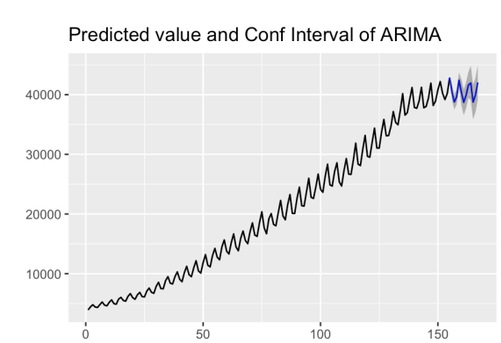
predict(arima_model, number_to_predict)

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))



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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

layer_repeat_vector() Repeats the input n times

layer_lambda(object, f) Wraps arbitrary expression as a layer

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)
```

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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

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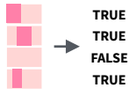
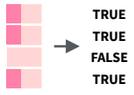
String manipulation with stringr : : **CHEAT SHEET**

The **stringr** package provides a set of internally consistent tools for working with character strings, i.e. sequences of characters surrounded by quotation marks.

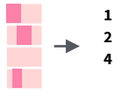
Detect Matches



str_detect(string, **pattern**, negate = FALSE**)** Detect the presence of a pattern match in a string. Also **str_like()**. str_detect(fruit, "a")

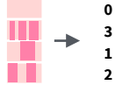


str_starts(string, **pattern**, negate = FALSE**)** Detect the presence of a pattern match at the beginning of a string. Also **str_ends()**. str_starts(fruit, "a")



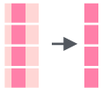
str_which(string, **pattern**, negate = FALSE**)** Find the indexes of strings that contain a pattern match. str_which(fruit, "a")

str_locate(string, **pattern**) Locate the positions of pattern matches in a string. Also **str_locate_all()**. str_locate(fruit, "a")

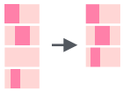


str_count(string, **pattern**) Count the number of matches in a string. str_count(fruit, "a")

Subset Strings



str_sub(string, start = 1L, end = -1L**)** Extract substrings from a character vector. str_sub(fruit, 1, 3); str_sub(fruit, -2)

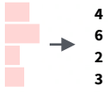


str_subset(string, **pattern**, negate = FALSE**)** Return only the strings that contain a pattern match. str_subset(fruit, "p")

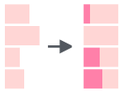
str_extract(string, **pattern**) Return the first pattern match found in each string, as a vector. Also **str_extract_all()** to return every pattern match. str_extract(fruit, "[aeiou]")

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

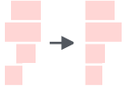


str_length(string**)** The width of strings (i.e. number of code points, which generally equals the number of characters). str_length(fruit)



str_pad(string, width, side = c("left", "right", "both"), pad = " "**)** Pad strings to constant width. str_pad(fruit, 17)

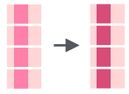
str_trunc(string, width, side = c("right", "left", "center"), ellipsis = "..."**)** Truncate the width of strings, replacing content with ellipsis. str_trunc(sentences, 6)



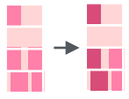
str_trim(string, side = c("both", "left", "right"))** Trim whitespace from the start and/or end of a string. str_trim(str_pad(fruit, 17))

str_squish(string**)** Trim whitespace from each end and collapse multiple spaces into single spaces. str_squish(str_pad(fruit, 17, "both"))

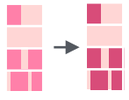
Mutate Strings



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)

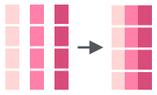
a string
↓
A STRING

str_to_upper(string, locale = "en"**)**[1] Convert strings to upper case. str_to_upper(sentences)

a string
↓
A String

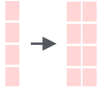
str_to_title(string, locale = "en"**)**[1] Convert strings to title case. Also **str_to_sentence()**. str_to_title(sentences)

Join and Split

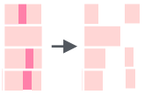


str_c(..., sep = "", collapse = NULL**)** Join multiple strings into a single string. str_c(letters, LETTERS)

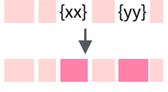
str_flatten(string, collapse = ""**)** Combines into a single string, separated by collapse. str_flatten(fruit, ", ")



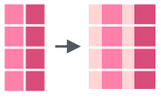
str_dup(string, times**)** Repeat strings times times. Also **str_unique()** to remove duplicates. str_dup(fruit, times = 2)



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)

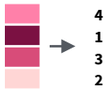


str_glue(..., .sep = "", .envir = parent.frame()**)** Create a string from strings and {expressions} to evaluate. str_glue("Pi is {pi}")



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)]

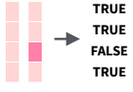
str_sort(x, decreasing = FALSE, na_last = TRUE, locale = "en", numeric = FALSE, ...**)**[1] Sort a character vector. str_sort(fruit)

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.

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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

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

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R For Data Science *Cheat Sheet*

Tidyverse for Beginners

Learn More R for Data Science Interactively at www.datacamp.com

Tidyverse

The **tidyverse** is a powerful collection of R packages that are actually data tools for transforming and visualizing data. All packages of the tidyverse share an underlying philosophy and common APIs.

The core packages are:

- **ggplot2**, which implements the grammar of graphics. You can use it to visualize your data.
- **dplyr** is a grammar of data manipulation. You can use it to solve the most common data manipulation challenges.
- **tidyr** helps you to create tidy data or data where each variable is in a column, each observation is a row end each value is a cell.
- **readr** is a fast and friendly way to read rectangular data.
- **purrr** enhances R's functional programming (FP) toolkit by providing a complete and consistent set of tools for working with functions and vectors.
- **tibble** is a modern re-imaginging of the data frame.
- **stringr** provides a cohesive set of functions designed to make working with strings as easy as posssible
- **forcats** provide a suite of useful tools that solve common problems with factors.

You can install the complete tidyverse with:

```
> install.packages("tidyverse")
```

Then, load the core tidyverse and make it available in your current R session by running:

```
> library(tidyverse)
```

Note: there are many other tidyverse packages with more specialised usage. They are not loaded automatically with library(tidyverse), so you'll need to load each one with its own call to `library()`.

Useful Functions

`> tidyverse_conflicts()`	Conflicts between tidyverse and other packages
`> tidyverse_deps()`	List all tidyverse dependencies
`> tidyverse_logo()`	Get tidyverse logo, using ASCII or unicode characters
`> tidyverse_packages()`	List all tidyverse packages
`> tidyverse_update()`	Update tidyverse packages

Loading in the data

`> library(datasets)`	Load the datasets package
`> library(gapminder)`	Load the gapminder package
`> attach(iris)`	Attach iris data to the R search path

dplyr

Filter

`filter()` allows you to select a subset of rows in a data frame.

`> iris %>%` `  filter(Species=="virginica")`	Select iris data of species "virginica"

`> iris %>%`
`  filter(Species=="virginica",`
`  Sepal.Length > 6)`
	Select iris data of species "virginica" and sepal length greater than 6.

Arrange

`arrange()` sorts the observations in a dataset in ascending or descending order based on one of its variables.

`> iris %>%` `  arrange(Sepal.Length)`	Sort in ascending order of sepal length
`> iris %>%` `  arrange(desc(Sepal.Length))`	Sort in descending order of sepal length

Combine multiple `dplyr` verbs in a row with the pipe operator `%>%`:

`> iris %>%`
`  filter(Species=="virginica") %>%`
`  arrange(desc(Sepal.Length))`
	Filter for species "virginica" then arrange in descending order of sepal length

Mutate

`mutate()` allows you to update or create new columns of a data frame.

`> iris %>%` `  mutate(Sepal.Length=Sepal.Length*10)`	Change Sepal.Length to be in millimeters
`> iris %>%` `  mutate(SLMm=Sepal.Length*10)`	Create a new column called SLMm

Combine the verbs `filter()`, `arrange()`, and `mutate()`:

```
> iris %>%
  filter(Species=="Virginica") %>%
  mutate(SLMm=Sepal.Length*10) %>%
  arrange(desc(SLMm))
```

Summarize

`summarize()` allows you to turn many observations into a single data point.

`> iris %>%` `  summarize(medianSL=median(Sepal.Length))`	Summarize to find the median sepal length

`> iris %>%`
`  filter(Species=="virginica") %>%`
`  summarize(medianSL=median(Sepal.Length))`
	Filter for virginica then summarize the median sepal length

You can also summarize multiple variables at once:

```
> iris %>%
  filter(Species=="virginica") %>%
  summarize(medianSL=median(Sepal.Length),
            maxSL=max(Sepal.Length))
```

`group_by()` allows you to summarize within groups instead of summarizing the entire dataset:

`> iris %>%`
`  group_by(Species) %>%`
`  summarize(medianSL=median(Sepal.Length),`
`  maxSL=max(Sepal.Length))`
	Find median and max sepal length of each species

`> iris %>%`
`  filter(Sepal.Length>6) %>%`
`  group_by(Species) %>%`
`  summarize(medianPL=median(Petal.Length),`
`  maxPL=max(Petal.Length))`
	Find median and max petal length of each species with sepal length > 6

ggplot2

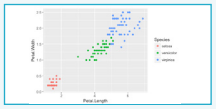
Scatter plot

Scatter plots allow you to compare two variables within your data. To do this with ggplot2, you use `geom_point()`

`> iris_small <- iris %>%`
`  filter(Sepal.Length > 5)`
`> ggplot(iris_small, aes(x=Petal.Length,`
`  y=Petal.Width)) +`
`  geom_point()`
	Compare petal width and length

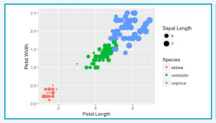
Additional Aesthetics

- Color



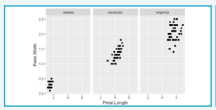
```
> ggplot(iris_small, aes(x=Petal.Length,
  y=Petal.Width,
  color=Species)) +
  geom_point()
```

- Size



```
> ggplot(iris_small, aes(x=Petal.Length,
  y=Petal.Width,
  color=Species,
  size=Sepal.Length)) +
  geom_point()
```

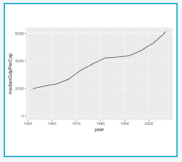
Faceting



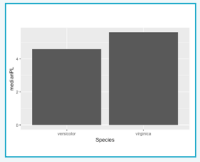
```
> ggplot(iris_small, aes(x=Petal.Length,
  y=Petal.Width)) +
  geom_point()+
  facet_wrap(~Species)
```

Line Plots

```
> by_year <- gapminder %>%
  group_by(year) %>%
  summarize(medianGdpPerCap=median(gdpPercap))
> ggplot(by_year, aes(x=year,
  y=medianGdpPerCap))+
  geom_line()+
  expand_limits(y=0)
```



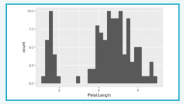
Bar Plots



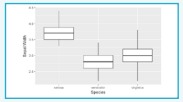
```
> by_species <- iris %>%
  filter(Sepal.Length>6) %>%
  group_by(Species) %>%
  summarize(medianPL=median(Petal.Length))
> ggplot(by_species, aes(x=Species,
  y=medianPL)) +
  geom_col()
```

Histograms

```
> ggplot(iris_small, aes(x=Petal.Length))+
  geom_histogram()
```



Box Plots



```
> ggplot(iris_small, aes(x=Species,
  y=Sepal.Width))+
  geom_boxplot()
```

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>) +            ] Not required, sensible defaults supplied
<COORDINATE_FUNCTION> +
<FACET_FUNCTION> +
<SCALE_FUNCTION> +
<THEME_FUNCTION>
```

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")

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

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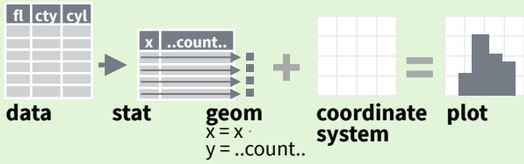
Stats An alternative way to build a layer.

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)**)**

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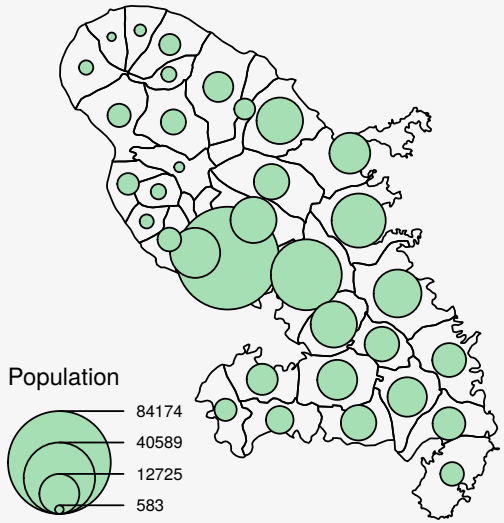
Thematic maps with cartography : : **CHEAT SHEET**

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

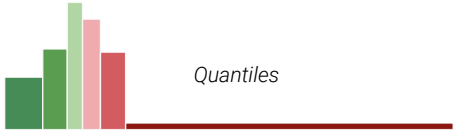
```
library(cartography)
library(sf)
mtq <- st_read("martinique.shp")
plot(st_geometry(mtq))
propSymbolsLayer(x = mtq, var = "P13_POP",
 legend.title.txt = "Population",
 col = "#a7dfb4")
```



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")
```

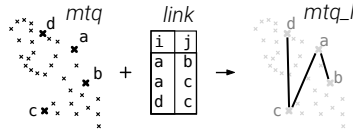
Labels
```
labelLayer(x = mtq, txt = "myvar",
 halo = TRUE, overlap = FALSE)
```

Transformations

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

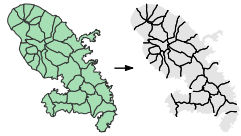
Grids layers can be used by choroLayer() or propSymbolsLayer().

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



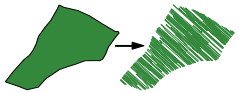
Links layers can be used by *LinkLayer().

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



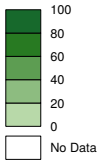
Borders layers can be used by discLayer() function

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



Legends

legendChoro()

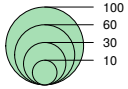



```
legendChoro(pos = "topleft",
 title.txt = "legendChoro()",
 breaks = c(0,20,40,60,80,100),
 col = carto.pal("green.pal", 5),
 nodata = TRUE, nodata.txt = "No Data")
```

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)
```

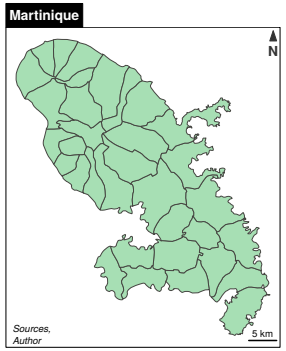
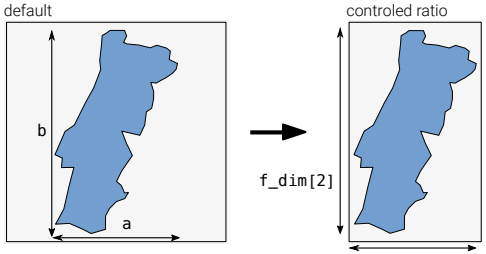


Figure Dimensions

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()
```



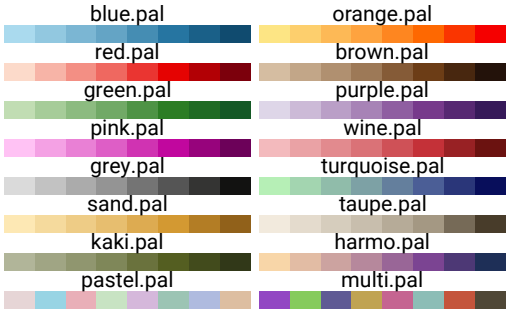
a / b == f_dim[1] / f_dim[2]

f_dim[1]

Color Palettes

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

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

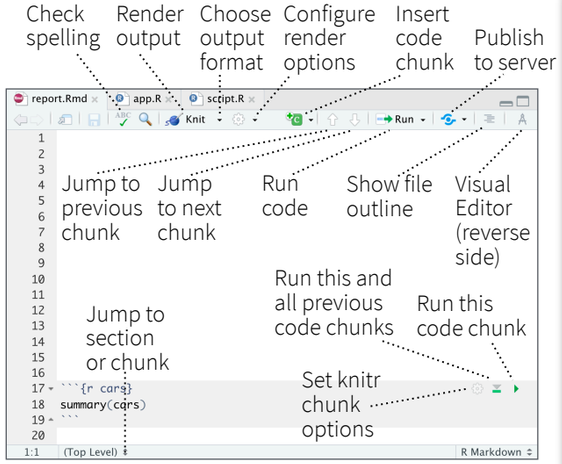


cartography - https://github.com/riatelab/cartography - CC BY SA Timothée Giraud - 2018-07

RStudio IDE : : **CHEAT SHEET**

Documents and Apps

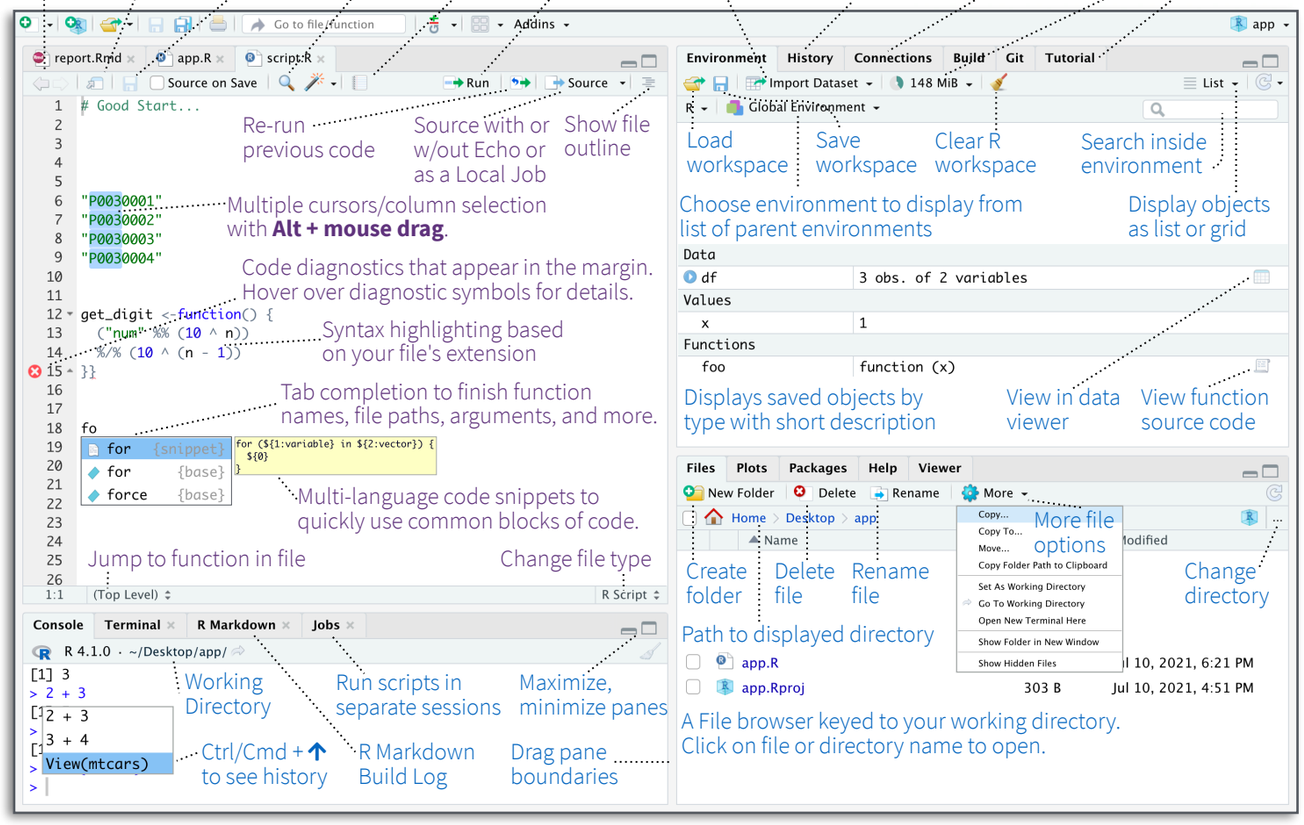
Open Shiny, R Markdown, knitr, Sweave, LaTeX, .Rd files and more in Source Pane



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

Source Editor

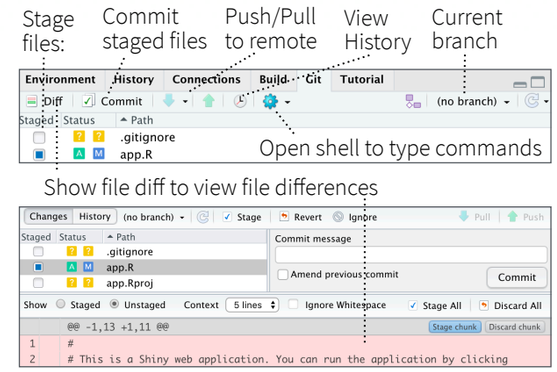


Tab Panes

Version Control

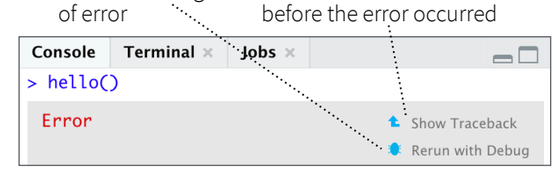
Turn on at **Tools > Project Options > Git/SVN**

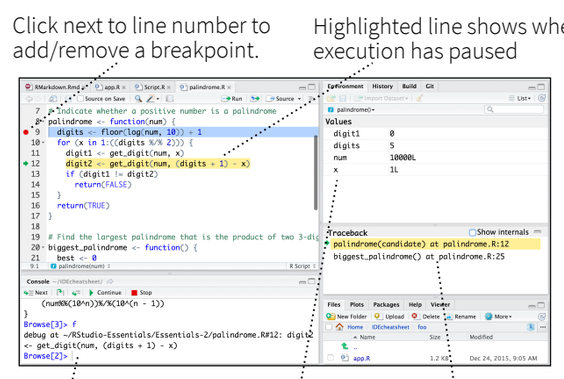
A Added M Modified ? Untracked
D Deleted R Renamed

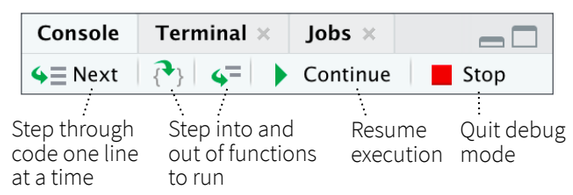


Debug Mode

Use **debug(), browser(),** or a breakpoint and execute your code to open the debugger mode.







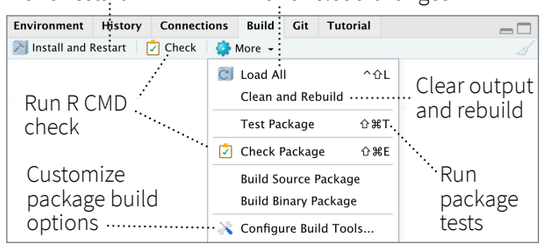
Package Development

Create a new package with
File > New Project > New Directory > R Package

Enable roxygen documentation with
Tools > Project Options > Build Tools

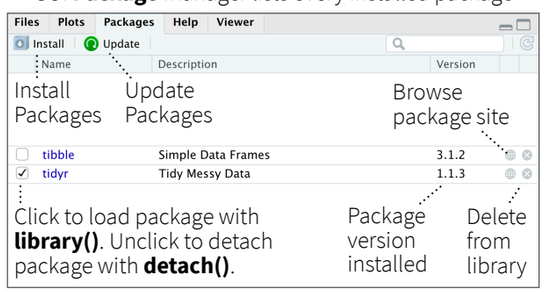
Roxygen guide at **Help > Roxygen Quick Reference**

See package information in the **Build Tab**

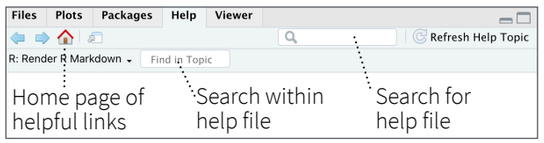


RStudio opens plots in a dedicated **Plots** pane

GUI **Package** manager lists every installed package

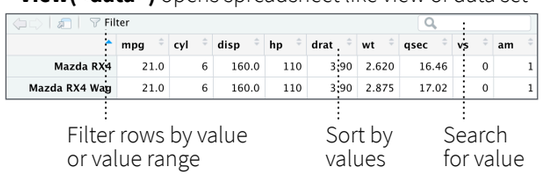


RStudio opens documentation in a dedicated **Help** pane



Viewer pane displays HTML content, such as Shiny apps, RMarkdown reports, and interactive visualizations

View(<data>) opens spreadsheet like view of data set



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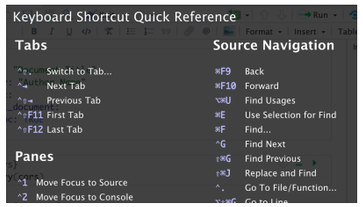
Keyboard Shortcuts

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

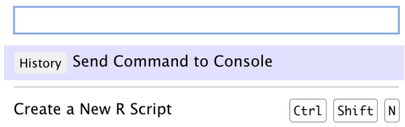
MAKE PACKAGES	Windows/Linux	Mac
Load All (devtools)	Ctrl+Shift+L	Cmd+Shift+L
Test Package (Desktop)	Ctrl+Shift+T	Cmd+Shift+T
Document Package	Ctrl+Shift+D	Cmd+Shift+D

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

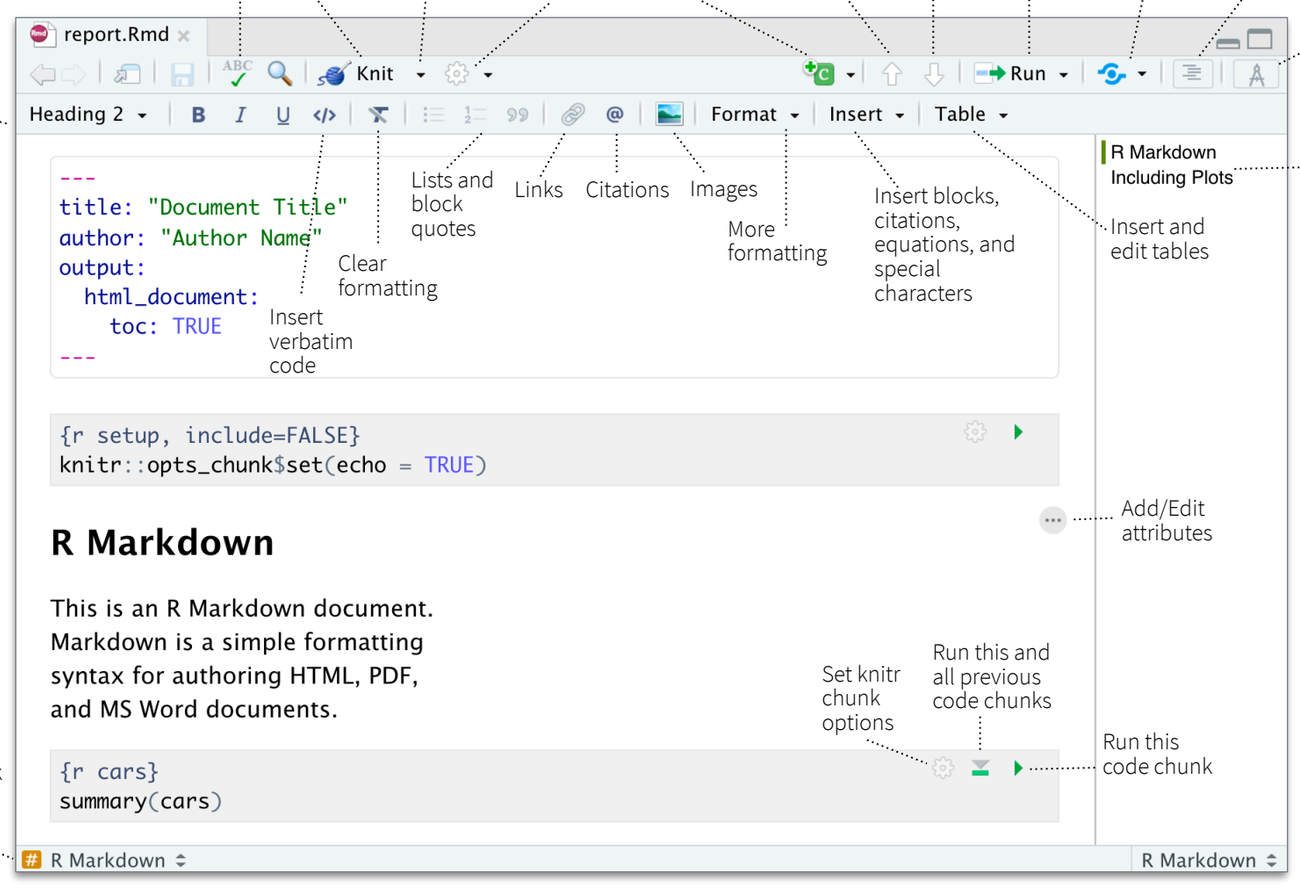
View the Keyboard Shortcut Quick Reference with **Tools > Keyboard Shortcuts** or **Alt/Option + Shift + K**



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:

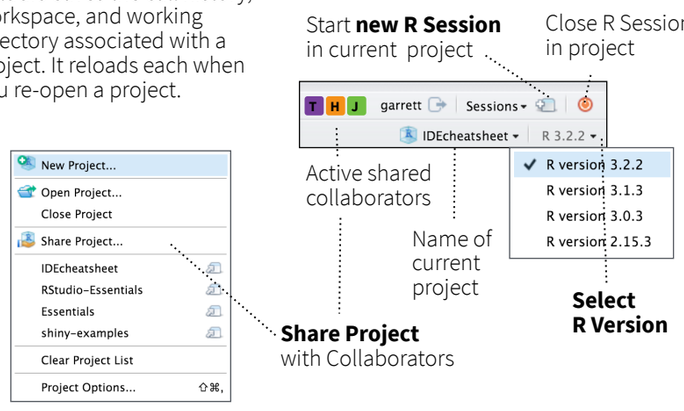
- open and run multiple R sessions at once
- tune your resources to improve performance
- administrative tools for managing user sessions
- collaborate real-time with others in shared projects
- switch easily from one version of R to a different version
- integrate with your authentication, authorization, 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

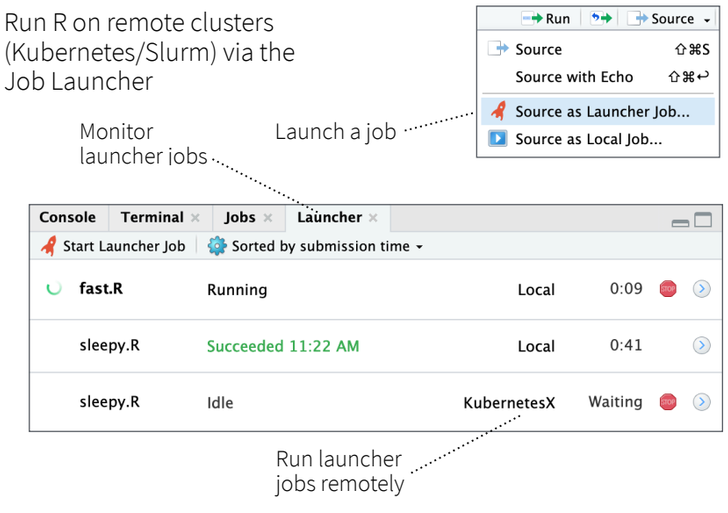
File > New Project

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



R Reference Card for Data Mining

by Yanchang Zhao, yanchang@rdatamining.com, January 3, 2013
The latest version is available at http://www.RDataMining.com. Click the link also for document *R and Data Mining: Examples and Case Studies*.
The package names are in parentheses.

Association Rules & Frequent Itemsets

APRIORI Algorithm

a level-wise, breadth-first algorithm which counts transactions to find frequent itemsets

apriori() mine associations with APRIORI algorithm (*arules*)

ECLAT Algorithm

employs equivalence classes, depth-first search and set intersection instead of counting

eclat() mine frequent itemsets with the Eclat algorithm (*arules*)

Packages

arules mine frequent itemsets, maximal frequent itemsets, closed frequent itemsets and association rules. It includes two algorithms, Apriori and Eclat.
arulesViz visualizing association rules

Sequential Patterns

Functions

cspade() mining frequent sequential patterns with the cSPADE algorithm (*arulesSequences*)
seqefsub() searching for frequent subsequences (*TraMineR*)

Packages

arulesSequences add-on for *arules* to handle and mine frequent sequences
TraMineR mining, describing and visualizing sequences of states or events

Classification & Prediction

Decision Trees

ctree() conditional inference trees, recursive partitioning for continuous, censored, ordered, nominal and multivariate response variables in a conditional inference framework (*party*)
rpart() recursive partitioning and regression trees (*rpart*)
mob() model-based recursive partitioning, yielding a tree with fitted models associated with each terminal node (*party*)

Random Forest

cforest() random forest and bagging ensemble (*party*)
randomForest() random forest (*randomForest*)
varimp() variable importance (*party*)
importance() variable importance (*randomForest*)

Neural Networks

nnet() fit single-hidden-layer neural network (*nnet*)

Support Vector Machine (SVM)

svm() train a support vector machine for regression, classification or density-estimation (*e1071*)
ksvm() support vector machines (*kernlab*)

Performance Evaluation

performance() provide various measures for evaluating performance of prediction and classification models (*ROCR*)
roc() build a ROC curve (*pROC*)
auc() compute the area under the ROC curve (*pROC*)
ROC() draw a ROC curve (*DiagnosisMed*)
PRcurve() precision-recall curves (*DMwR*)
CRchart() cumulative recall charts (*DMwR*)

Packages

rpart recursive partitioning and regression trees
party recursive partitioning
randomForest classification and regression based on a forest of trees using random inputs
rpartOrdinal ordinal classification trees, deriving a classification tree when the response to be predicted is ordinal
rpart.plot plots rpart models with an enhanced version of plot.rpart in the *rpart* package
ROCR visualize the performance of scoring classifiers
pROC display and analyze ROC curves

Regression

Functions

lm() linear regression
glm() generalized linear regression
nls() non-linear regression
predict() predict with models
residuals() residuals, the difference between observed values and fitted values
gls() fit a linear model using generalized least squares (*nlme*)
gnls() fit a nonlinear model using generalized least squares (*nlme*)

Packages

nlme linear and nonlinear mixed effects models

Clustering

Partitioning based Clustering

partition the data into k groups first and then try to improve the quality of clustering by moving objects from one group to another

kmeans() perform k-means clustering on a data matrix
kmeansCBI() interface function for kmeans (*fpc*)
kmeansruns() call kmeans for the k-means clustering method and includes estimation of the number of clusters and finding an optimal solution from several starting points (*fpc*)
pam() the Partitioning Around Medoids (PAM) clustering method (*cluster*)
pamk() the Partitioning Around Medoids (PAM) clustering method with estimation of number of clusters (*fpc*)
cluster.optimal() search for the optimal k-clustering of the dataset (*bayesclust*)
clara() Clustering Large Applications (*cluster*)
fanny(x,k,...) compute a fuzzy clustering of the data into k clusters (*cluster*)
kcca() k-centroids clustering (*flexclust*)
ccfkms() clustering with Conjugate Convex Functions (*cba*)
apcluster() affinity propagation clustering for a given similarity matrix (*apcluster*)
apclusterK() affinity propagation clustering to get K clusters (*apcluster*)
cclust() Convex Clustering, incl. k-means and two other clustering algorithms (*cclust*)
KMeansSparseCluster() sparse k-means clustering (*sparcl*)
tclust(x,k,alpha,...) trimmed k-means with which a proportion alpha of observations may be trimmed (*tclust*)

Hierarchical Clustering

a hierarchical decomposition of data in either bottom-up (agglomerative) or top-down (divisive) way

hclust(d, method, ...) hierarchical cluster analysis on a set of dissimilarities d using the method for agglomeration
birch() the BIRCH algorithm that clusters very large data with a CF-tree (*birch*)
pvclust() hierarchical clustering with p-values via multi-scale bootstrap resampling (*pvclust*)
agnes() agglomerative hierarchical clustering (*cluster*)
diana() divisive hierarchical clustering (*cluster*)
mona() divisive hierarchical clustering of a dataset with binary variables only (*cluster*)
rockCluster() cluster a data matrix using the Rock algorithm (*cba*)
proximus() cluster the rows of a logical matrix using the Proximus algorithm (*cba*)
isopam() Isopam clustering algorithm (*isopam*)
LLAhclust() hierarchical clustering based on likelihood linkage analysis (*LLAhclust*)
flashClust() optimal hierarchical clustering (*flashClust*)
fastcluster() fast hierarchical clustering (*fastcluster*)
cutreeDynamic(), cutreeHybrid() detection of clusters in hierarchical clustering dendrograms (*dynamicTreeCut*)
HierarchicalSparseCluster() hierarchical sparse clustering (*sparcl*)

Model based Clustering

Mclust() model-based clustering (*mclust*)
HDDC() a model-based method for high dimensional data clustering (*HDclassif*)
fixmahal() Mahalanobis Fixed Point Clustering (*fpc*)
fixreg() Regression Fixed Point Clustering (*fpc*)
mergenormals() clustering by merging Gaussian mixture components (*fpc*)

Density based Clustering

generate clusters by connecting dense regions

dbscan(data,eps,MinPts,...) generate a density based clustering of arbitrary shapes, with neighborhood radius set as eps and density threshold as MinPts (*fpc*)
pdfCluster() clustering via kernel density estimation (*pdfCluster*)

Other Clustering Techniques

mixer() random graph clustering (*mixer*)
nncluster() fast clustering with restarted minimum spanning tree (*nnclust*)
orclus() ORCLUS subspace clustering (*orclus*)

Plotting Clustering Solutions

plotcluster() visualisation of a clustering or grouping in data (*fpc*)
bannerplot() a horizontal barplot visualizing a hierarchical clustering (*cluster*)

Cluster Validation

`silhouette()` compute or extract silhouette information (*cluster*)
`cluster.stats()` compute several cluster validity statistics from a clustering and a dissimilarity matrix (*fpc*)
`clValid()` calculate validation measures for a given set of clustering algorithms and number of clusters (*clValid*)
`clustIndex()` calculate the values of several clustering indexes, which can be independently used to determine the number of clusters existing in a data set (*cclust*)
`NbClust()` provide 30 indices for cluster validation and determining the number of clusters (*NbClust*)

Packages

cluster cluster analysis
fpc various methods for clustering and cluster validation
mclust model-based clustering and normal mixture modeling
birch clustering very large datasets using the BIRCH algorithm
pvclust hierarchical clustering with p-values
apcluster Affinity Propagation Clustering
cclust Convex Clustering methods, including k-means algorithm, On-line Update algorithm and Neural Gas algorithm and calculation of indexes for finding the number of clusters in a data set
cba Clustering for Business Analytics, including clustering techniques such as Proximus and Rock
bclust Bayesian clustering using spike-and-slab hierarchical model, suitable for clustering high-dimensional data
biclust algorithms to find bi-clusters in two-dimensional data
clue cluster ensembles
clues clustering method based on local shrinking
clValid validation of clustering results
clv cluster validation techniques, contains popular internal and external cluster validation methods for outputs produced by package *cluster*
bayesclust tests/searches for significant clusters in genetic data
clustvarsel variable selection for model-based clustering
clustsig significant cluster analysis, tests to see which (if any) clusters are statistically different
clusterfly explore clustering interactively
clusterSim search for optimal clustering procedure for a data set
clusterGeneration random cluster generation
clusterCons calculate the consensus clustering result from re-sampled clustering experiments with the option of using multiple algorithms and parameter
gcExplorer graphical cluster explorer
hybridHclust hybrid hierarchical clustering via mutual clusters
Modalclust hierarchical modal Clustering
iCluster integrative clustering of multiple genomic data types
EMCC evolutionary Monte Carlo (EMC) methods for clustering
rEMM extensible Markov Model (EMM) for data stream clustering

Outlier Detection

Functions

`boxplot.stats()$out` list data points lying beyond the extremes of the whiskers
`lofactor()` calculate local outlier factors using the LOF algorithm (*DMwR* or *dprep*)
`lof()` a parallel implementation of the LOF algorithm (*Rlof*)

Packages

extremevalues detect extreme values in one-dimensional data
mvoutlier multivariate outlier detection based on robust methods
outliers some tests commonly used for identifying outliers
Rlof a parallel implementation of the LOF algorithm

Time Series Analysis

Construction & Plot

`ts()` create time-series objects (*stats*)
`plot.ts()` plot time-series objects (*stats*)
`smoothts()` time series smoothing (*ast*)
`sfilter()` remove seasonal fluctuation using moving average (*ast*)

Decomposition

`decomp()` time series decomposition by square-root filter (*timsac*)
`decompose()` classical seasonal decomposition by moving averages (*stats*)
`stl()` seasonal decomposition of time series by `loess` (*stats*)
`tsr()` time series decomposition (*ast*)
`ardec()` time series autoregressive decomposition (*ArDec*)

Forecasting

`arima()` fit an ARIMA model to a univariate time series (*stats*)
`predict.Arima()` forecast from models fitted by `arima` (*stats*)
`auto.arima()` fit best ARIMA model to univariate time series (*forecast*)
`forecast.stl(), forecast.ets(), forecast.Arima()` forecast time series using `stl`, `ets` and `arima` models (*forecast*)

Packages

forecast displaying and analysing univariate time series forecasts
timsac time series analysis and control program
ast time series analysis
ArDec time series autoregressive-based decomposition
ares a toolbox for time series analyses using generalized additive models
dse tools for multivariate, linear, time-invariant, time series models

Text Mining

Functions

`Corpus()` build a corpus, which is a collection of text documents (*tm*)
`tm_map()` transform text documents, e.g., stemming, stopword removal (*tm*)
`tm_filter()` filtering out documents (*tm*)
`TermDocumentMatrix(), DocumentTermMatrix()` construct a term-document matrix or a document-term matrix (*tm*)
`Dictionary()` construct a dictionary from a character vector or a term-document matrix (*tm*)
`findAssocs()` find associations in a term-document matrix (*tm*)
`findFreqTerms()` find frequent terms in a term-document matrix (*tm*)
`stemDocument()` stem words in a text document (*tm*)
`stemCompletion()` complete stemmed words (*tm*)
`termFreq()` generate a term frequency vector from a text document (*tm*)
`stopwords(language)` return stopwords in different languages (*tm*)
`removeNumbers(), removePunctuation(), removeWords()` remove numbers, punctuation marks, or a set of words from a text document (*tm*)
`removeSparseTerms()` remove sparse terms from a term-document matrix (*tm*)
`textcat()` n-gram based text categorization (*textcat*)
`SnowballStemmer()` Snowball word stemmers (*Snowball*)
`LDA()` fit a LDA (latent Dirichlet allocation) model (*topicmodels*)
`CTM()` fit a CTM (correlated topics model) model (*topicmodels*)
`terms()` extract the most likely terms for each topic (*topicmodels*)
`topics()` extract the most likely topics for each document (*topicmodels*)

Packages

tm a framework for text mining applications
lda fit topic models with LDA
topicmodels fit topic models with LDA and CTM
RTextTools automatic text classification via supervised learning
tm.plugin.dc a plug-in for package *tm* to support distributed text mining
tm.plugin.mail a plug-in for package *tm* to handle mail
RcmdrPlugin.TextMining GUI for demonstration of text mining concepts and *tm* package
textir a suite of tools for inference about text documents and associated sentiment
tau utilities for text analysis
textcat n-gram based text categorization
YjdnJlp Japanese text analysis by Yahoo! Japan Developer Network

Social Network Analysis and Graph Mining

Functions

`graph(), graph.edgelist(), graph.adjacency(), graph.incidence()` create graph objects respectively from edges, an edge list, an adjacency matrix and an incidence matrix (*igraph*)
`plot(), tkplot()` static and interactive plotting of graphs (*igraph*)
`gplot(), gplot3d()` plot graphs (*sna*)
`V(), E()` vertex/edge sequence of igraph (*igraph*)
`are.connected()` check whether two nodes are connected (*igraph*)
`degree(), betweenness(), closeness()` various centrality scores (*igraph, sna*)
`add.edges(), add.vertices(), delete.edges(), delete.vertices()` add and delete edges and vertices (*igraph*)
`neighborhood()` neighborhood of graph vertices (*igraph, sna*)
`get.adjlist()` adjacency lists for edges or vertices (*igraph*)
`nei(), adj(), from(), to()` vertex/edge sequence indexing (*igraph*)
`cliques()` find cliques, ie. complete subgraphs (*igraph*)
`clusters()` maximal connected components of a graph (*igraph*)
`%->%, %<-%, %--%` edge sequence indexing (*igraph*)
`get.edgelist()` return an edge list in a two-column matrix (*igraph*)
`read.graph(), write.graph()` read and writ graphs from and to files (*igraph*)

Packages

sna social network analysis
igraph network analysis and visualization
statnet a set of tools for the representation, visualization, analysis and simulation of network data
egonet ego-centric measures in social network analysis
snort social network-analysis on relational tables
network tools to create and modify network objects
bipartite visualising bipartite networks and calculating some (ecological) indices
blockmodeling generalized and classical blockmodeling of valued networks
diagram visualising simple graphs (networks), plotting flow diagrams
NetCluster clustering for networks
NetData network data for McFarland's SNA R labs

RDM

NetIndices estimating network indices, including trophic structure of foodwebs in R
NetworkAnalysis statistical inference on populations of weighted or unweighted networks
tnet analysis of weighted, two-mode, and longitudinal networks
triads triad census for networks

Spatial Data Analysis

Functions

`geocode()` geocodes a location using Google Maps (*ggmap*)
`qmap()` quick map plot (*ggmap*)
`get_map()` queries the Google Maps, OpenStreetMap, or Stamen Maps server for a map at a certain location (*ggmap*)
`gvisGeoChart(), gvisGeoMap(), gvisIntensityMap(), gvisMap()` Google geo charts and maps (*googleVis*)
`GetMap()` download a static map from the Google server (*RgoogleMaps*)
`ColorMap()` plot levels of a variable in a colour-coded map (*RgoogleMaps*)
`PlotOnStaticMap()` overlay plot on background image of map tile (*RgoogleMaps*)
`TextOnStaticMap()` plot text on map (*RgoogleMaps*)

Packages

plotGoogleMaps plot spatial data as HTML map mushup over Google Maps
RgoogleMaps overlay on Google map tiles in R
plotKML visualization of spatial and spatio-temporal objects in Google Earth
ggmap Spatial visualization with Google Maps and OpenStreetMap
clustTool GUI for clustering data with spatial information
SGCS Spatial Graph based Clustering Summaries for spatial point patterns
spdep spatial dependence: weighting schemes, statistics and models

Statistics

Summarization

`summary()` summarize data
`describe()` concise statistical description of data (*Hmisc*)
`boxplot.stats()` box plot statistics

Analysis of Variance

`aov()` fit an analysis of variance model (*stats*)
`anova()` compute analysis of variance (or deviance) tables for one or more fitted model objects (*stats*)

Statistical Test

`t.test()` student's t-test (*stats*)
`prop.test()` test of equal or given proportions (*stats*)
`binom.test()` exact binomial test (*stats*)

Mixed Effects Models

`lme()` fit a linear mixed-effects model (*nlme*)
`nlme()` fit a nonlinear mixed-effects model (*nlme*)

Principal Components and Factor Analysis

`princomp()` principal components analysis (*stats*)
`prcomp()` principal components analysis (*stats*)

Other Functions

`var(), cov(), cor()` variance, covariance, and correlation (*stats*)
`density()` compute kernel density estimates (*stats*)

Packages

nlme linear and nonlinear mixed effects models

Graphics

Functions

`plot()` generic function for plotting (*graphics*)
`barplot(), pie(), hist()` bar chart, pie chart and histogram (*graphics*)
`boxplot()` box-and-whisker plot (*graphics*)
`stripchart()` one dimensional scatter plot (*graphics*)
`dotchart()` Cleveland dot plot (*graphics*)
`qqnorm(), qqplot(), qqline()` QQ (quantile-quantile) plot (*stats*)
`coplot()` conditioning plot (*graphics*)
`splom()` conditional scatter plot matrices (*lattice*)
`pairs()` a matrix of scatterplots (*graphics*)
`cpairs()` enhanced scatterplot matrix (*gclus*)
`parcoord()` parallel coordinate plot (*MASS*)
`cparcoord()` enhanced parallel coordinate plot (*gclus*)
`paracoor()` parallel coordinates plot (*denpro*)
`parallelplot()` parallel coordinates plot (*lattice*)
`densityplot()` kernel density plot (*lattice*)
`contour(), filled.contour()` contour plot (*graphics*)
`levelplot(), contourplot()` level plots and contour plots (*lattice*)
`smoothScatter()` scatterplots with smoothed densities color representation; capable of visualizing large datasets (*graphics*)
`sunflowerplot()` a sunflower scatter plot (*graphics*)
`assocplot()` association plot (*graphics*)
`mosaicplot()` mosaic plot (*graphics*)
`matplot()` plot the columns of one matrix against the columns of another (*graphics*)
`fourfoldplot()` a fourfold display of a $2 \times 2 \times k$ contingency table (*graphics*)
`persp()` perspective plots of surfaces over the x?y plane (*graphics*)
`cloud(), wireframe()` 3d scatter plots and surfaces (*lattice*)
`interaction.plot()` two-way interaction plot (*stats*)
`iplot(), ihist(), ibar(), ipcp()` interactive scatter plot, histogram, bar plot, and parallel coordinates plot (*iplots*)
`pdf(), postscript(), win.metafile(), jpeg(), bmp(), png(), tiff()` save graphs into files of various formats
`gvisAnnotatedTimeLine(), gvisAreaChart(), gvisBarChart(), gvisBubbleChart(), gvisCandlestickChart(), gvisColumnChart(), gvisComboChart(), gvisGauge(), gvisGeoChart(), gvisGeoMap(), gvisIntensityMap(), gvisLineChart(), gvisMap(), gvisMerge(), gvisMotionChart(), gvisOrgChart(), gvisPieChart(), gvisScatterChart(), gvisSteppedAreaChart(), gvisTable(), gvisTreeMap()` various interactive charts produced with the Google Visualisation API (*googleVis*)
`gvisMerge()` merge two *googleVis* charts into one (*googleVis*)

Packages

ggplot2 an implementation of the Grammar of Graphics
googleVis an interface between R and the Google Visualisation API to create interactive charts
lattice a powerful high-level data visualization system, with an emphasis on multivariate data
vcd visualizing categorical data
denpro visualization of multivariate, functions, sets, and data
iplots interactive graphics

Data Manipulation

Functions

`transform()` transform a data frame
`scale()` scaling and centering of matrix-like objects
`t()` matrix transpose
`aperm()` array transpose
`sample()` sampling
`table(), tabulate(), xtabs()` cross tabulation (*stats*)
`stack(), unstack()` stacking vectors
`split(), unsplit()` divide data into groups and reassemble
`reshape()` reshape a data frame between "wide" and "long" format (*stats*)
`merge()` merge two data frames; similar to database `join` operations
`aggregate()` compute summary statistics of data subsets (*stats*)
`by()` apply a function to a data frame split by factors
`melt(), cast()` melt and then cast data into the reshaped or aggregated form you want (*reshape*)
`complete.cases()` find complete cases, i.e., cases without missing values
`na.fail, na.omit, na.exclude, na.pass` handle missing values

Packages

reshape flexibly restructure and aggregate data
data.table extension of data.frame for fast indexing, ordered joins, assignment, and grouping and list columns
gdata various tools for data manipulation

Data Access

Functions

`save(), load()` save and load R data objects
`read.csv(), write.csv()` import from and export to .CSV files
`read.table(), write.table(), scan(), write()` read and write data
`write.matrix()` write a matrix or data frame (*MASS*)
`readLines(), writeLines()` read/write text lines from/to a connection, such as a text file
`sqlQuery()` submit an SQL query to an ODBC database (*RODBC*)
`sqlFetch()` read a table from an ODBC database (*RODBC*)
`sqlSave(), sqlUpdate()` write or update a table in an ODBC database (*RODBC*)
`sqlColumns()` enquire about the column structure of tables (*RODBC*)
`sqlTables()` list tables on an ODBC connection (*RODBC*)
`odbcConnect(), odbcClose(), odbcCloseAll()` open/close connections to ODBC databases (*RODBC*)
`dbSendQuery` execute an SQL statement on a given database connection (*DBI*)
`dbConnect(), dbDisconnect()` create/close a connection to a DBMS (*DBI*)

Packages

RODBC ODBC database access
DBI a database interface (DBI) between R and relational DBMS
RMySQL interface to the MySQL database
RJDBC access to databases through the JDBC interface
RSQLite SQLite interface for R
ROracle Oracle database interface (DBI) driver
RpgSQL DBI/RJDBC interface to PostgreSQL database
RODM interface to Oracle Data Mining
xlsReadWrite read and write Excel files
WriteXLS create Excel 2003 (XLS) files from data frames

Big Data

Functions

`as.ffdf()` coerce a dataframe to an `ffdf` (*ff*)
`read.table.ffdf(), read.csv.ffdf()` read data from a flat file to an `ffdf` object (*ff*)
`write.table.ffdf(), write.csv.ffdf()` write an `ffdf` object to a flat file (*ff*)
`ffdfappend()` append a dataframe or an `ffdf` to an existing `ffdf` (*ffdf*)
`big.matrix()` create a standard `big.matrix`, which is constrained to available RAM (*bigmemory*)
`read.big.matrix()` create a `big.matrix` by reading from an ASCII file (*bigmemory*)
`write.big.matrix()` write a `big.matrix` to a file (*bigmemory*)
`filebacked.big.matrix()` create a file-backed `big.matrix`, which may exceed available RAM by using hard drive space (*bigmemory*)
`mwhich()` expanded "which"-like functionality (*bigmemory*)

Packages

ff memory-efficient storage of large data on disk and fast access functions
ffbase basic statistical functions for package *ff*
filehash a simple key-value database for handling large data
g.data create and maintain delayed-data packages
BufferedMatrix a matrix data storage object held in temporary files
biglm regression for data too large to fit in memory
bigmemory manage massive matrices with shared memory and memory-mapped files
biganalytics extend the *bigmemory* package with various analytics
bigtabulate table-, tapply-, and split-like functionality for matrix and `big.matrix` objects

Parallel Computing

Functions

`foreach(...)` **`%dopar%`** looping in parallel (*foreach*)
`registerDoSEQ(), registerDoSNOW(), registerDoMC()` register respectively the sequential, SNOW and multicore parallel backend with the *foreach* package (*foreach, doSNOW, doMC*)
`sfInit(), sfStop()` initialize and stop the cluster (*snowfall*)
`sfLapply(), sfSapply(), sfApply()` parallel versions of `lapply(), sapply(), apply()` (*snowfall*)

Packages

multicore parallel processing of R code on machines with multiple cores or CPUs
snow simple parallel computing in R
snowfall usability wrapper around *snow* for easier development of parallel R programs
snowFT extension of *snow* supporting fault tolerant and reproducible applications, and easy-to-use parallel programming
Rmpi interface (Wrapper) to MPI (Message-Passing Interface)
rpvm R interface to PVM (Parallel Virtual Machine)
nws provide coordination and parallel execution facilities
foreach foreach looping construct for R
doMC foreach parallel adaptor for the *multicore* package
doSNOW foreach parallel adaptor for the *snow* package
doMPI foreach parallel adaptor for the *Rmpi* package
doParallel foreach parallel adaptor for the *multicore* package
doRNG generic reproducible parallel backend for `foreach` Loops
GridR execute functions on remote hosts, clusters or grids
fork R functions for handling multiple processes

Generating Reports

`Sweave()` mixing text and R/S code for automatic report generation (*utils*)
knitr a general-purpose package for dynamic report generation in R
R2HTML making HTML reports
R2PPT generating Microsoft PowerPoint presentations

Interface to Weka

Package ***RWeka*** is an R interface to Weka, and enables to use the following Weka functions in R.

Association rules:
`Apriori(), Tertius()`
Regression and classification:
`LinearRegression(), Logistic(), SMO()`
Lazy classifiers:
`IBk(), LBR()`
Meta classifiers:
`AdaBoostM1(), Bagging(), LogitBoost(), MultiBoostAB(), Stacking(), CostSensitiveClassifier()`
Rule classifiers:
`JRip(), M5Rules(), OneR(), PART()`
Regression and classification trees:
`J48(), LMT(), M5P(), DecisionStump()`
Clustering:
`Cobweb(), FarthestFirst(), SimpleKMeans(), XMeans(), DBScan()`
Filters:
`Normalize(), Discretize()`
Word stemmers:
`IteratedLovinsStemmer(), LovinsStemmer()`
Tokenizers:
`AlphabeticTokenizer(), NGramTokenizer(), WordTokenizer()`

Editors/GUIs

Tinn-R a free GUI for R language and environment
RStudio a free integrated development environment (IDE) for R
rattle graphical user interface for data mining in R
Rpad workbook-style, web-based interface to R
RPMG graphical user interface (GUI) for interactive R analysis sessions
gWidgets a toolkit-independent API for building interactive GUIs
Red-R An open source visual programming GUI interface for R
R AnalyticFlow a software which enables data analysis by drawing analysis flowcharts
latticist a graphical user interface for exploratory visualisation

Other R Reference Cards

R Reference Card, by Tom Short
`http://rpad.googlecode.com/svn-history/r76/Rpad_homepage/R-refcard.pdf` or
`http://cran.r-project.org/doc/contrib/Short-refcard.pdf`
R Reference Card, by Jonathan Baron
`http://cran.r-project.org/doc/contrib/refcard.pdf`
R Functions for Regression Analysis, by Vito Ricci
`http://cran.r-project.org/doc/contrib/Ricci-refcard-regression.pdf`
R Functions for Time Series Analysis, by Vito Ricci
`http://cran.r-project.org/doc/contrib/Ricci-refcard-ts.pdf`

RDataMining Website, Package, Twitter & Groups

RDataMining Website:	`http://www.rdatamining.com`
Group on LinkedIn:	`http://group.rdatamining.com`
Group on Google:	`http://group2.rdatamining.com`
Twitter:	`http://twitter.com/rdatamining`
RDataMining Package:	`http://www.rdatamining.com/package`
	`http://package.rdatamining.com`