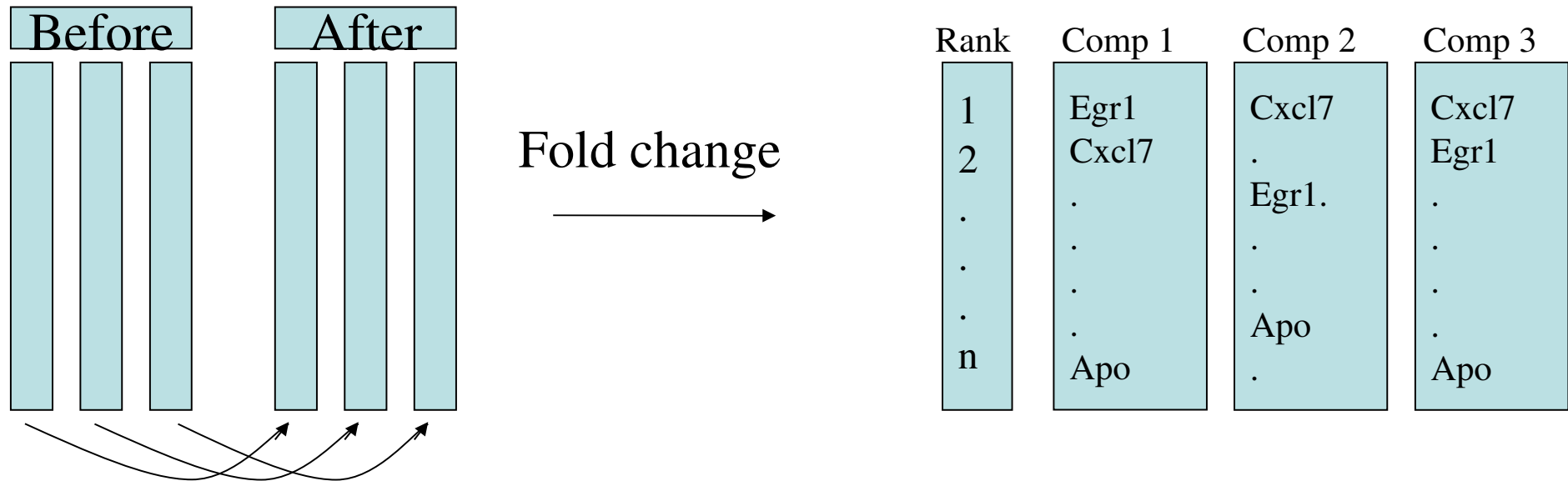


# Meta analysis using Rank Product

# Rank Product recap



- Makes no assumption about distribution of the data
- No calculation of variance across samples

# Rank Product recap

1/n	Egr1	1/n	Cxcl7	1/n	Cxcl7
2/n	Cxcl7	2/n	.	2/n	Egr1
./n	.	./n	Egr1.	./n	.
./n	.	./n	.	./n	.
./n	.	./n	.	./n	.
./n	.	./n	Apo	./n	.
n/n	Apo	n/n	.	n/n	Apo

- $RP(Cxcl7) = 2/n * 1/n * 1/n$

# Advantages

Flexible format for each list: rank

Find consistencies between samples

Find consistencies between experiments

# Drawbacks

- Few assumptions leads to less predictive power
- Used in meta-analysis, the number of replicates are normally low

# Several independent experiments

- Need a common identifier, e.g. Gene Symbol
- Only data points from the individual lists that overlap can be used
- Alternatively, impute missing values in some lists if necessary/desired.

# Example 1: The same experiment performed two independent times

Properties for Top q<=5%

Values Value Distribution Info fields and settings

Changes in this table are permanent  Submit changes to meta info

Probe_ID	Ge...	Score	e-val	q-val	SY...	DEFINITION	ENTREZ_...	New ident...	Rank Exp1	Rank Exp2
ILMN_273...	M...	1.514380...	0.0	0.0	MM...	Mus musc...	17386		-1.0	-1.0
ILMN_274...	Dcn	1.817257...	0.0025	0.00125	PGI...	Mus musc...	13179		-6.0	-2.0
ILMN_271...	S1...	4.543142...	0.01	0.00275	Ca...	Mus musc...	20201		-3.0	-10.0
ILMN_271...	Gp...	6.057523...	0.0125	0.00275	OCI...	Mus musc...	14734		-5.0	-8.0
ILMN_289...	Tnn	6.966152...	0.0175	0.00275	Tn...	Mus musc...	329278		-2.0	-23.0
ILMN_275...	Avil	1.029779...	0.0275	0.00275	DO...	Mus musc...	11567		-4.0	-17.0
ILMN_283...	Gp...	1.272080...	0.0275	0.00275	OCI...	Mus musc...	14734		-7.0	-12.0
ILMN_275...	M...	1.590100...	0.0275	0.00275	ST...	Mus musc...	17392		-35.0	-3.0
ILMN_271...	Ctsk	1.635531...	0.0275	0.00275	MM...	Mus musc...	13038		-18.0	-6.0
ILMN_259...	Dcn	1.665819...	0.0275	0.00275	PGI...	Mus musc...	13179		-10.0	-11.0
ILMN_298...	Pla...	3.392213...	0.045	0.003653...	D5...	Mus musc...	231507		-16.0	-14.0
ILMN_261...	C2	3.816240...	0.0475	0.003653...		Mus musc...	12263		-28.0	-9.0
ILMN_123...	Rb...	3.816240...	0.0475	0.003653...					-9.0	-28.0
ILMN_289...	M...	4.558286...	0.06	0.003906...	ST...	Mus musc...	17392		-43.0	-7.0
ILMN_125...	Igf...	4.603718...	0.0625	0.003906...	De...	Mus musc...	16010		-19.0	-16.0
ILMN_275...	Il1...	4.921738...	0.0625	0.003906...	T1...	Mus musc...	17082		-25.0	-13.0
ILMN_270...	M...	5.815223...	0.08	0.004705...	ST...	Mus musc...	17392		-96.0	-4.0
ILMN_270...	Ilg...	6.542125...	0.095	0.005277...	47...	Mus musc...	319480		-8.0	-54.0
ILMN_269...	Igf...	8.344239...	0.1425	0.0075					-29.0	-19.0
ILMN_271...	Lcn2	9.616319...	0.1625	0.007800...	AW...	Mus musc...	16819		-127.0	-5.0
ILMN_260...	Ch...	1.035836...	0.1775	0.007800...	AW...	Mus musc...	12654		-38.0	-18.0
ILMN_260...	Pr...	1.044922...	0.1775	0.007800...	60...	Mus musc...	244954		-15.0	-46.0
ILMN_124...	Ms...	1.099440...	0.1875	0.007800...	Ho...	Mus musc...	17701		-11.0	-66.0
ILMN_273...	Rp...	1.123670...	0.195	0.007800...	11...	Mus musc...			-14.0	-53.0
ILMN_276...	Lrr...	1.126699...	0.195	0.007800...	49...	Mus musc...	231549		-24.0	-31.0
ILMN_121...	Rg...	1.393230...	0.2425	0.008857...					-23.0	-40.0
ILMN_273...	Co...	1.465920...	0.2525	0.008857...	en...	Mus musc...	12822		-44.0	-22.0
ILMN_313...	Snca	1.590100...	0.27	0.008857...	NA...	Mus musc...	20617		-21.0	-50.0

# Example 2: Comparable samples from several research groups

- Sjögren's Syndrome studies in Bergen and Boston,
  - Common design: healthy ctrl vs diagnosed patients
  - Different technologies/platforms not a show stopper
- Additional results from public sources

# Example 3: MA and PR

Properties for RP Early vs Late MA and PR combined

Values Value Distribution Info fields and settings

Changes in this table are permanent  Submit changes to meta info

Protein Na...	Acc no	annotation 2	Biol proc	Pathway	Human En...	score	e-val	q-val	New ident...	inv Rank PR	inv Rank MA
Transient ...	Q8R455	TRPM8	Biological ...	NULL	79054	1.125525...	1.227	0.53625		-3.0	-134.0
Myelin ba...	P02688	MBP	NULL	NULL	4155	1.134601...	1.23	0.53625		-15.0	-29.0
Xylosyltra...	Q9H1B5	XYLT2	NULL	NULL	64132	1.794183...	2.075	0.53625		-1.0	-644.0
Myelin pro...	P60201	MYPR	NULL	NULL	5354	1.839567...	2.145	0.53625		-80.0	-8.0
Sphingosi...	P48303	EDG1	G-protein...	NULL	1901	4.190463...	5.5975	0.820277...		-1,463.0	-1.0
Apolipopr...	Q9QUH3	APOA5	Lipid and ...	NULL	116519	4.483946...	6.02	0.820277...		-27.0	-63.0
Inter-alph...	Q63416	ITIH3	Proteolysis	NULL	3699	4.834916...	6.5675	0.820277...		-852.0	-2.0
Plasma m...	Q64568	AT2B3	NULL	NULL	492	5.252450...	7.2625	0.820277...		-467.0	-4.0
ATPase fa...	Q505J9	ATAD1	Protein m...	NULL	84896	5.325064...	7.3825	0.820277...		-22.0	-89.0
Protein TS...	Q5XIB1	TSSC4	Biological ...	NULL	10078	7.757651...	10.65	0.838963...		-2.0	-1,424.0
Protein ki...	Q9Z0W5	PACN1	NULL	NULL	29993	8.586667...	11.7625	0.838963...		-511.0	-6.0
Organic c...	Q6AY78	ORCT2	NULL	NULL	5002	8.810562...	12.0325	0.838963...		-16.0	-194.0
Leucine-ri...	Q8N145	LGI3	Biological ...	NULL	203190	9.560912...	12.9275	0.838963...		-20.0	-170.0
Neurofila...	P19527	NFL	NULL	NULL	4747	9.802960...	13.25	0.838963...		-57.0	-66.0
Breast car...	Q3ZB98	BCAS1	NULL	NULL	8537	9.984496...	13.4675	0.838963...		-64.0	-61.0
Eukaryotic...	Q14152	IF3A	NULL	NULL	8661	0.001008...	13.605	0.838963...		-4.0	-906.0
Huntingtin...	P97924	HAPIP	NULL	NULL	8997	0.001409...	18.21	0.838963...		-1,639.0	-3.0
SPARC-rel...	Q9H4F8	SMOC1	NULL	NULL	64093	0.001418...	18.3125	0.838963...		-45.0	-119.0
Ras-relat...	Q63487	RRAGB	NULL	NULL	10325	0.001420...	18.335	0.838963...		-5.0	-1,024.0
Visinin-lik...	P62762	VISL1	NULL	NULL	7447	0.001448...	18.665	0.838963...		-426.0	-12.0
Histone H...	Q00729	H2B1A	NULL	NULL	255626	0.001479...	19.0275	0.838963...		-71.0	-81.0
Reelin pre...	P58751	RELN	NULL	NULL	5649	0.001658...	21.2525	0.838963...		-1,163.0	-5.0
Inositol 1...	P29994	ITPR1	NULL	NULL	3708	0.001756...	22.435	0.838963...		-225.0	-31.0
Alpha-syn...	P37377	SNCA	NULL	NULL	5522	0.001770...	22.5675	0.838963...		-570.0	-11.0
Synaptoso...	P60880	SYN1	NULL	NULL	5522	0.001770...	22.5675	0.838963...		-216.0	-33.0
Septin-4 (...)	O43236	SEPT4	NULL	NULL	5522	0.001770...	22.5675	0.838963...		-282.0	-27.0
Protein-gl...	Q08188	GLY1	NULL	NULL	5522	0.001770...	22.5675	0.838963...		-23.0	-298.0
Lipoprotei...	P25222	LDL1	NULL	NULL	5522	0.001770...	22.5675	0.838963...		-297.0	-22.0

Gene-protein pair measurements must be present in both data sets.

# Rank of sets evaluated on several datasets

- Evaluate gene sets e.g. KEGG Pathways individually on several data sets
- Identify PW with support from more than one data set.
- Does not need to be the corresponding genes/proteins that support a given pathway, they may be complementing the picture