

Introducing an Outstanding Publicly Available Data Set

Zhang B, Gaiteri C, Bodea LG, Wang Z, McElwee J, Podtelezchnikov AA, Zhang C, Xie T, Tran L, Dobrin R, Fluder E, Clurman B, Melquist S, Narayanan M, Suver C, Shah H, Mahajan M, Gillis T, Mysore J, MacDonald ME, Lamb JR, Bennett DA, Molony C, Stone DJ, Gudnason V, Myers AJ, Schadt EE, Neumann H, Zhu J, Emilsson V. **Integrated systems approach identifies genetic nodes and networks in late-onset Alzheimer's disease.** Cell. 2013 Apr 25;153(3):707-20. doi: 10.1016/j.cell.2013.03.030. PMID: 23622250; PMCID: PMC3677161.

The genetics of complex disease produce alterations in the molecular interactions of cellular pathways whose collective effect may become clear through the organized structure of molecular networks. To characterize molecular systems associated with **late-onset Alzheimer's disease (LOAD)**, we **constructed gene-regulatory networks** in **1,647 postmortem brain tissues** from LOAD patients and nondemented subjects, and we demonstrate that LOAD reconfigures specific portions of the molecular interaction structure. Through an integrative network-based approach, we rank-ordered these network structures for relevance to LOAD pathology, highlighting an immune- and microglia-specific module that is dominated by genes involved in pathogen phagocytosis, contains TYROBP as a key regulator, and is upregulated in LOAD. Mouse microglia cells overexpressing intact or truncated TYROBP revealed expression changes that significantly overlapped the human brain TYROBP network. Thus the causal network structure is a useful predictor of response to gene perturbations and presents a framework to test models of disease mechanisms underlying LOAD.

Check various visualization plots used in the article!

Multi-tissue gene expression profiles of human brain



Zhang B, Gaiteri C, Bodea LG, Wang Z et al. Integrated systems approach identifies genetic nodes and networks in late-onset Alzheimer's disease. Cell 2013 Apr 25;153(3):707-20. PMID: 23622250

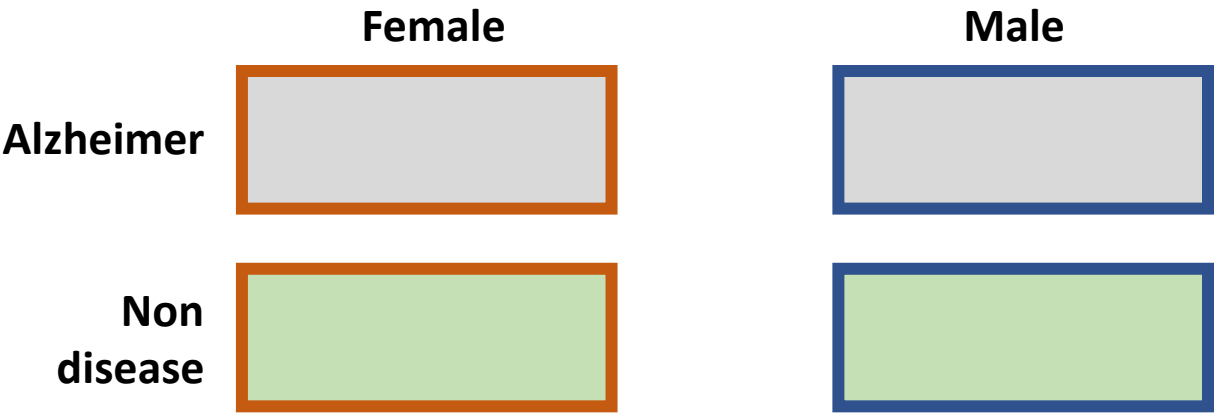
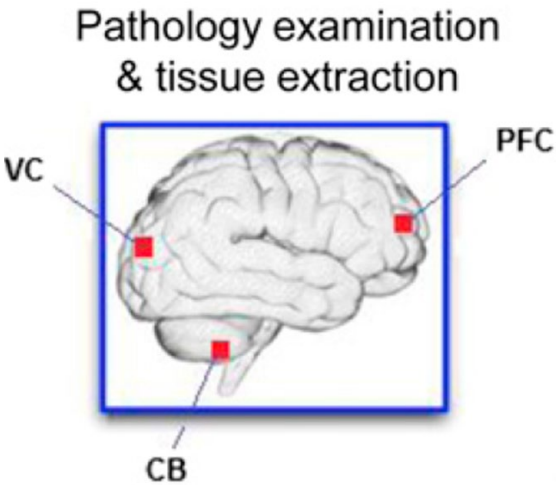
This SuperSeries is composed of the following SubSeries:

- GSE44768 Multi-tissue gene expression profiles of human brain (CR)
- GSE44770 Multi-tissue gene expression profiles of human brain (PFC)
- GSE44771 Multi-tissue gene expression profiles of human brain (VC)

Samples (690)
[More...](#)

- GSM1090267 1_CR
- GSM1090268 2_CR
- GSM1090269 3_CR

Samples:
230 CR
230 PFC
230 VC



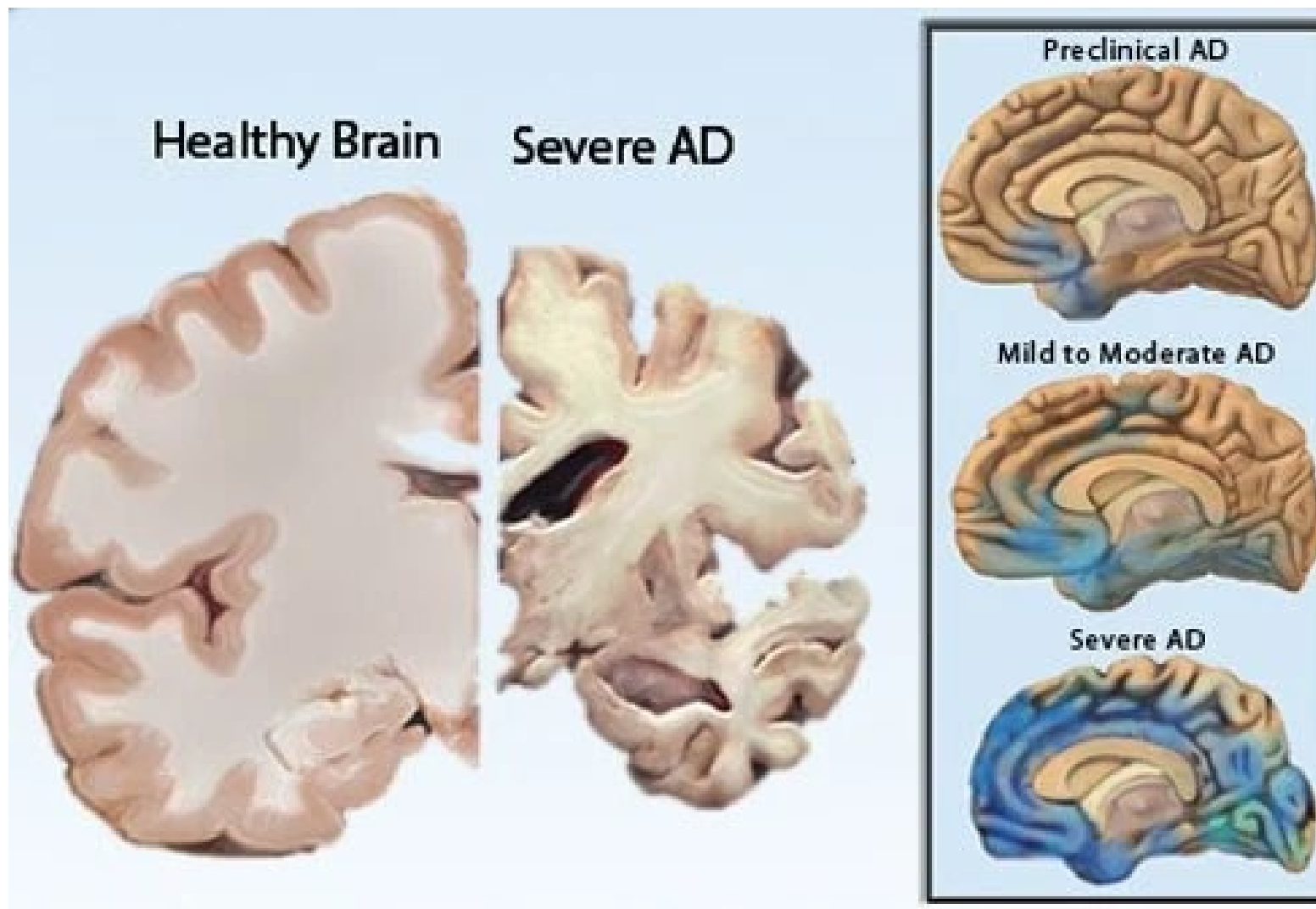
Four subpopulation for each tissue study

Picture of Alzheimer's Disease

Analyze mRNA
gene expression
data



Construct
gene-regulatory
networks



nd = non- disease

A = Alzheimer's



Quick Facts

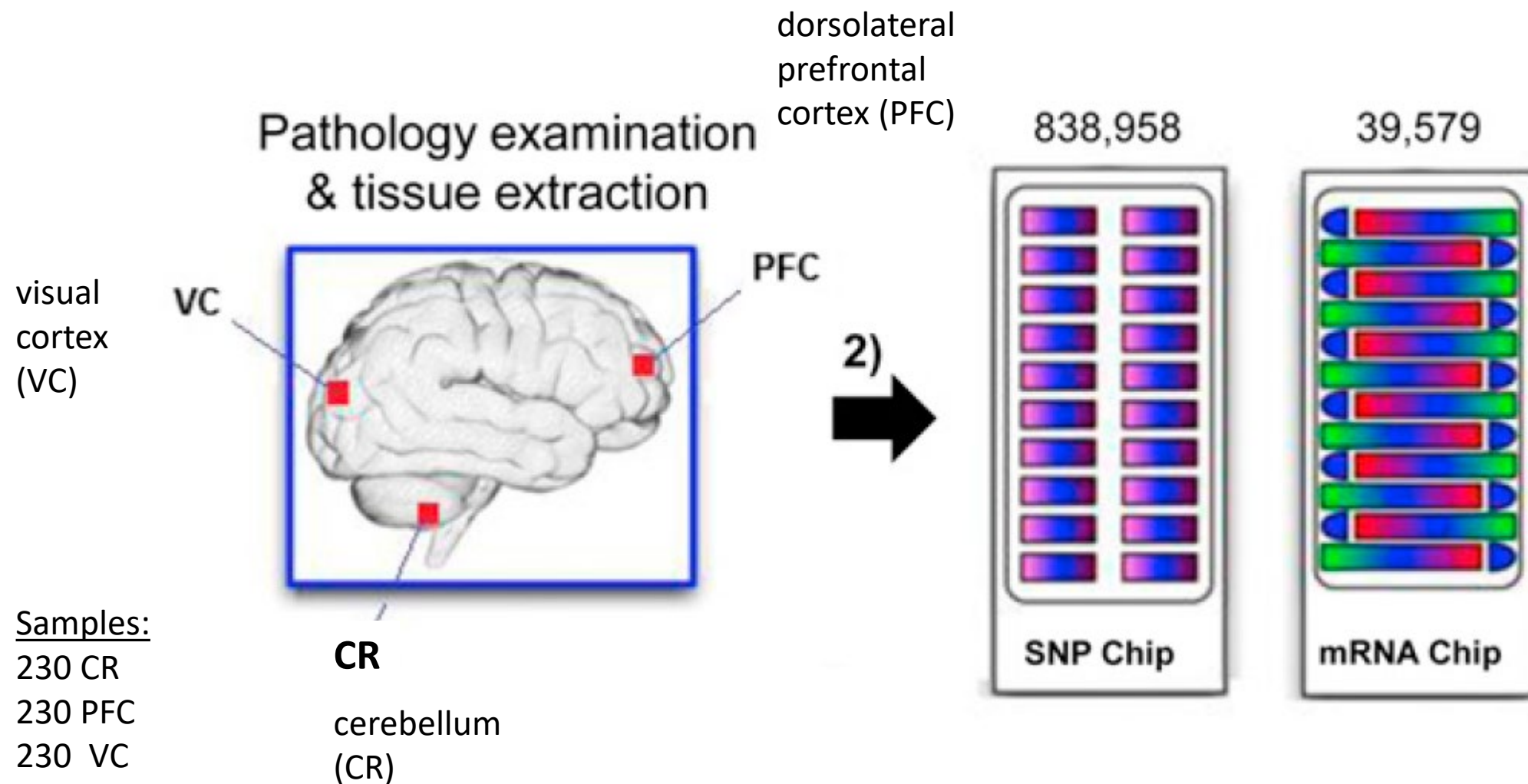
MORE THAN **6 MILLION** AMERICANS ARE LIVING WITH ALZHEIMER'S. BY 2050, THIS NUMBER IS PROJECTED TO RISE TO NEARLY 13 MILLION.

IN THE UNITED STATES, ALZHEIMER'S AND DEMENTIA DEATHS HAVE **INCREASED 16%** DURING THE COVID-19 PANDEMIC.

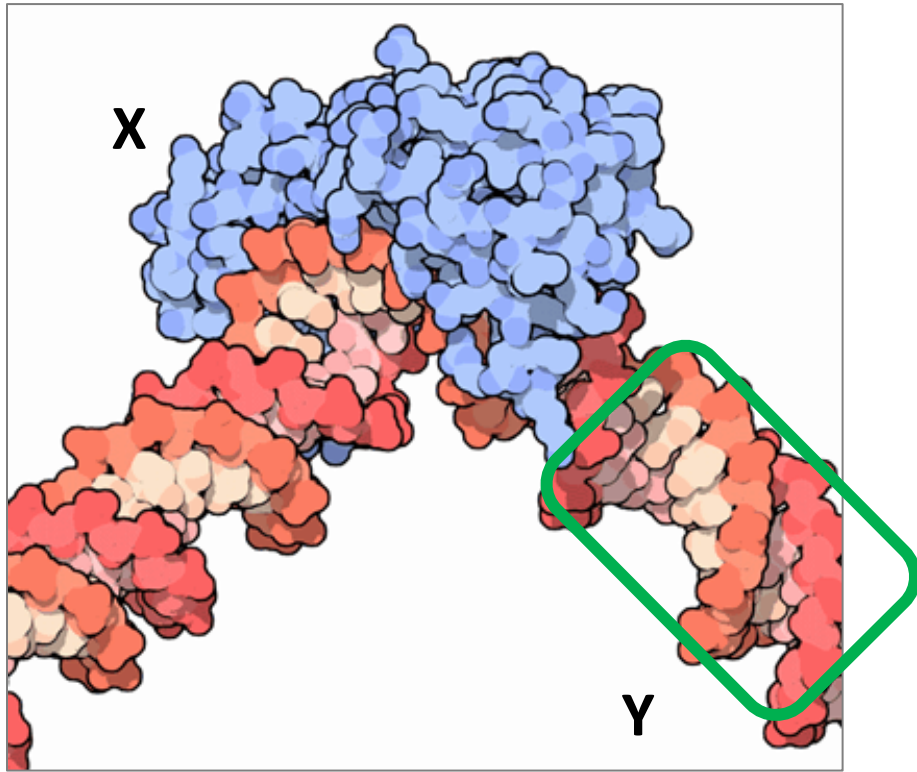
1 IN 3 SENIORS DIES WITH ALZHEIMER'S OR ANOTHER DEMENTIA. IT KILLS MORE THAN BREAST CANCER AND PROSTATE CANCER COMBINED.

We are in the business of training next generation work force who can combat this and other human health related issues!

Multi-tissue gene expression profiles of human brain (CR)



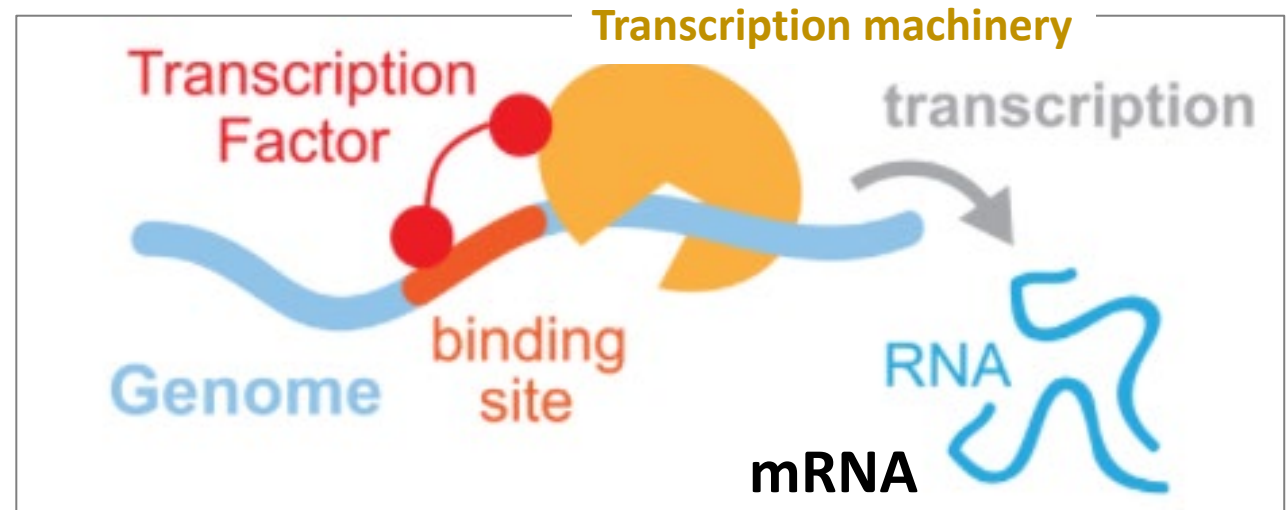
Gene X may activate expression of gene Y.
Gene X may inhibit expression of gene Y.



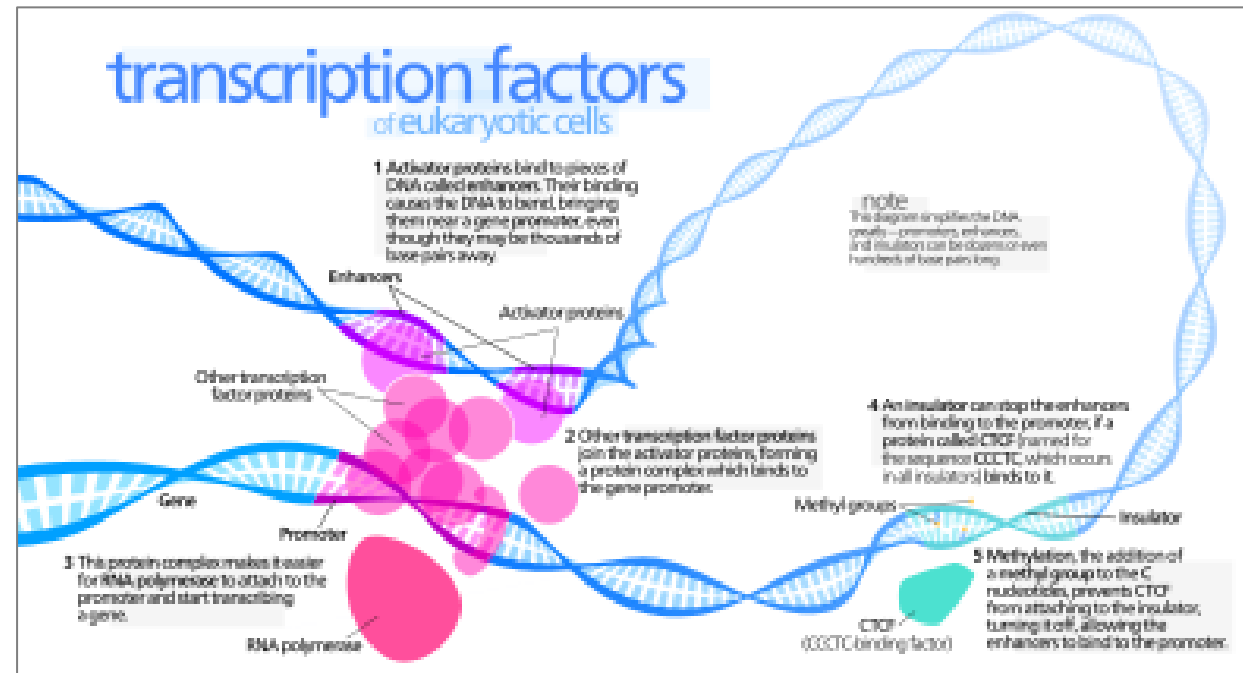
The transcription factor **TATA binding protein** (blue) bound to **DNA** (red).

Image by David S. Goodsell based on the crystal structure 1cdw from the Protein Data Bank.

http://en.wikipedia.org/wiki/Transcription_factor



doi: <https://doi.org/10.1371/journal.pcbi.1004891.g001>



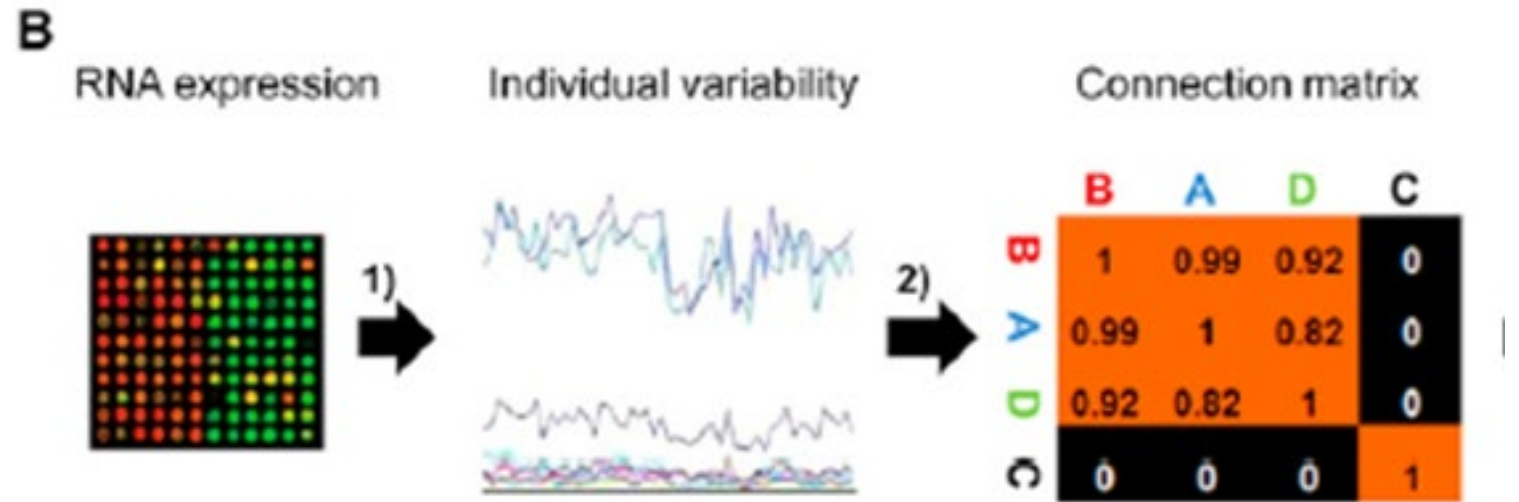
https://en.wikipedia.org/wiki/Transcription_factor

First Step of Analysis

Construct Pearson Correlation coefficient matrix for the subset of genes of you are focusing.

Example:

node1	node2	r_val
TYROBP	DOCK2	0.927
TYROBP	FCER1G	0.885
TYROBP	GSTA4	-0.7
TYROBP	ABCC2	0.028
DOCK2	FCER1G	0.841
DOCK2	GSTA4	-0.647
DOCK2	ABCC2	0.071
FCER1G	GSTA4	0.841
FCER1G	ABCC2	0.206
GSTA4	ABCC2	-0.085



HW3

GSE44768_CR_alz_female_reduced.csv Data Set

Available at HuskyCT Data_Files folder.

mRNA intensity values in log10 

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	
1	GSM_ID	disease	age	gender	pmi	pH	rin	pres	batch	tissue	XIST	TYROBP	DOCK2	FCER1G	GSTA4	ABCC2	TIMELESS	ACBD5	LM
2	GSM1090268	A	90	F	12.6	6.164	6.3	LNV	1	brain	0.301474	0.209515	0.161961	0.310937	-0.17929	-0.00925	0.027849	0.057428	-0
3	GSM1090271	A	90	F	9.25	6.057	6.7	LNV	1	brain	0.460495	-0.16217	-0.0896	-0.13201	-0.01009	0.02753	-0.00782	-0.00669	-0
4	GSM1090272	A	77	F	6.86	6.793	7.2	LNV	1	brain	0.238641	0.280428	0.313562	0.267188	-0.10473	0.130515	0.228776	-0.0761	-0
5	GSM1090274	A	100	F	24.28	6.576	7.1	LNV	1	brain	0.276038	0.400028	0.251573	0.275051	-0.33018	0.137491	0.105215	-0.09633	-0
6	GSM1090276	A	89	F	13.8	6.145	6.4	LNV	1	brain	0.435775	-0.29332	-0.2628	-0.13867	-0.01655	0.013355	-0.00629	-0.25949	-0
7	GSM1090277	A	61	F	14.1	6.115	7.5	LNV	1	brain	0.245945	-0.42066	-0.35032	-0.31697	-0.14612	0.10048	0.095884	0.024655	-0
8	GSM1090282	A	77	F	10.75	6.58	6.4	LNV	1	brain	0.440187	0.199408	-0.09561	0.384826	-0.11276	0.163864	-0.19778	-0.1274	-0
9	GSM1090284	A	76	F	21.83	6.388	6.3	LNV	1	brain	0.366115	-0.03379	-0.09254	0.150413	0.099431	-0.01735	-0.10217	-0.04408	0.
10	GSM1090285	A	66	F	17.58	6.452	6.4	LNV	1	brain	0.342604	-0.19143	-0.16528	-0.04182	-0.31651	0.122101	-0.02727	-0.18149	0.
11	GSM1090291	A	89	F	7.66	6.689	7.2	LNV	1	brain	0.497142	-0.29836	-0.22498	-0.23675	0.108094	-0.0842	0.028409	-0.1799	-0
12	GSM1090292	A	85	F	6.25	6.654	6.5	LNV	1	brain	0.346257	0.147478	0.16301	0.221962	-0.14166	0.063308	0.114311	-0.07164	-0
13	GSM1090293	A	87	F	13.83	6.86	5.9	Dry-Ice	3	brain	0.256477	-0.05275	-0.12644	0.165657	-0.03902	0.148996	-0.00269	-0.28127	-0
14	GSM1090296	A	90	F	6.58	6.386	6.5	LNV	1	brain	0.373623	-0.18457	-0.14394	-0.10204	-0.04138	0.090129	0.018457	-0.17351	-0
15	GSM1090297	A	92	F	7.08	5.838	6.7	LNV	1	brain	0.44892	-0.2411	-0.17966	-0.15971	-0.06525	0.161733	0.098187	-0.09937	-0
16	GSM1090298	A	91	F	9.58	6.29	6.1	Dry-Ice	2	brain	0.335216	-0.31143	-0.27651	-0.15292	-0.03993	0.014787	0.024292	-0.28976	-0
17	GSM1090300	A	70	F	20	6.058	6.2	Dry-Ice	2	brain	0.245378	-0.5246	-0.44006	-0.24046	0.041687	0.021471	0.082919	-0.39599	-0
18	GSM1090301	A	83	F	13	5.667	6.4	LNV	1	brain	0.383436	-0.20521	-0.21682	-0.07422	-0.08448	0.039032	0.033073	-0.04243	-0
19	GSM1090302	A	75	F	10.62	6.764	6.6	LNV	1	brain	0.251072	0.151106	0.042112	0.025138	-0.25303	0.087672	-0.03997	-0.00613	-0
20	GSM1090305	A	87	F	20.58	6.77	6.9	LNV	1	brain	0.308346	0.100023	0.103067	0.347627	0.016947	-0.01039	0.041217	-0.12216	-0
21	GSM1090307	A	74	F	34.25	6.449	6.3	LNV	1	brain	0.508474	-0.2744	-0.27189	0.079182	-0.01166	0.086366	-0.1255	-0.31437	-0
22	GSM1090309	A	83	F	19.25	6.707	6.9	LNV	1	brain	0.354007	0.075023	0.072999	0.160714	-0.05104	-0.096	0.086144	-0.08198	0

Samples

Total 67 patients

RNA quality measure

Genes from which mRNA abundance level is obtained.

GSE44768_CR_alz_female_reduced.csv Data Set

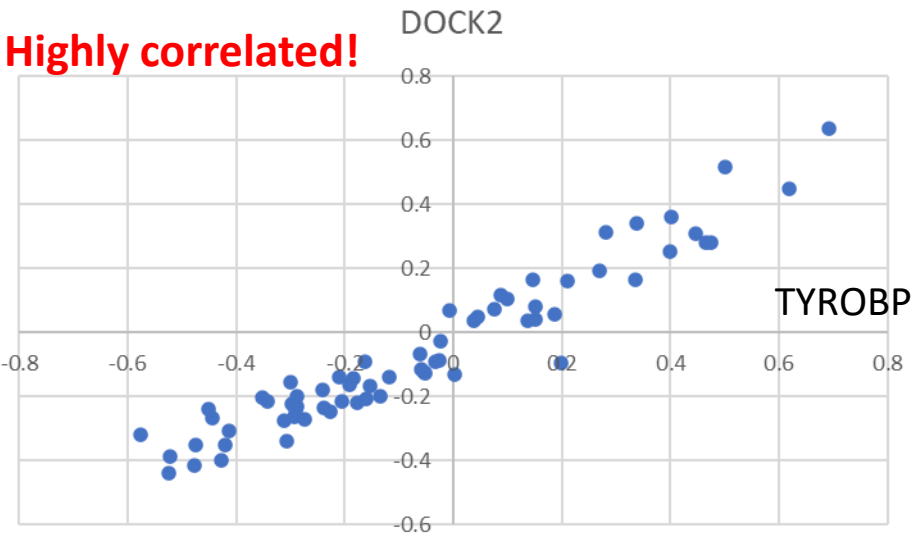


Available at HuskyCT Data_Files folder.

mRNA intensity values in log10

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	
1	GSM_ID	disease	age	gender	pmi	pH	rin	pres	batch	tissue	XIST	TYROBP	DOCK2	FCER1G	GSTA4	ABCC2	TIMELESS	ACBD5	LM
2	GSM1090268	A	90	F	12.6	6.164	6.3	LNV	1	brain	0.301474	0.209515	0.161961	0.310937	-0.17929	-0.00925	0.027849	0.057428	-0
3	GSM1090271	A	90	F	9.25	6.057	6.7	LNV	1	brain	0.460495	-0.16217	-0.0896	-0.13201	-0.01009	0.02753	-0.00782	-0.00669	-0
4	GSM1090272	A	77	F	6.86	6.793	7.2	LNV	1	brain	0.238641	0.280428	0.313562	0.267188	-0.10473	0.130515	0.228776	-0.0761	-0
5	GSM1090274	A	100	F	24.28	6.576	7.1	LNV	1	brain	0.276038	0.400028	0.251573	0.275051	-0.33018	0.137491	0.105215	-0.09633	-0
6	GSM109027										0.435775	-0.29332	-0.2628	-0.13867	-0.01655	0.013355	-0.00629	-0.25949	-0
7	GSM109027										0.245945	-0.42066	-0.35032	-0.31697	-0.14612	0.10048	0.095884	0.024655	-0
8	GSM109028										0.440187	0.199408	-0.09561	0.384826	-0.11276	0.163864	-0.19778	-0.1274	-0
9	GSM109028										0.366115	-0.03379	-0.09254	0.150413	0.099431	-0.01735	-0.10217	-0.04408	0.
10	GSM109028										0.342604	-0.19143	-0.16528	-0.04182	-0.31651	0.122101	-0.02727	-0.18149	0.
11	GSM109029										0.497142	-0.29836	-0.22498	-0.23675	0.108094	-0.0842	0.028409	-0.1799	-0
12	GSM109029										0.346257	0.147478	0.16301	0.221962	-0.14166	0.063308	0.114311	-0.07164	-0
13	GSM109029										0.256477	-0.05275	-0.12644	0.165657	-0.03902	0.148996	-0.00269	-0.28127	-0
14	GSM109029										0.373623	-0.18457	-0.14394	-0.10204	-0.04138	0.090129	0.018457	-0.17351	-0
15	GSM109029										0.44892	-0.2411	-0.17966	-0.15971	-0.06525	0.161733	0.098187	-0.09937	-0
16	GSM109029										0.335216	-0.31143	-0.27651	-0.15292	-0.03993	0.014787	0.024292	-0.28976	-0
17	GSM109030										0.245378	-0.5246	-0.44006	-0.24046	0.041687	0.021471	0.082919	-0.39599	-0
18	GSM1090301	A	83	F	13	5.667	6.4	LNV	1	brain	0.383436	-0.20521	-0.21682	-0.07422	-0.08448	0.039032	0.033073	-0.04243	-0
19	GSM1090302	A	75	F	10.62	6.764	6.6	LNV	1	brain	0.251072	0.151106	0.042112	0.025138	-0.25303	0.087672	-0.03997	-0.00613	-0
20	GSM1090305	A	87	F	20.58	6.77	6.9	LNV	1	brain	0.308346	0.100023	0.103067	0.347627	0.016947	-0.01039	0.041217	-0.12216	-0
21	GSM1090307	A	74	F	34.25	6.449	6.3	LNV	1	brain	0.508474	-0.2744	-0.27189	0.079182	-0.01166	0.086366	-0.1255	-0.31437	-0
22	GSM1090309	A	83	F	19.25	6.707	6.9	LNV	1	brain	0.354007	0.075023	0.072999	0.160714	-0.05104	-0.096	0.086144	-0.08198	0

Highly correlated!



Samples

Total 67 patients

RNA quality measure

Genes from which mRNA abundance level is obtained.

GSE44768_CR_alz_female_reduced.csv Data Set

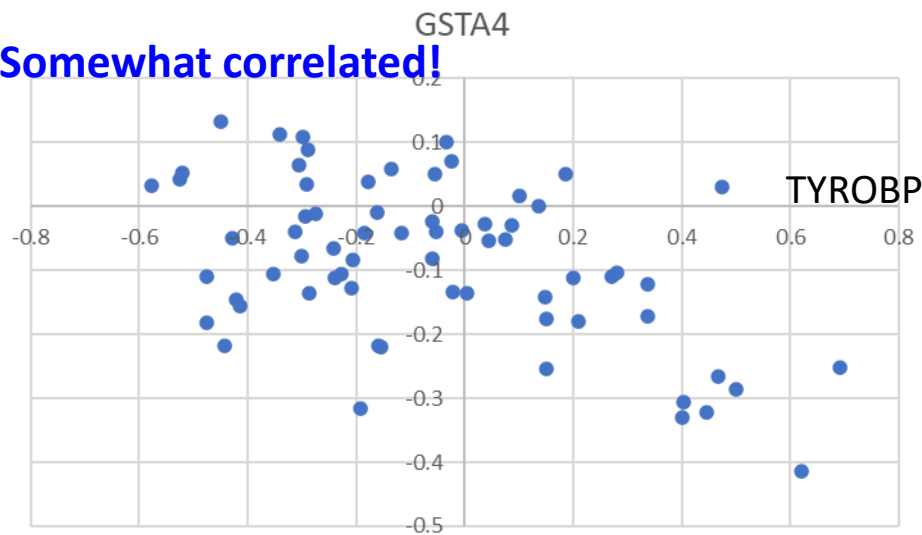


Available at HuskyCT Data_Files folder.

mRNA intensity values in log10

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	
1	GSM_ID	disease	age	gender	pmi	pH	rin	pres	batch	tissue	XIST	TYROBP	DOCK2	FCER1G	GSTA4	ABCC2	TIMELESS	ACBD5	LM
2	GSM1090268	A	90	F	12.6	6.164	6.3	LNV	1	brain	0.301474	0.209515	0.161961	0.310937	-0.17929	-0.00925	0.027849	0.057428	-0
3	GSM1090271	A	90	F	9.25	6.057	6.7	LNV	1	brain	0.460495	-0.16217	-0.0896	-0.13201	-0.01009	0.02753	-0.00782	-0.00669	-0
4	GSM1090272	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.238641	0.280428	0.313562	0.267188	-0.10473	0.130515	0.228776	-0.0761	-0
5	GSM1090273	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.276038	0.400028	0.251573	0.275051	-0.33018	0.137491	0.105215	-0.09633	-0
6	GSM1090274	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.435775	-0.29332	-0.2628	-0.13867	-0.01655	0.013355	-0.00629	-0.25949	-0
7	GSM1090275	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.245945	-0.42066	-0.35032	-0.31697	-0.14612	0.10048	0.095884	0.024655	-0
8	GSM1090276	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.440187	0.199408	-0.09561	0.384826	-0.11276	0.163864	-0.19778	-0.1274	-0
9	GSM1090277	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.366115	-0.03379	-0.09254	0.150413	0.099431	-0.01735	-0.10217	-0.04408	0
10	GSM1090278	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.342604	-0.19143	-0.16528	-0.04182	-0.31651	0.122101	-0.02727	-0.18149	0
11	GSM1090279	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.497142	-0.29836	-0.22498	-0.23675	0.108094	-0.0842	0.028409	-0.1799	-0
12	GSM1090280	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.346257	0.147478	0.16301	0.221962	-0.14166	0.063308	0.114311	-0.07164	-0
13	GSM1090281	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.256477	-0.05275	-0.12644	0.165657	-0.03902	0.148996	-0.00269	-0.28127	-0
14	GSM1090282	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.373623	-0.18457	-0.14394	-0.10204	-0.04138	0.090129	0.018457	-0.17351	-0
15	GSM1090283	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.44892	-0.2411	-0.17966	-0.15971	-0.06525	0.161733	0.098187	-0.09937	-0
16	GSM1090284	A	77	F	6.86	6.782	7.2	LNV	1	brain	0.335216	-0.31143	-0.27651	-0.15292	-0.03993	0.014787	0.024292	-0.28976	-0
17	GSM1090300	A	70	F	20	6.058	6.2	Dry-Ice	2	brain	0.245378	-0.5246	-0.44006	-0.24046	0.041687	0.021471	0.082919	-0.39599	-0
18	GSM1090301	A	83	F	13	5.667	6.4	LNV	1	brain	0.383436	-0.20521	-0.21682	-0.07422	-0.08448	0.039032	0.033073	-0.04243	-0
19	GSM1090302	A	75	F	10.62	6.764	6.6	LNV	1	brain	0.251072	0.151106	0.042112	0.025138	-0.25303	0.087672	-0.03997	-0.00613	-0
20	GSM1090305	A	87	F	20.58	6.77	6.9	LNV	1	brain	0.308346	0.100023	0.103067	0.347627	0.016947	-0.01039	0.041217	-0.12216	-0
21	GSM1090307	A	74	F	34.25	6.449	6.3	LNV	1	brain	0.508474	-0.2744	-0.27189	0.079182	-0.01166	0.086366	-0.1255	-0.31437	-0
22	GSM1090309	A	83	F	19.25	6.707	6.9	LNV	1	brain	0.354007	0.075023	0.072999	0.160714	-0.05104	-0.096	0.086144	-0.08198	0

Somewhat correlated!



Samples

What would be r?

Total 67 patients

Genes from which mRNA abundance level is obtained.

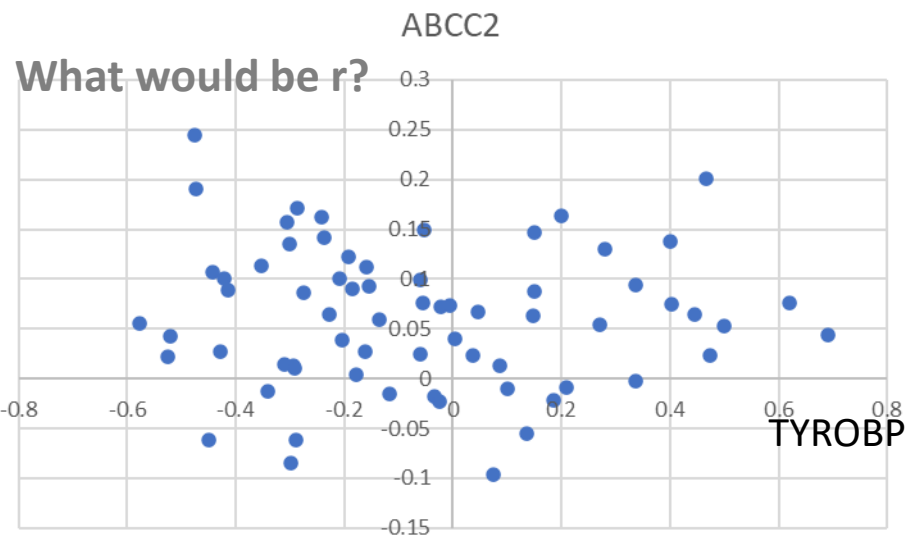
GSE44768_CR_alz_female_reduced.csv Data Set



Available at HuskyCT Data_Files folder.

mRNA intensity values in log10

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	
1	GSM_ID	disease	age	gender	pmi	pH	rin	pres	batch	tissue	XIST	TYROBP	DOCK2	FCER1G	GSTA4	ABCC2	TIMELESS	ACBD5	LM
2	GSM1090268	A	90	F	12.6	6.164	6.3	LNV	1	brain	0.301474	0.209515	0.161961	0.310937	-0.17929	-0.00925	0.027849	0.057428	-0
3	GSM1090271	A	90	F	9.25	6.057	6.7	LNV	1	brain	0.460495	-0.16217	-0.0896	-0.13201	-0.01009	0.02753	-0.00782	-0.00669	-0
4	GSM1090272	A	77	F	6.86	6.793	7.2	LNV	1	brain	0.238641	0.280428	0.313562	0.267188	-0.10473	0.130515	0.228776	-0.0761	-0
5	GSM1090274	A	100	F	24.28	6.576	7.1	LNV	1	brain	0.276038	0.400028	0.251573	0.275051	-0.33018	0.137491	0.105215	-0.09633	-0
6	GSM109									rain	0.435775	-0.29332	-0.2628	-0.13867	-0.01655	0.013355	-0.00629	-0.25949	-0
7	GSM109									rain	0.245945	-0.42066	-0.35032	-0.31697	-0.14612	0.10048	0.095884	0.024655	-0
8	GSM109									rain	0.440187	0.199408	-0.09561	0.384826	-0.11276	0.163864	-0.19778	-0.1274	-0
9	GSM109									rain	0.366115	-0.03379	-0.09254	0.150413	0.099431	-0.01735	-0.10217	-0.04408	0.
10	GSM109									rain	0.342604	-0.19143	-0.16528	-0.04182	-0.31651	0.122101	-0.02727	-0.18149	0.
11	GSM109									rain	0.497142	-0.29836	-0.22498	-0.23675	0.108094	-0.0842	0.028409	-0.1799	-0
12	GSM109									rain	0.346257	0.147478	0.16301	0.221962	-0.14166	0.063308	0.114311	-0.07164	-0
13	GSM109									rain	0.256477	-0.05275	-0.12644	0.165657	-0.03902	0.148996	-0.00269	-0.28127	-0
14	GSM109									rain	0.373623	-0.18457	-0.14394	-0.10204	-0.04138	0.090129	0.018457	-0.17351	-0
15	GSM109									rain	0.44892	-0.2411	-0.17966	-0.15971	-0.06525	0.161733	0.098187	-0.09937	-0
16	GSM109									rain	0.335216	-0.31143	-0.27651	-0.15292	-0.03993	0.014787	0.024292	-0.28976	-0
17	GSM109									rain	0.245378	-0.5246	-0.44006	-0.24046	0.041687	0.021471	0.082919	-0.39599	-0
18	GSM1090301	A	85	F	15	5.007	6.4	LNV	1	brain	0.383436	-0.20521	-0.21682	-0.07422	-0.08448	0.039032	0.033073	-0.04243	-0
19	GSM1090302	A	75	F	10.62	6.764	6.6	LNV	1	brain	0.251072	0.151106	0.042112	0.025138	-0.25303	0.087672	-0.03997	-0.00613	-0
20	GSM1090305	A	87	F	20.58	6.77	6.9	LNV	1	brain	0.308346	0.100023	0.103067	0.347627	0.016947	-0.01039	0.041217	-0.12216	-0
21	GSM1090307	A	74	F	34.25	6.449	6.3	LNV	1	brain	0.508474	-0.2744	-0.27189	0.079182	-0.01166	0.086366	-0.1255	-0.31437	-0
22	GSM1090309	A	83	F	19.25	6.707	6.9	LNV	1	brain	0.354007	0.075023	0.072999	0.160714	-0.05104	-0.096	0.086144	-0.08198	0



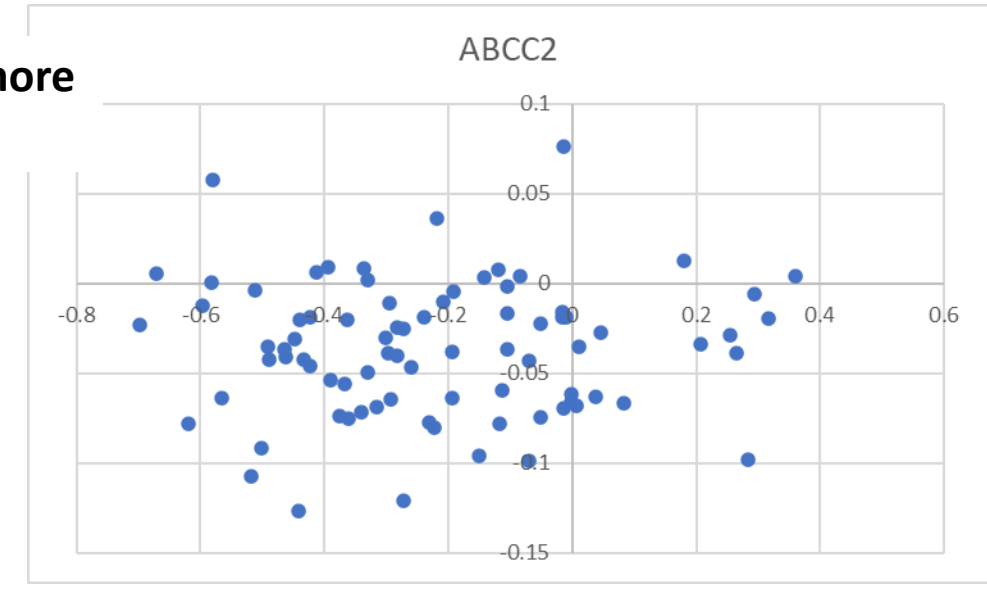
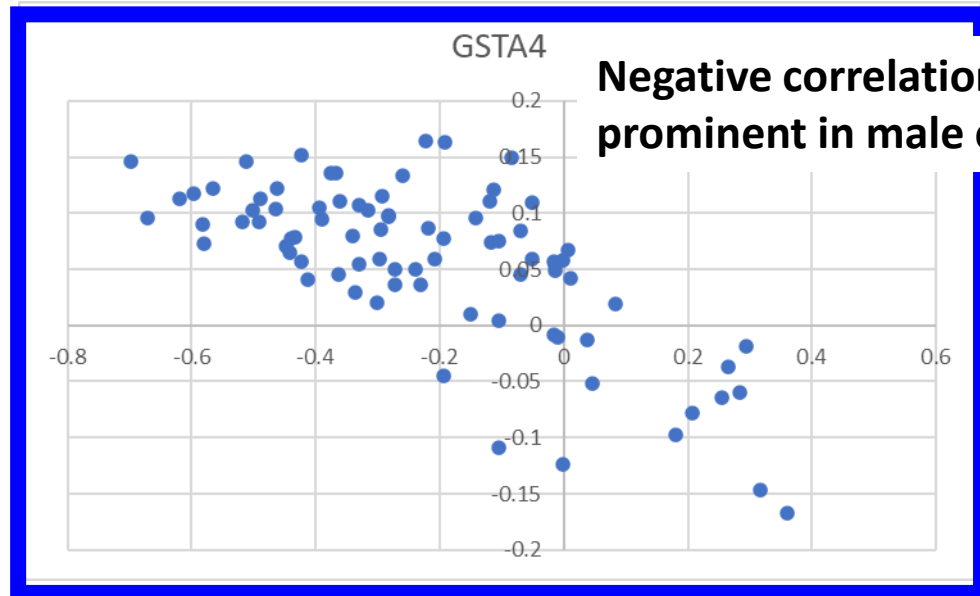
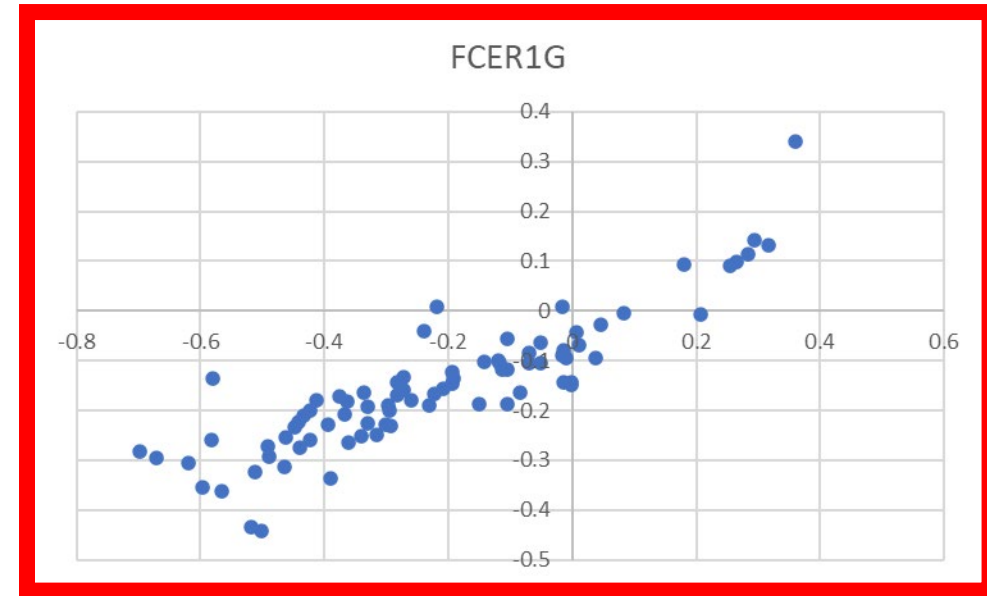
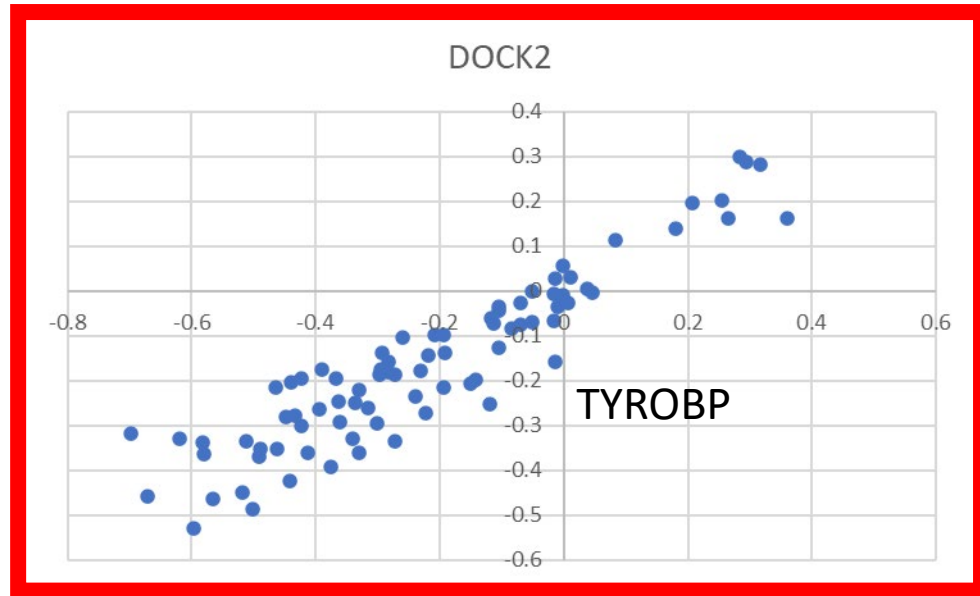
Samples

Total 67 patients

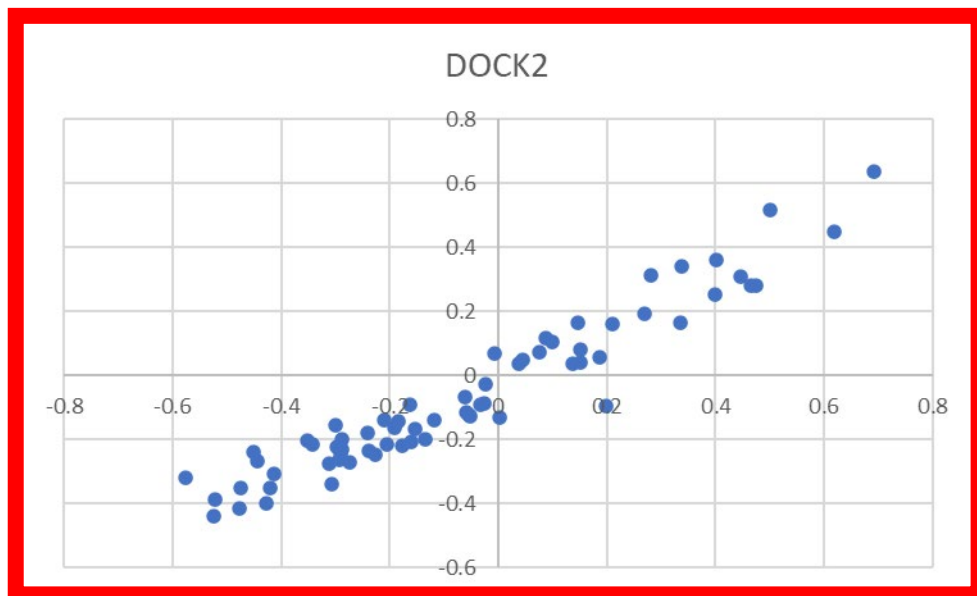
Genes from which mRNA abundance level is obtained.

Analysis outcome from CR nd Male Gene DOCK2, FCER1G ,GSTA4 and ABCC2 vs TYROBP

nd = non- disease

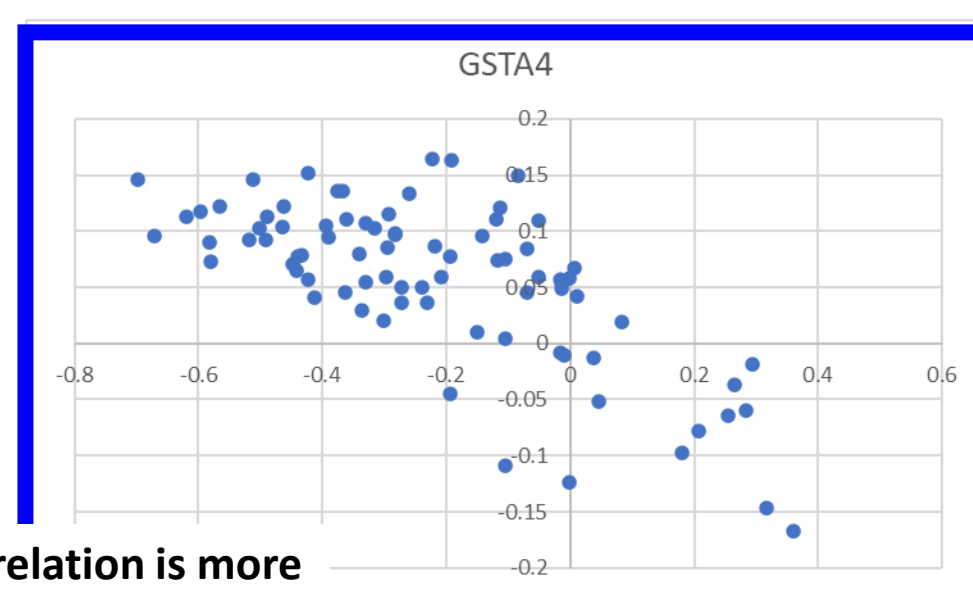
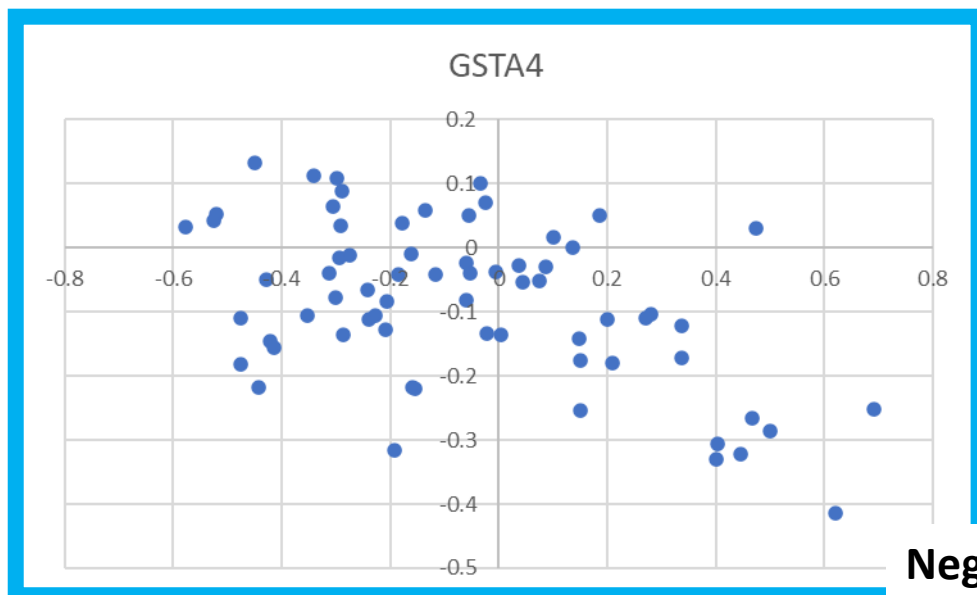
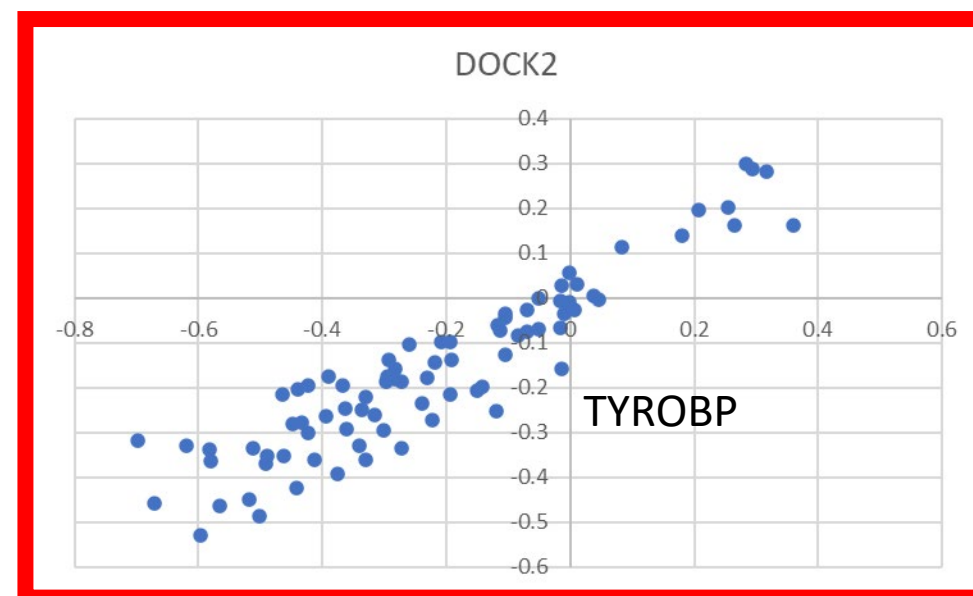


Analysis outcome from CR alz female



Analysis outcome from CR nd Male

nd = non-disease



Negative correlation is more prominent in male nd case!

Producing Heatmap from Correlation Matrix



```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sn

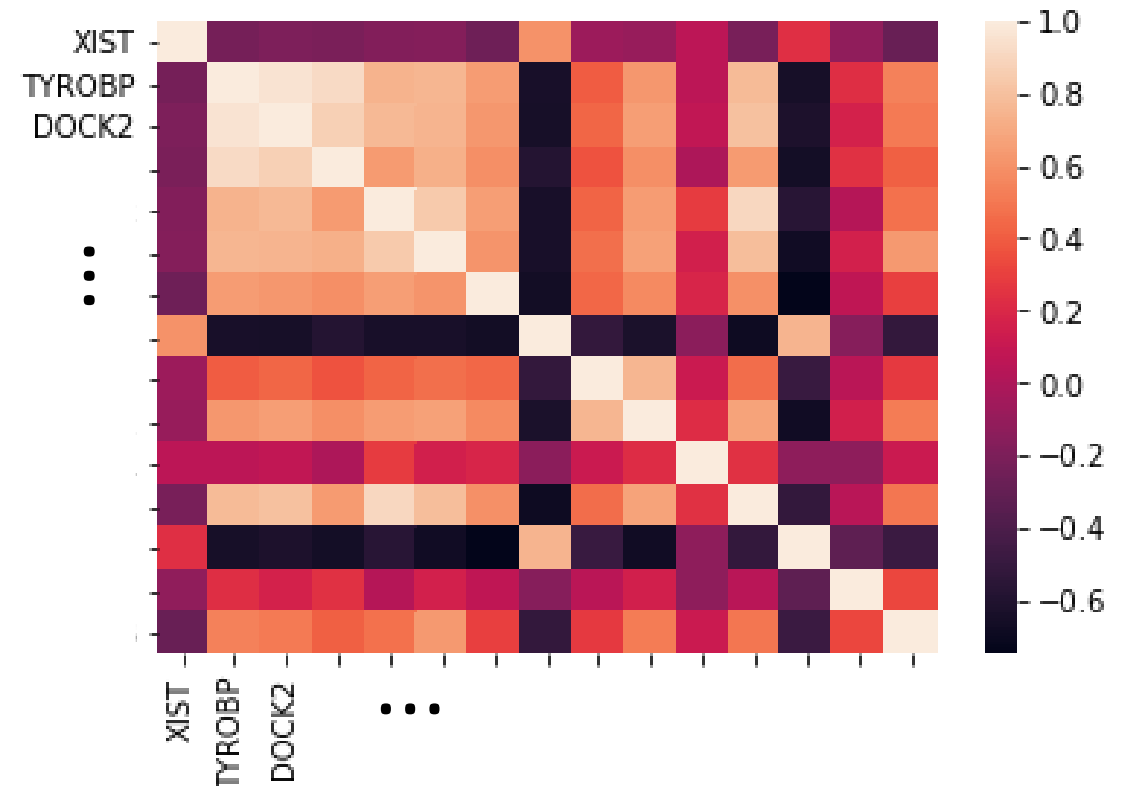
gene_names = ['XIST', 'TYROBP', 'DOCK2', ...] # pick genes to compare.
mylist_corr_matrix = mylist.loc[:,gene_names].corr()

sn.heatmap(mylist_corr_matrix, annot=False)
plt.show()
```

Alzheimer's Female

	XIST	TYROBP	DOCK2	...
XIST	1.000000	-0.222890	-0.194223	-0.202658 -0.168652 -0.162335 0.154905
TYROBP	-0.222890	1.000000	0.959502	0.919214 0.746210 0.758362 -0.036335
DOCK2	-0.194223	0.959502	1.000000	0.871248 0.769880 0.748357 -0.069060
...	-0.202658	0.919214	0.871248	1.000000 0.644477 0.727700 -0.028926
...	-0.168652	0.746210	0.769880	0.644477 1.000000 0.844514 -0.076622
...	-0.162335	0.758362	0.748357	0.727700 0.844514 1.000000 -0.084141
...	0.154905	-0.036335	-0.069060	-0.028926 -0.076622 -0.084141 1.000000

$${}_7C_2 = (7 \times 6) / (2 \times 1) = 21$$



How to Create a Seaborn Correlation Heatmap in Python?

<https://medium.com/@szabo.bibor/how-to-create-a-seaborn-correlation-heatmap-in-python-834c0686b88e>

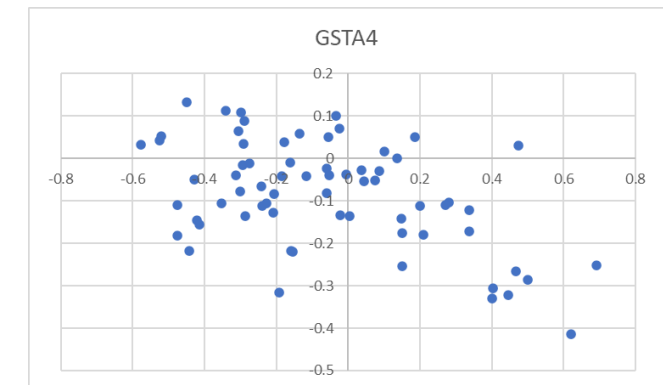
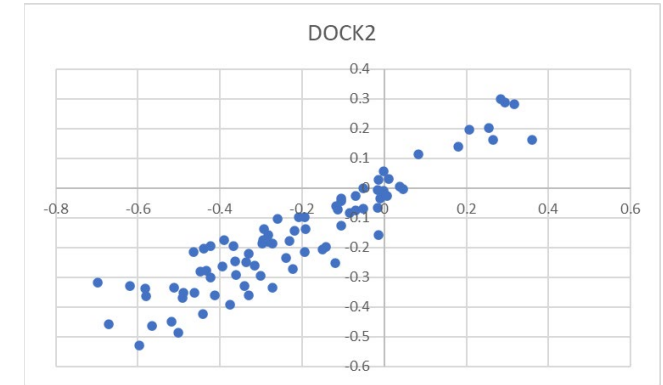
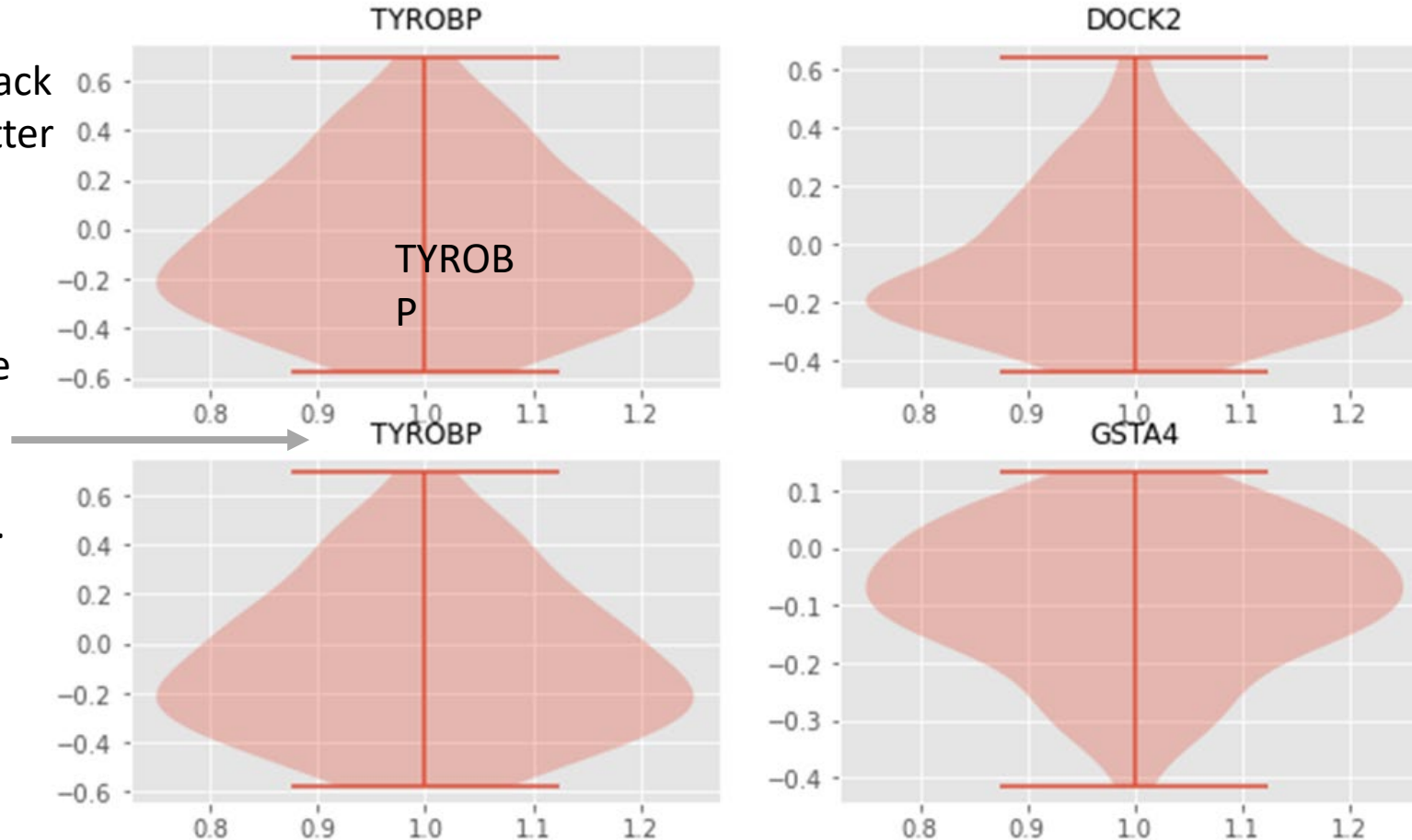
Combining multiple plots in a meaningful way.



Can you compare plots side by side, top to bottom to enhance interpretability of analysis outcome?

Can you stack images better than this?

Need some gap to improve readability.



μ and σ should be included somewhere in the plot (possibly in the title)

Display Multiple Plots



With the `subplots()` function you can draw multiple plots in one figure:

Example Draw 2 plots side by side:

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

```
#plot 1:
```

```
x = np.array([0, 1, 2, 3])
y = np.array([3, 8, 1, 10])
```

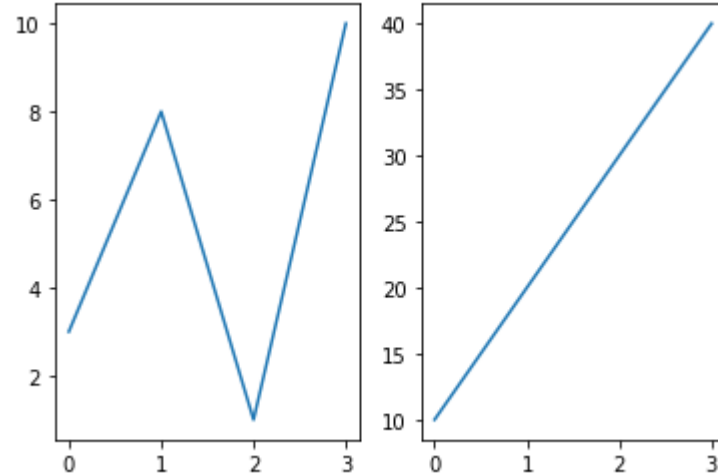
```
plt.subplot(1, 2, 1)
plt.plot(x,y)
```

```
#plot 2:
```

```
x = np.array([0, 1, 2, 3])
y = np.array([10, 20, 30, 40])
```

```
plt.subplot(1, 2, 2)
plt.plot(x,y)
```

```
plt.show()
```



Display Multiple Plots

The subplots() Function



subplots() allows you to draw multiple plots in one figure:

Example Draw 2 plots:

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

#plot 1:

```
x = np.array([0, 1, 2, 3])
y = np.array([3, 8, 1, 10])
```

```
plt.subplot(1, 2, 1)
plt.plot(x,y)
```

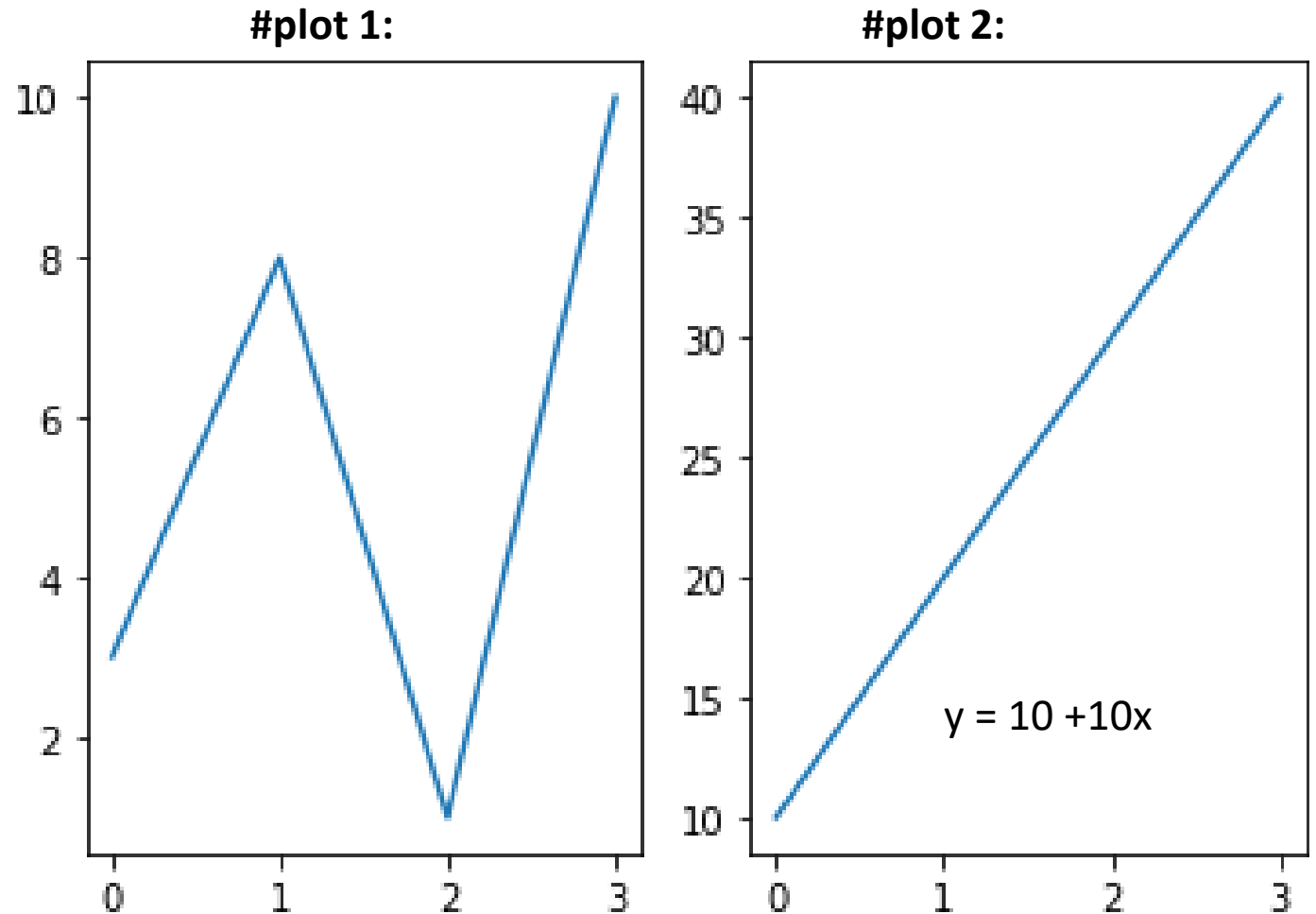
#plot 2:

```
x = np.array([0, 1, 2, 3])
y = np.array([10, 20, 30, 40])
```

```
plt.subplot(1, 2, 2)
plt.plot(x,y)
```

```
plt.show()
```

First two defines number of rows and columns and the **third** represents the index of the current plot.



The subplots() Function

What would be the plot in each case?



```
# plot 1:  
x = np.array([0, 1, 2, 3])  
y = np.array([3, 8, 1, 10])
```

```
# plt.subplot(1, 2, 1)  
plt.plot(x,y)
```

```
# plot 2:  
x = np.array([0, 1, 2, 3])  
y = np.array([10, 20, 30, 40])
```

```
plt.subplot(1, 2, 2)  
# plt.plot(x,y)
```

```
# plot 1:  
x = np.array([0, 1, 2, 3])  
y = np.array([3, 8, 1, 10])
```

```
# plt.subplot(1, 2, 1)  
plt.plot(x,y)
```

```
# plot 2:  
x = np.array([0, 1, 2, 3])  
y = np.array([10, 20, 30, 40])
```

```
plt.subplot(1, 2, 2)  
plt.plot(x,y)
```

```
# plot 1:  
x = np.array([0, 1, 2, 3])  
y = np.array([3, 8, 1, 10])
```

```
plt.subplot(1, 2, 1)  
# plt.plot(x,y)
```

```
# plot 2:  
x = np.array([0, 1, 2, 3])  
y = np.array([10, 20, 30, 40])
```

```
# plt.subplot(1, 2, 2)  
plt.plot(x,y)
```

```
# plot 1:  
x = np.array([0, 1, 2, 3])  
y = np.array([3, 8, 1, 10])
```

```
plt.subplot(1, 2, 1)  
plt.plot(x,y)
```

```
# plot 2:  
x = np.array([0, 1, 2, 3])  
y = np.array([10, 20, 30, 40])
```

```
plt.subplot(1, 2, 2)  
# plt.plot(x,y)
```

QUIZ??

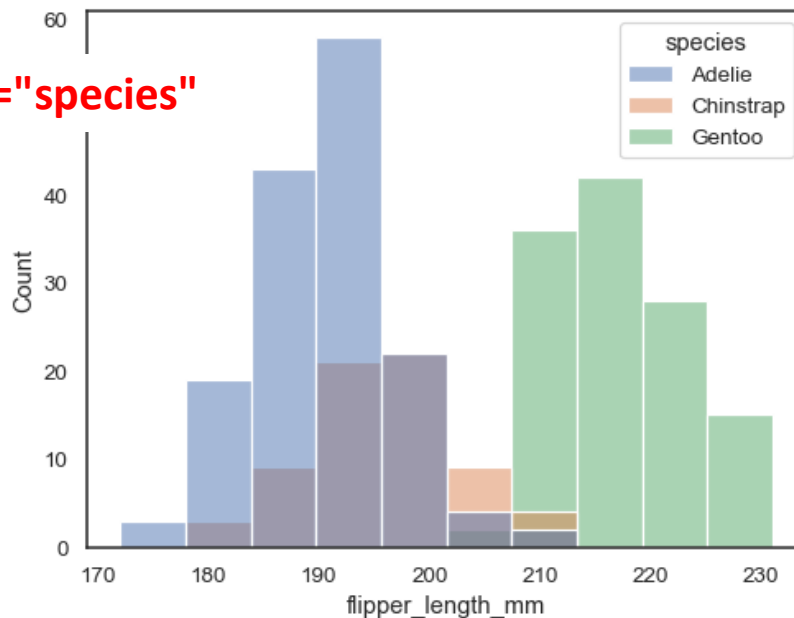
Can you merge related histograms in a meaningful way?



How many colors
do you see in each
plot?

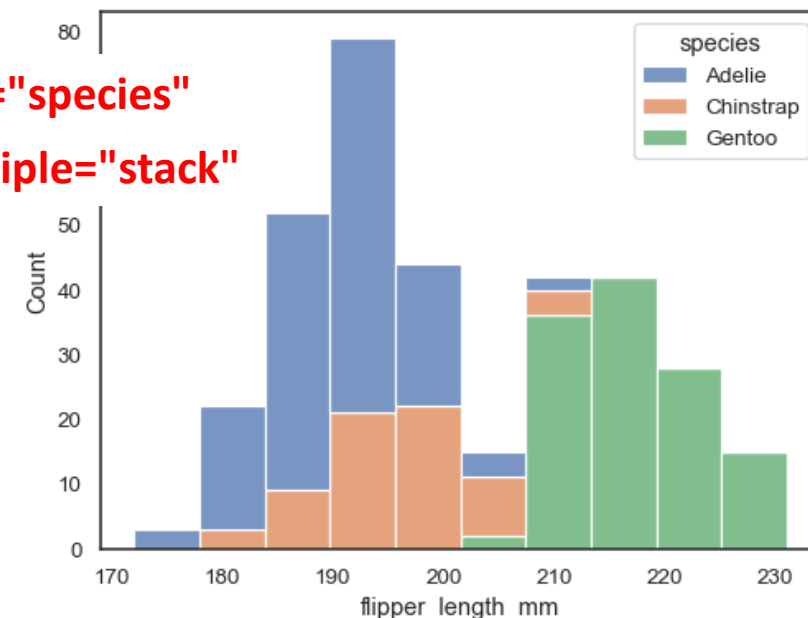
Is anyone plot more
meaningful than
others?

hue="species"



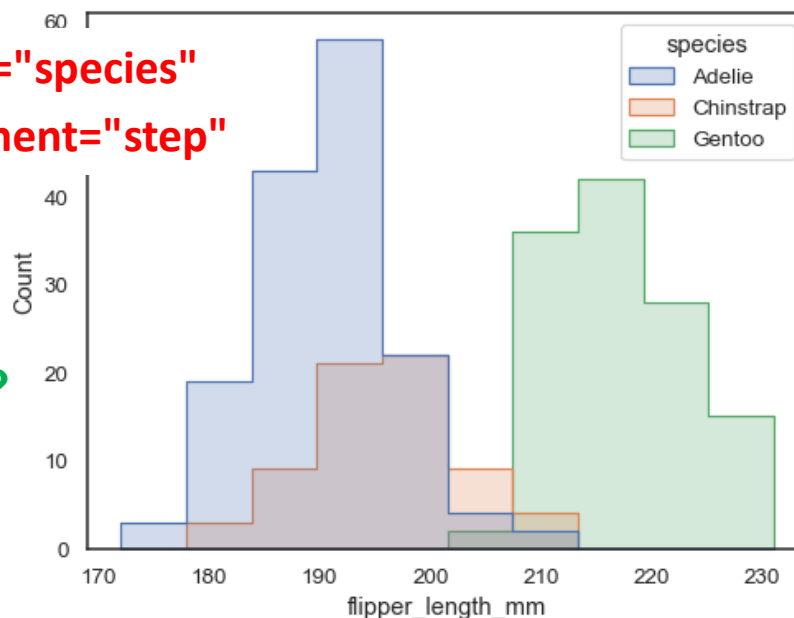
hue="species"

multiple="stack"



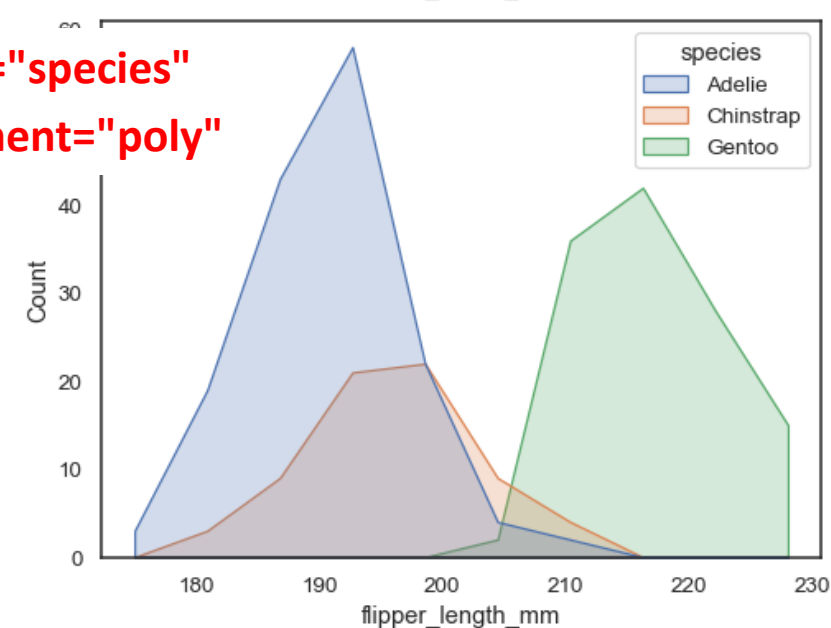
hue="species"

element="step"



hue="species"

element="poly"



“hue” is designed
to add semantics.

Should you create a new
data frame and use “hue”?

Or can you just merge two
histograms in one plot?

Can you merge TYROBP histograms from alz female and nd female?
If you do, would that comparison tell you anything?



	Female	Male
Alzheimer	67	
Non disease	19	

Would you say Gene X is possibly involved in the development of Alzheimer's Disease?

