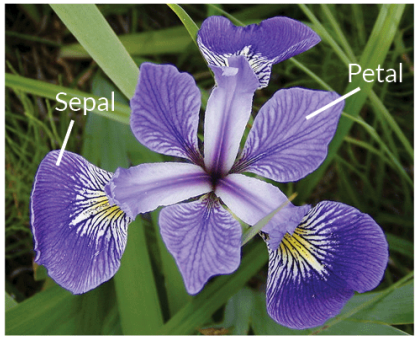
Introduction to dataframes

QB Bootcamp, Day 2
Wednesday, 6 September 2023
3:15pm - 3:30pm

What are dataframes?

Fisher's "Iris" dataset is a famous example dataset in statistics and dataviz



Iris Versicolor

Iris Setosa

Iris Virginica

150 rows
(50 per species)

	sepal_length	sepal_width	petal_length	petal_width	species
0	5.1	3.5	1.4	0.2	setosa
1	4.9	3.0	1.4	0.2	setosa
2	4.7	3.2	1.3	0.2	setosa
3	4.6	3.1	1.5	0.2	setosa
4	5.0	3.6	1.4	0.2	setosa

⋮

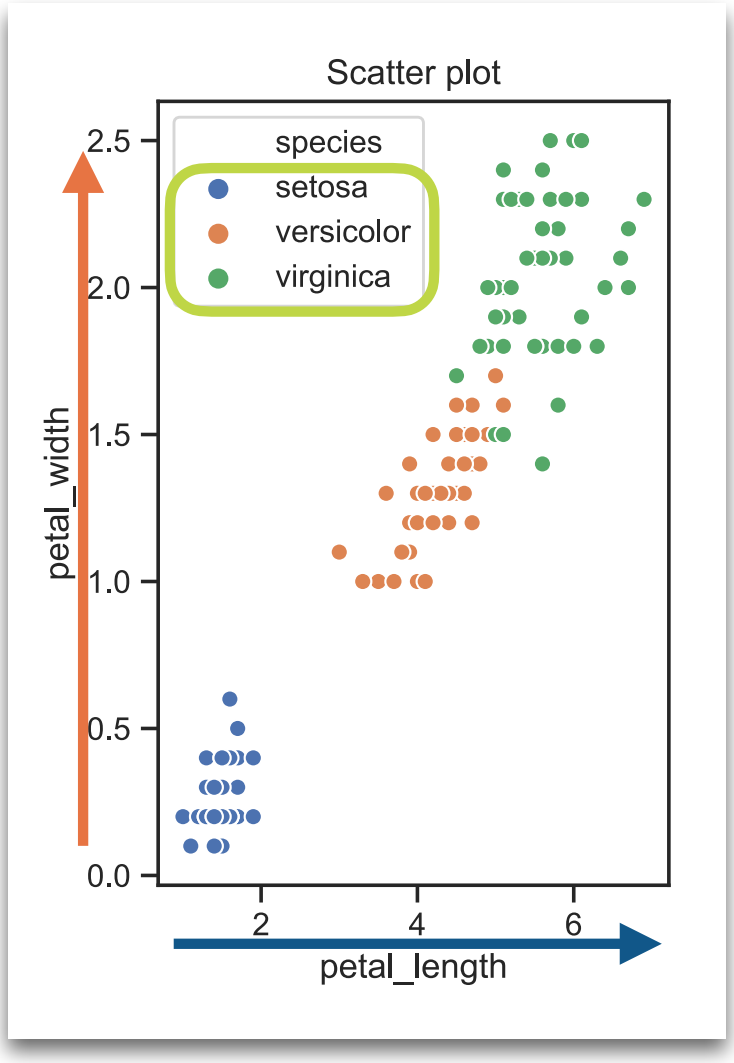
https://en.wikipedia.org/wiki/Iris_flower_data_set

https://www.datacamp.com/community/tutorials/machine-learning-in-r

Dataframes greatly facilitate data visualization

"aesthetics"

			x	y	color
	sepal_length	sepal_width	petal_length	petal_width	species
0	5.1	3.5	1.4	0.2	setosa
1	4.9	3.0	1.4	0.2	setosa
2	4.7	3.2	1.3	0.2	setosa
3	4.6	3.1	1.5	0.2	setosa
4	5.0	3.6	1.4	0.2	setosa
5	5.4	3.9	1.7	0.4	setosa
6	4.6	3.4	1.4	0.3	setosa
7	5.0	3.4	1.5	0.2	setosa
8	4.4	2.9	1.4	0.2	setosa
9	4.9	3.1	1.5	0.1	setosa
10	5.4	3.7	1.5	0.2	setosa
11	4.8	3.4	1.6	0.2	setosa
12	4.8	3.0	1.4	0.1	setosa
13	4.3	3.0	1.1	0.1	setosa
14	5.8	4.0	1.2	0.2	setosa



Dataframes facilitate important data-organizational transformations

	sepal_length	sepal_width	petal_length	petal_width	species
0	5.1	3.5	1.4	0.2	setosa
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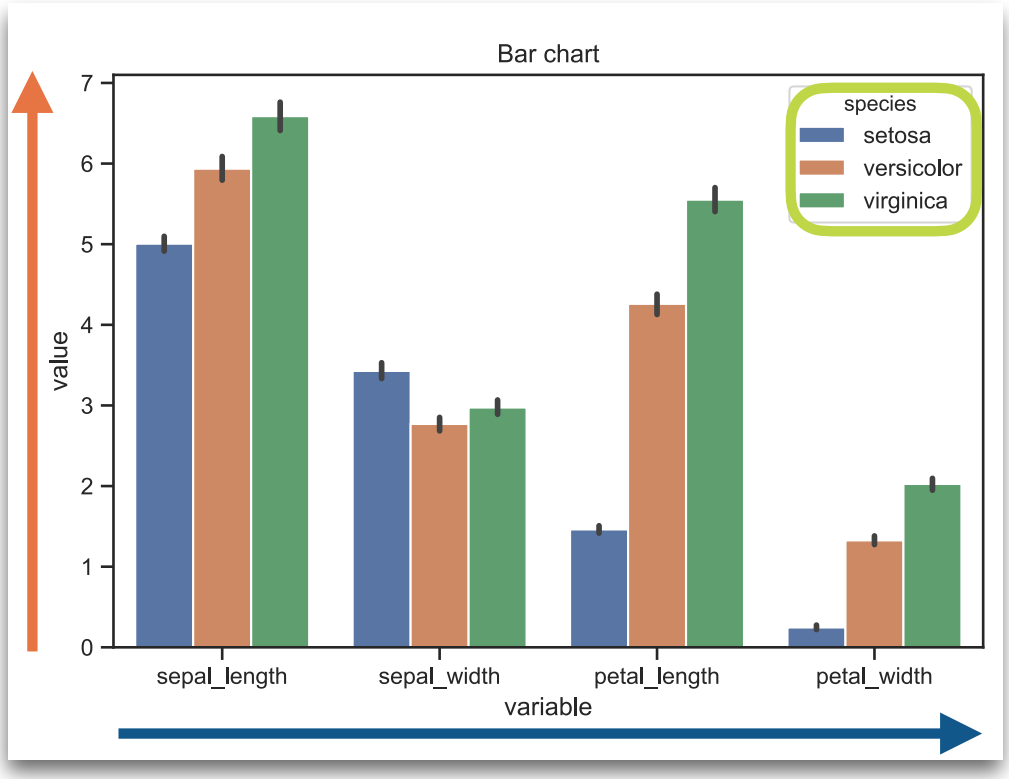
2	4.7	3.2	1.3	0.2	setosa
3	4.6	3.1	1.5	0.2	setosa
4	5.0	3.6	1.4	0.2	setosa

individual = 1 flower

melt

	species	variable	value
0	setosa	sepal_length	5.1
1	setosa	sepal_length	4.9
2	setosa	sepal_length	4.7
3	setosa	sepal_length	4.6
4	setosa	sepal_length	5.0

individual = 1 measurement



FULL DISCLOSURE:
Classical statistics is closely entwined with eugenics.

https://en.wikipedia.org/wiki/Ronald_Fisher

The Iris dataset comes from:

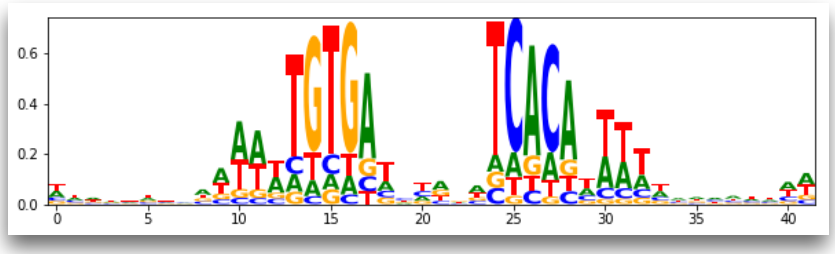
R. A. Fisher (1936).
"The use of multiple measurements
in taxonomic problems".
Annals of Eugenics. **7** (2): 179–188.
(data collected by Edgar Anderson)

What will we be doing today?

We will start by working with a dataframe listing transcription factor binding sites in the database RegulonDB

	tf	site
0	AcrR	gcgttagattTACATACATTTGTGAATGTATGTAccatagcacg
1	AcrR	cgtgctatggTACATACATTCACAAATGTATGTAaatctaacgc
2	AcrR	catcggtcaaTTCATTCATTtgacttatac
3	AcrR	tcactacacgCACATACAACggaggggggc
4	AcrR	atttattaccGTCATTCATTTCTGAATGTCTGTTtacccctatt
5	AcrR	gctttacctcAAGTTAACTTgaggaattat
6	AcrR	ataattcctcAAGTTAACTTgaggtaaagc
7	Ada	ttcagacgctGCGCTTTGCTTTCATATTCCGGTTgtcgcgacgg
8	Ada	ggtcaccatcACGCAAAAACCAACAATCTTGCGCtttaattttt
9	Ada	caacaatcttGCGCTTTAATTTTTTTCGCTGACAaggaagcttt
10	Ada	cgcattacatTGCTGGATAAGAATGTTTTAGCAAtctctttctg
11	AgaR	ttcgtaaaacTTTCGTTTCATTTCGTTTTGcctattaacg
12	AgaR	ttgcctattaACGCCTTTCTATTAAGCAAAtgcaagccca
13	AgaR	tttcagtgacTTTCATTATGTTTCTTTTGTgaatcagatc
14	AgaR	aaccattatcTTTCGTTTTATTTTTATCTCaccatgacgc

1. Load TF binding site database a Pandas dataframe
2. Filter for TF of choice
3. Filter for binding sites of the most common length
4. Make a sequence logo



CRP logo (from 358 sites)

We will then parse our computed replication profiles in the form of a data frame

	chromosome	start	stop	reads
0	chrI	1	31	2
1	chrI	32	62	0
2	chrI	63	93	1
3	chrI	94	124	0
4	chrI	125	155	3
5	chrI	156	186	0
6	chrI	187	217	0
7	chrI	218	248	0
8	chrI	249	279	0
9	chrI	280	310	0
10	chrI	311	341	0
11	chrI	342	372	0
12	chrI	373	403	0
13	chrI	404	434	0
14	chrI	435	465	1

1. Load a .bed file as a Pandas dataframe
2. Filter for the chromosome of choice
3. Smooth # reads as a function of position
4. Plot replication profile