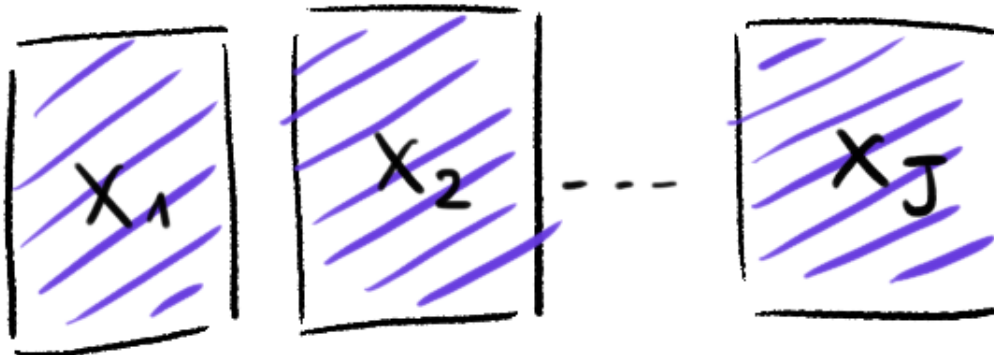


INTRODUCTION AUX TABLEAUX
DE DONNÉES MULTIPLES,
À L'ANALYSE
CANONIQUE,
À L'ANALYSE FACTORIELLE
MULTIPLE

Application aux données transcriptomiques

Objectifs

- Comprendre ce que l'on peut attendre des tableaux multiples
- Comprendre les motivations et le cadre de l'analyse canonique
- Comprendre l'analyse canonique généralisée
- Comprendre l'apport de l'analyse factorielle multiple vs. ACG



Plan



- Ce que vous savez faire
- Ce que vous avez envie de faire et pourquoi vous en avez envie
- Comment le faire
- Comment le mettre en pratique

Les données



- 40 souris
- 2 génotypes (sauvages, PPAR α -déficiantes)
- 5 régimes (dha, efad, lin, ref, tsol)
- 120 gènes (données d'expression)
- 21 concentration d'acides gras hépathiques

PPAR α

- Le **peroxisome proliferator-activated receptor** est une protéine liant naturellement les lipides et agissant comme facteur de transcription des gènes cibles impliqués notamment dans le métabolisme et l'adipogénèse.
- α (alpha) - exprimé dans le foie, les reins, le cœur, les muscles, le tissu adipeux, et autres.



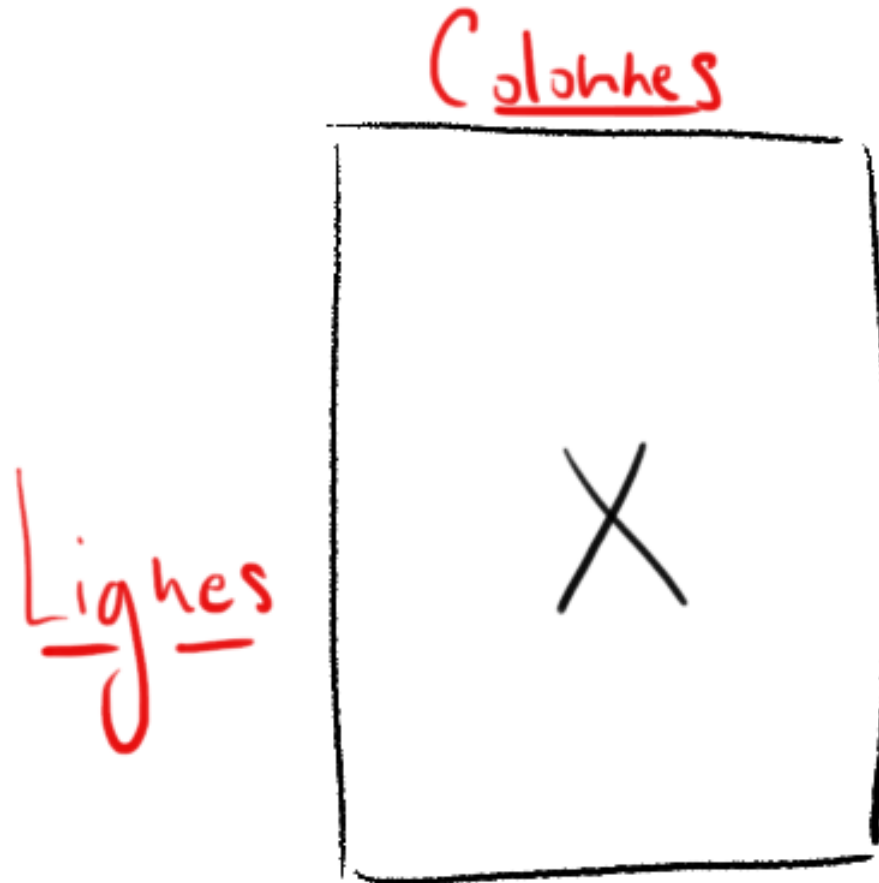
Les régimes

- dha : régime enrichi en acides gras de la famille Oméga 3 et particulièrement en acide docosahexaénoïque (DHA), à base d'huile de poisson ;
- efad (Essential Fatty Acid Deficient) : régime constitué uniquement d'acides gras saturés, à base d'huile de coco hydrogénée ;
- lin : régime riche en Oméga 3, à base d'huile de lin ;
- ref : régime dont l'apport en Oméga 6 et en Oméga 3 est adapté des Apports Nutritionnels Conseillés pour la population française, sept fois plus d'Oméga 6 que d'Oméga 3 ;
- tsol : riche en Oméga 6, à base d'huile de tournesol.

Problématique



Le tableau de données



Le tableau de données

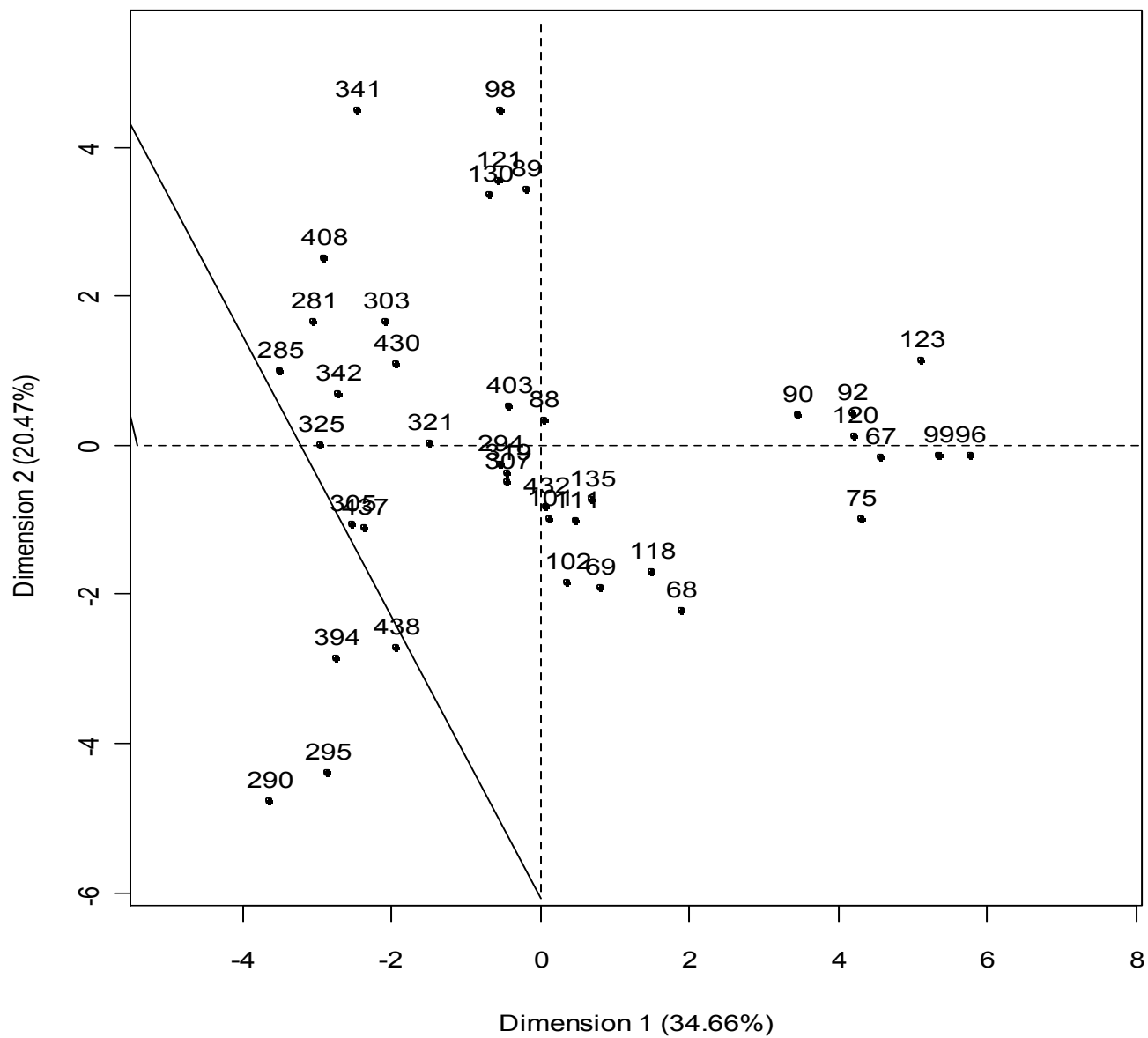
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	
1	Souris	Regime	Genotype	C14.0	C16.0	C18.0	C16.1n.9	C16.1n.7	C18.1n.9	X36b4	ACAT1	ACAT2	ACBP	ACC1	ACC2	ACO
2	67	lin	1	0.34	26.45	10.22	0.35	3.10	16.98	-0.42	-0.65	-0.84	-0.34	-1.29	-1.13	-0.93
3	68	tournesol	1	0.38	24.04	9.93	0.55	2.54	20.07	-0.44	-0.68	-0.91	-0.32	-1.23	-1.06	-0.99
4	69	tournesol	1	0.36	23.70	8.96	0.55	2.65	22.89	-0.48	-0.74	-1.1	-0.46	-1.3	-1.09	-1.06
5	75	dha	1	0.22	25.48	8.14	0.49	2.82	21.92	-0.45	-0.69	-0.65	-0.41	-1.26	-1.09	-0.93
6	88	ref	1	0.37	24.80	9.63	0.46	2.85	21.38	-0.42	-0.71	-0.54	-0.38	-1.21	-0.89	
7	89	efad	1	1.70	26.04	6.59	0.66	7.26	28.23	-0.43	-0.69	-0.8	-0.32	-1.13	-0.79	-0.93
8	90	lin	1	0.35	25.94	9.68	0.36	3.60	17.62	-0.53	-0.62	-1	-0.44	-1.22	-1	-0.94
9	92	lin	1	0.34	28.63	9.95	0.29	3.27	17.02	-0.49	-0.69	-0.91	-0.37	-1.29	-1.06	-1.05
10	96	dha	1	0.22	25.34	8.81	0.44	2.36	18.39	-0.36	-0.66	-0.74	-0.39	-1.15	-1.08	-0.88
11	98	efad	1	1.38	28.49	5.63	0.90	7.01	36.68	-0.5	-0.62	-0.79	-0.36	-1.21	-0.82	-0.92
12	99	dha	1	0.26	25.73	8.30	0.43	2.74	21.75	-0.4	-0.6	-0.55	-0.25	-1.22	-1.13	-0.81
13	101	ref	1	0.44	24.28	8.63	0.53	3.33	23.86	-0.52	-0.66	-0.66	-0.41	-1.28	-1.1	-0.95
14	102	tournesol	1	0.32	24.63	9.99	0.45	2.39	17.93	-0.52	-0.63	-0.99	-0.43	-1.24	-0.96	-0.96
15	111	ref	1	0.34	26.04	9.81	0.35	2.36	20.14	-0.47	-0.71	-0.44	-0.45	-1.44	-1.17	-1.02
16	118	tournesol	1	0.35	24.76	9.38	0.54	2.47	19.66	-0.42	-0.66	-0.88	-0.33	-1.24	-1.03	-0.92
17	120	lin	1	0.24	26.46	10.97	0.31	2.81	14.69	-0.4	-0.62	-0.85	-0.42	-1.33	-1.19	-0.91
18	121	efad	1	1.21	23.45	5.59	0.67	6.31	33.84	-0.46	-0.69	-0.45	-0.32	-1.31	-0.93	-1.06
19	123	dha	1	0.30	29.72	8.95	0.45	2.86	17.79	-0.36	-0.58	-0.71	-0.34	-1.2	-0.98	-0.92
20	130	efad	1	1.30	27.00	5.72	0.81	7.86	33.50	-0.35	-0.62	-0.56	-0.24	-1.24	-0.88	-0.95
21	135	ref	1	0.38	24.09	8.22	0.60	3.89	24.61	-0.44	-0.75	-0.7	-0.33	-1.35	-1.04	-0.99
22	281	efad	2	3.24	23.59	2.68	1.11	13.09	35.61	-0.48	-0.71	-0.63	-0.55	-1.27	-1.03	-0.88
23	285	ref	2	0.60	19.95	3.18	1.21	4.89	35.91	-0.5	-0.69	-0.86	-0.58	-1.31	-1.06	-0.88
24	290	tournesol	2	0.38	17.64	6.99	0.74	2.58	21.23	-0.54	-0.69	-1.02	-0.51	-1.32	-1.2	-0.96
25	294	dha	2	0.44	22.73	4.71	0.75	2.27	25.10	-0.39	-0.7	-0.83	-0.47	-1.27	-1.09	-0.91
26	295	tournesol	2	0.47	14.65	4.29	0.66	2.88	23.15	-0.54	-0.63	-0.86	-0.56	-1.35	-1.17	-0.88
27	303	ref	2	0.64	20.49	2.71	1.09	4.05	38.32	-0.35	-0.52	-0.74	-0.4	-1.07	-0.83	-0.73
28	305	ref	2	0.52	18.44	5.21	0.87	3.37	32.04	-0.46	-0.69	-0.53	-0.51	-1.33	-0.99	-0.9
29	307	lin	2	0.49	17.72	6.02	0.58	3.77	21.04	-0.42	-0.56	-0.86	-0.57	-1.23	-1.04	-0.75
30	319	dha	2	0.40	21.70	6.12	0.78	2.07	22.49	-0.51	-0.7	-0.68	-0.46	-1.34	-1.13	-0.94
31	321	lin	2	0.61	16.25	4.55	0.61	5.42	21.43	-0.47	-0.74	-0.88	-0.58	-1.3	-1.03	-0.83
32	325	efad	2	3.19	22.91	3.60	0.99	13.90	33.55	-0.54	-0.64	-0.39	-0.46	-1.3	-1.03	-0.85

Les données

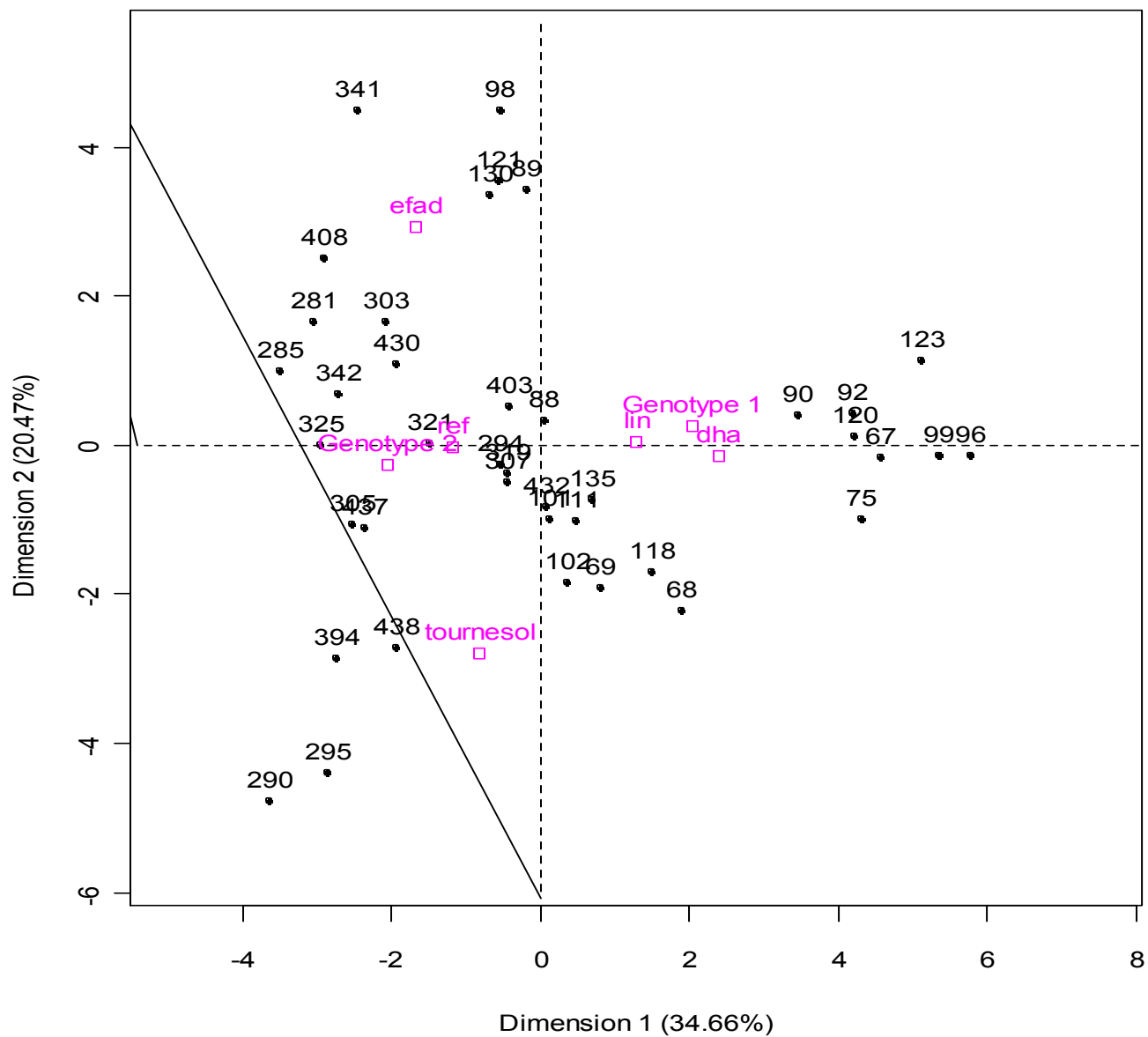
The diagram illustrates a transformation from a matrix X to a matrix Σ . On the left, a rectangular box contains the letter X . A red 'I' is written to the left of the box, and a red 'J' is written above the box. An arrow points from this box to a second rectangular box on the right. This second box contains the Greek letter Σ . A red 'J' is written above this box. Below the second box, the expression $\Sigma = (\pi(j, j'))$ is written.

$$\begin{matrix} \text{I} & & & & \text{J} \\ & \boxed{X} & \Rightarrow & \boxed{\Sigma} & \\ & & & \text{J} & \end{matrix}$$
$$\Sigma = (\pi(j, j'))$$

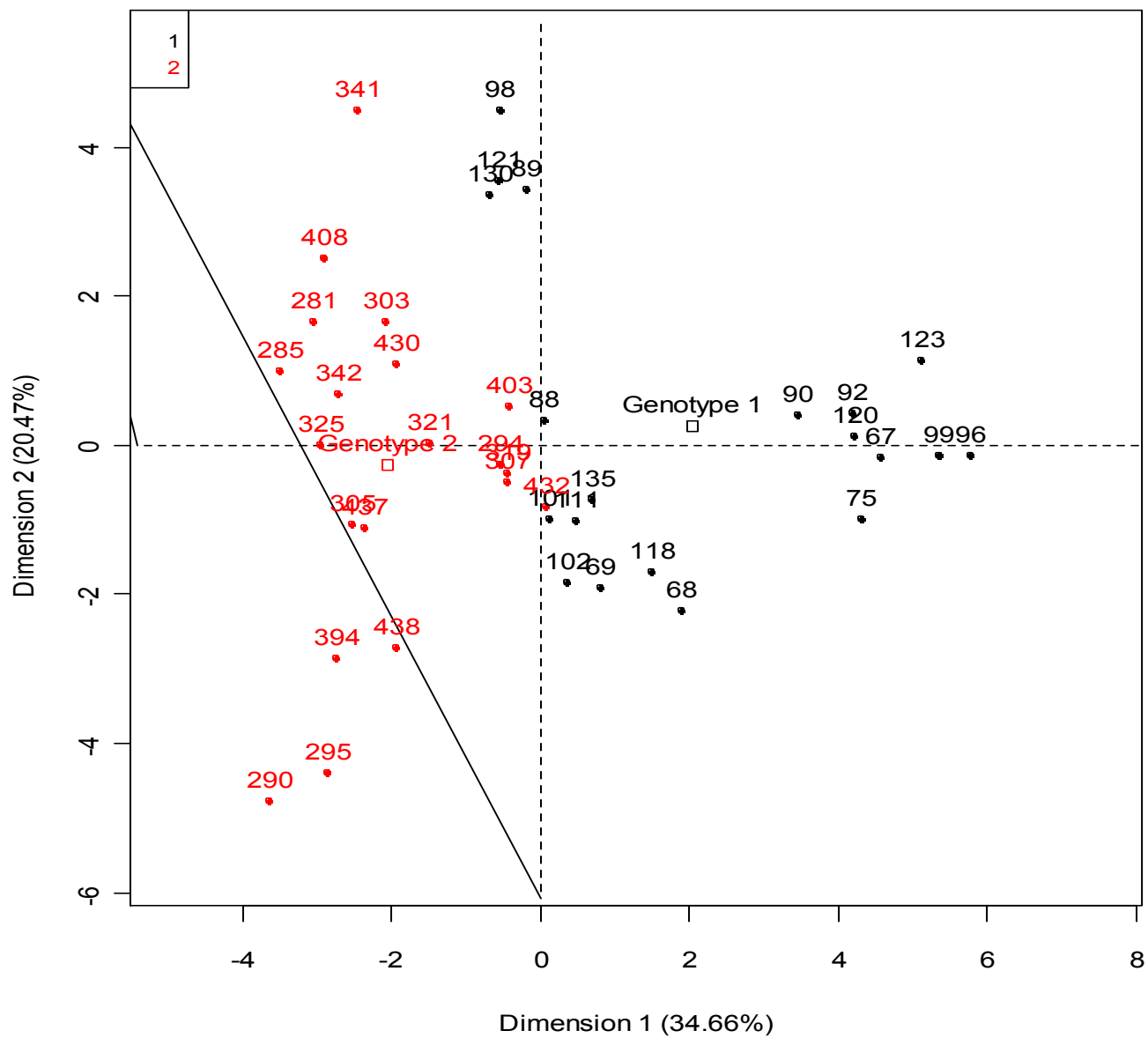
Individuals factor map (PCA)



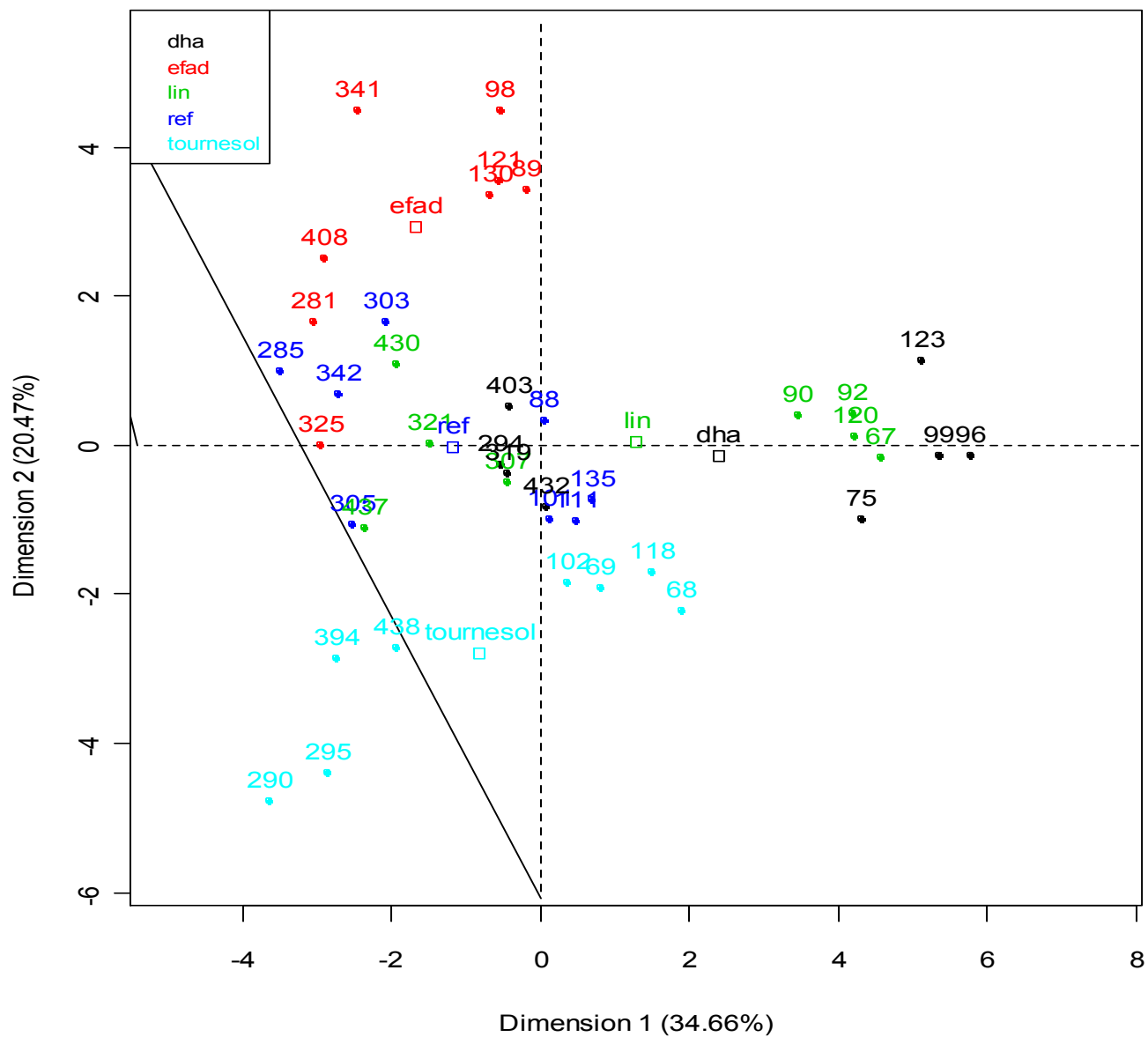
Individuals factor map (PCA)



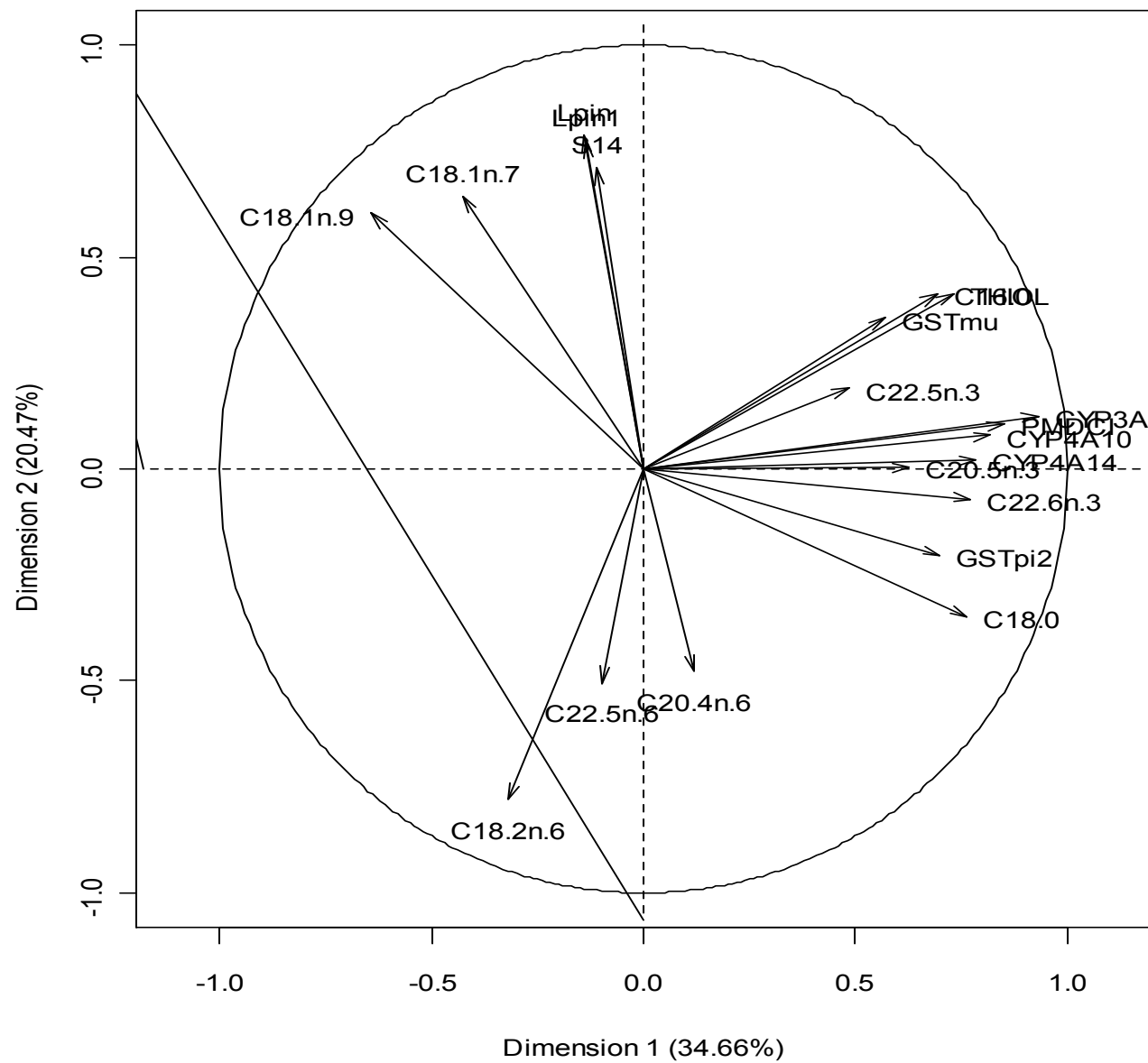
Individuals factor map (PCA)



Individuals factor map (PCA)



Variables factor map (PCA)



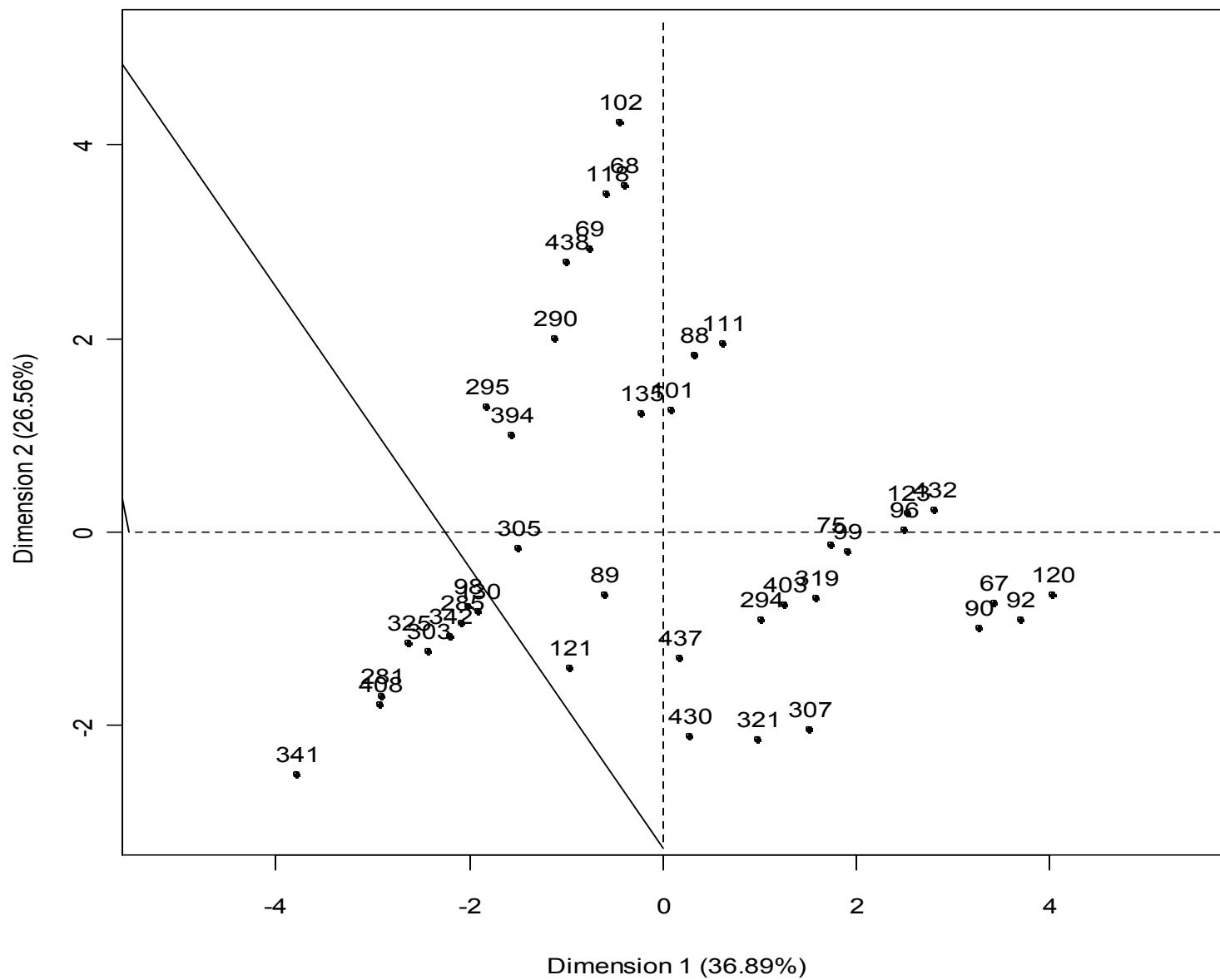
Les données

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	
1	Souris	Regime	Genotype	C14.0	C16.0	C18.0	C16.1n.9	C16.1n.7	C18.1n.9	X36b4	ACAT1	ACAT2	ACBP	ACC1	ACC2	ACO
2	67	lin	1	0.34	26.45	10.22	0.35	3.10	16.98	-0.42	-0.65	-0.84	-0.34	-1.29	-1.13	-0.93
3	68	tournesol	1	0.38	24.04	9.93	0.55	2.54	20.07	-0.44	-0.68	-0.91	-0.32	-1.23	-1.06	-0.99
4	69	tournesol	1	0.36	23.70	8.96	0.55	2.65	22.89	-0.48	-0.74	-1.1	-0.46	-1.3	-1.09	-1.06
5	75	dha	1	0.22	25.48	8.14	0.49	2.82	21.92	-0.45	-0.69	-0.65	-0.41	-1.26	-1.09	-0.93
6	88	ref	1	0.37	24.80	9.63	0.46	2.85	21.38	-0.42	-0.71	-0.54	-0.38	-1.21	-0.89	
7	89	efad	1	1.70	26.04	6.59	0.66	7.26	28.23	-0.43	-0.69	-0.8	-0.32	-1.13	-0.79	-0.93
8	90	lin	1	0.35	25.94	9.68	0.36	3.60	17.62	-0.53	-0.62	-1	-0.44	-1.22	-1	-0.94
9	92	lin	1	0.34	28.63	9.95	0.29	3.27	17.02	-0.49	-0.69	-0.91	-0.37	-1.29	-1.06	-1.05
10	96	dha	1	0.22	25.34	8.81	0.44	2.36	18.39	-0.36	-0.66	-0.74	-0.39	-1.15	-1.08	-0.88
11	98	efad	1	1.38	28.49	5.63	0.90	7.01	36.68	-0.5	-0.62	-0.79	-0.36	-1.21	-0.82	-0.92
12	99	dha	1	0.26	25.73	8.30	0.43	2.74	21.75	-0.4	-0.6	-0.55	-0.25	-1.22	-1.13	-0.81
13	101	ref	1	0.44	24.28	8.63	0.53	3.33	23.86	-0.52	-0.66	-0.66	-0.41	-1.28	-1.1	-0.95
14	102	tournesol	1	0.32	24.63	9.99	0.45	2.39	17.93	-0.52	-0.63	-0.99	-0.43	-1.24	-0.96	-0.96
15	111	ref	1	0.34	26.04	9.81	0.35	2.36	20.14	-0.47	-0.71	-0.44	-0.45	-1.44	-1.17	-1.02
16	118	tournesol	1	0.35	24.76	9.38	0.5	2.47	19.66	-0.42	-0.66	-0.88	-0.33	-1.24	-1.03	-0.92
17	120	lin	1	0.24	26.46	10.97	0.41	2.81	14.69	-0.58	-0.62	-0.85	-0.1	-1.33	-1.19	-0.91
18	121	efad	1	1.21	23.45	5.59	0.8	6.21	33.84	-0.46	-0.69	-0.45	-0.32	-1.21	-0.93	-1.06
19	123	dha	1	0.30	29.72	8.95	0.45	2.16	17.79	-0.36	-0.58	-0.71	-0.34	-1.2	-0.98	-0.92
20	130	efad	1	1.30	27.00	5.72	0.81	7.16	33.50	-0.35	-0.62	-0.56	-0.24	-1.2	-0.88	-0.95
21	135	ref	1	0.38	24.09	8.22	0.60	3.9	24.61	-0.44	-0.75	-0.7	-0.33	-1.25	-1.04	-0.99
22	281	efad	2	3.24	23.59	2.68	1.11	13.09	35.61	-0.48	-0.71	-0.63	-0.55	-1.27	-1.03	-0.88
23	285	ref	2	0.60	19.95	3.18	1.21	4.89	35.91	-0.5	-0.69	-0.86	-0.58	-1.31	-1.06	-0.88
24	290	tournesol	2	0.38	17.64	6.99	0.74	2.58	21.23	-0.54	-0.69	-1.02	-0.51	-1.32	-1.2	-0.96
25	294	dha	2	0.44	22.73	4.71	0.75	2.27	25.10	-0.39	-0.7	-0.83	-0.47	-1.27	-1.09	-0.91
26	295	tournesol	2	0.47	14.65	4.29	0.66	2.88	23.15	-0.54	-0.63	-0.86	-0.56	-1.35	-1.17	-0.88
27	303	ref	2	0.64	20.49	2.71	1.09	4.05	38.32	-0.35	-0.52	-0.74	-0.4	-1.07	-0.83	-0.73
28	305	ref	2	0.52	18.44	5.21	0.87	3.37	32.04	-0.46	-0.69	-0.53	-0.51	-1.33	-0.99	-0.9
29	307	lin	2	0.49	17.72	6.02	0.58	3.77	21.04	-0.42	-0.56	-0.86	-0.57	-1.23	-1.04	-0.75
30	319	dha	2	0.40	21.70	6.12	0.78	2.07	22.49	-0.51	-0.7	-0.68	-0.46	-1.34	-1.13	-0.94
31	321	lin	2	0.61	16.25	4.55	0.61	5.42	21.43	-0.47	-0.74	-0.88	-0.58	-1.3	-1.03	-0.83
32	325	efad	2	3.19	22.91	3.60	0.99	13.90	33.55	-0.54	-0.64	-0.39	-0.46	-1.3	-1.03	-0.85

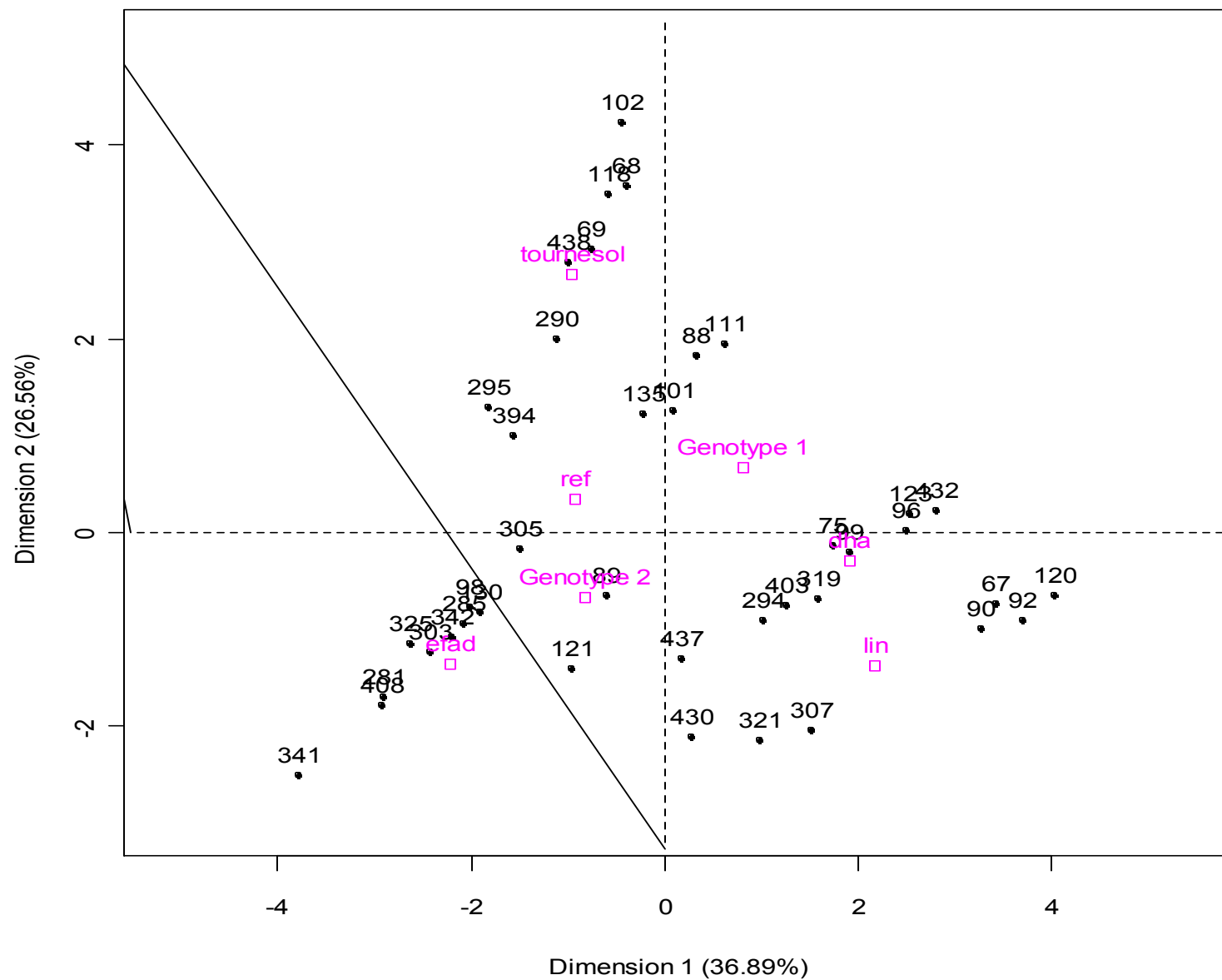
Les données

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	
1	Souris	Regime	Genotype	C14.0	C16.0	C18.0	C16.1n.9	C16.1n.7	C18.1n.9	X36b4	ACAT1	ACAT2	ACBP	ACC1	ACC2	ACO
2	67	lin	1	0.34	26.45	10.22	0.35	3.10	16.98	-0.42	-0.65	-0.84	-0.34	-1.29	-1.13	-0.93
3	68	tournesol	1	0.38	24.04	9.93	0.55	2.54	20.07	-0.44	-0.68	-0.91	-0.32	-1.23	-1.06	-0.99
4	69	tournesol	1	0.36	23.70	8.96	0.55	2.65	22.89	-0.48	-0.74	-1.1	-0.46	-1.3	-1.09	-1.06
5	75	dha	1	0.22	25.48	8.14	0.49	2.82	21.92	-0.45	-0.69	-0.65	-0.41	-1.26	-1.09	-0.93
6	88	ref	1	0.37	24.80	9.63	0.46	2.85	21.38	-0.42	-0.71	-0.54	-0.38	-1.21	-0.89	
7	89	efad	1	1.70	26.04	6.59	0.66	7.26	28.23	-0.43	-0.69	-0.8	-0.32	-1.13	-0.79	-0.93
8	90	lin	1	0.35	25.94	9.68	0.36	3.60	17.62	-0.53	-0.62	-1	-0.44	-1.22	-1	-0.94
9	92	lin	1	0.34	28.63	9.95	0.29	3.27	17.02	-0.49	-0.69	-0.91	-0.37	-1.29	-1.06	-1.05
10	96	dha	1	0.22	25.34	8.81	0.44	2.36	18.39	-0.36	-0.66	-0.74	-0.39	-1.15	-1.08	-0.88
11	98	efad	1	1.38	28.49	5.63	0.90	7.01	36.68	-0.5	-0.62	-0.79	-0.36	-1.21	-0.82	-0.92
12	99	dha	1	0.26	25.73	8.30	0.43	2.74	21.75	-0.4	-0.6	-0.55	-0.25	-1.22	-1.13	-0.81
13	101	ref	1	0.44	24.28	8.63	0.53	3.33	23.86	-0.52	-0.66	-0.66	-0.41	-1.28	-1.1	-0.95
14	102	tournesol	1	0.32	24.63	9.99	0.45	2.39	17.93	-0.52	-0.63	-0.99	-0.43	-1.24	-0.96	-0.96
15	111	ref	1	0.34	26.04	9.81	0.35	2.36	20.14	-0.47	-0.71	-0.44	-0.45	-1.44	-1.17	-1.02
16	118	tournesol	1	0.35	24.76	9.38	0.5	2.47	19.66	-0.42	-0.66	-0.88	-0.33	-1.24	-1.03	-0.92
17	120	lin	1	0.24	26.46	10.97	0.41	2.81	14.69	-0.58	-0.62	-0.85	-0	-1.33	-1.19	-0.91
18	121	efad	1	1.21	23.45	5.59	0.8	6.21	33.84	-0.46	-0.69	-0.45	-0.32	-1.21	-0.93	-1.06
19	123	dha	1	0.30	29.72	8.95	0.45	2.16	17.79	-0.36	-0.58	-0.71	-0.34	-1.2	-0.98	-0.92
20	130	efad	1	1.30	27.00	5.72	0.81	7.16	33.50	-0.35	-0.62	-0.56	-0.24	-1.2	-0.88	-0.95
21	135	ref	1	0.38	24.09	8.22	0.60	3.9	24.61	-0.44	-0.75	-0.7	-0.33	-1.25	-1.04	-0.99
22	281	efad	2	3.24	23.59	2.68	1.11	13.09	35.61	-0.48	-0.71	-0.63	-0.55	-1.27	-1.03	-0.88
23	285	ref	2	0.60	19.95	3.18	1.21	4.89	35.91	-0.5	-0.69	-0.86	-0.58	-1.31	-1.06	-0.88
24	290	tournesol	2	0.38	17.64	6.99	0.74	2.58	21.23	-0.54	-0.69	-1.02	-0.51	-1.32	-1.2	-0.96
25	294	dha	2	0.44	22.73	4.71	0.75	2.27	25.10	-0.39	-0.7	-0.83	-0.47	-1.27	-1.09	-0.91
26	295	tournesol	2	0.47	14.65	4.29	0.66	2.88	23.15	-0.54	-0.63	-0.86	-0.56	-1.35	-1.17	-0.88
27	303	ref	2	0.64	20.49	2.71	1.09	4.05	38.32	-0.35	-0.52	-0.74	-0.4	-1.07	-0.83	-0.73
28	305	ref	2	0.52	18.44	5.21	0.87	3.37	32.04	-0.46	-0.69	-0.53	-0.51	-1.33	-0.99	-0.9
29	307	lin	2	0.49	17.72	6.02	0.58	3.77	21.04	-0.42	-0.56	-0.86	-0.57	-1.23	-1.04	-0.75
30	319	dha	2	0.40	21.70	6.12	0.78	2.07	22.49	-0.51	-0.7	-0.68	-0.46	-1.34	-1.13	-0.94
31	321	lin	2	0.61	16.25	4.55	0.61	5.42	21.43	-0.47	-0.74	-0.88	-0.58	-1.3	-1.03	-0.83
32	325	efad	2	3.19	22.91	3.60	0.99	13.90	33.55	-0.54	-0.64	-0.39	-0.46	-1.3	-1.03	-0.85

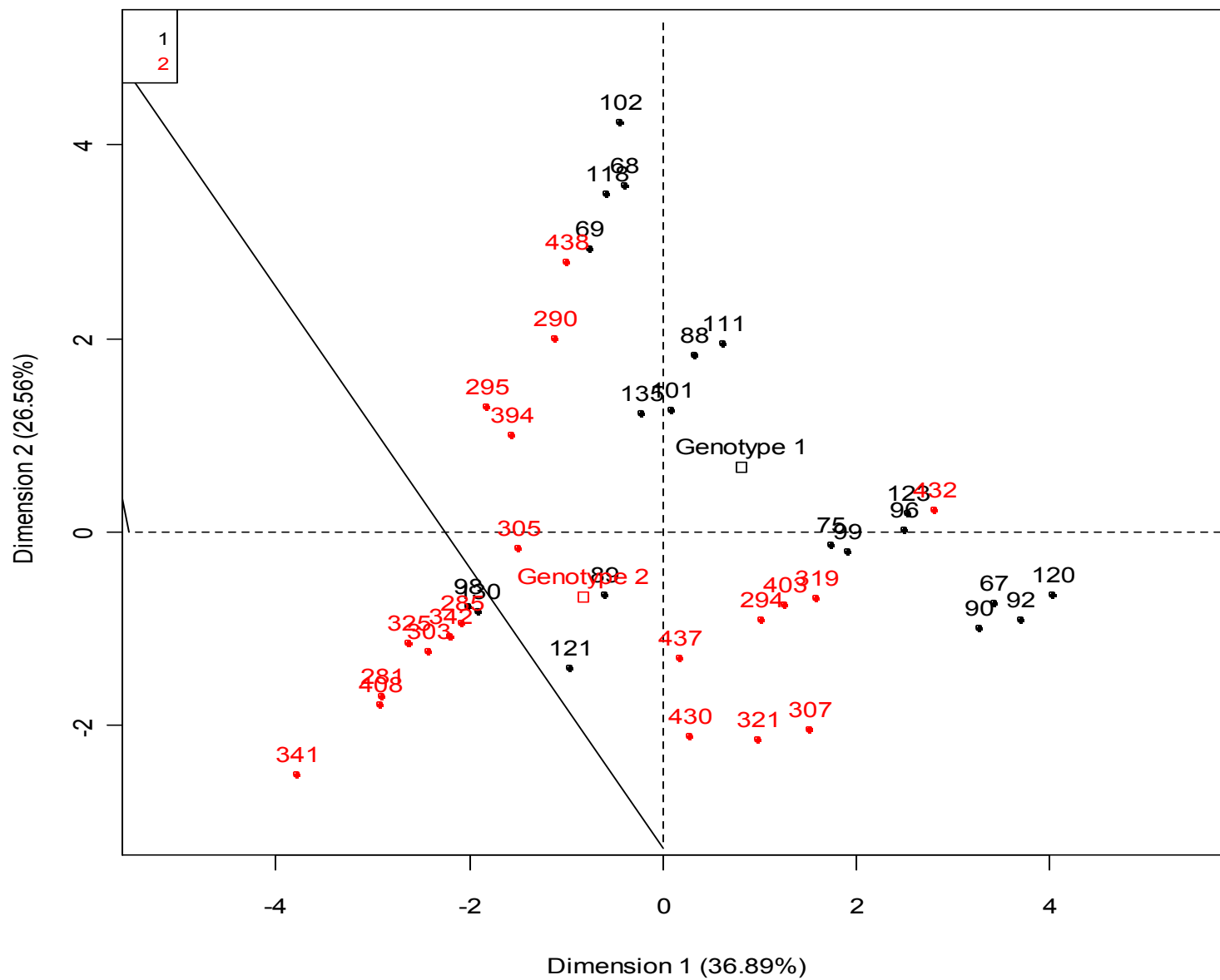
Individuals factor map (PCA)



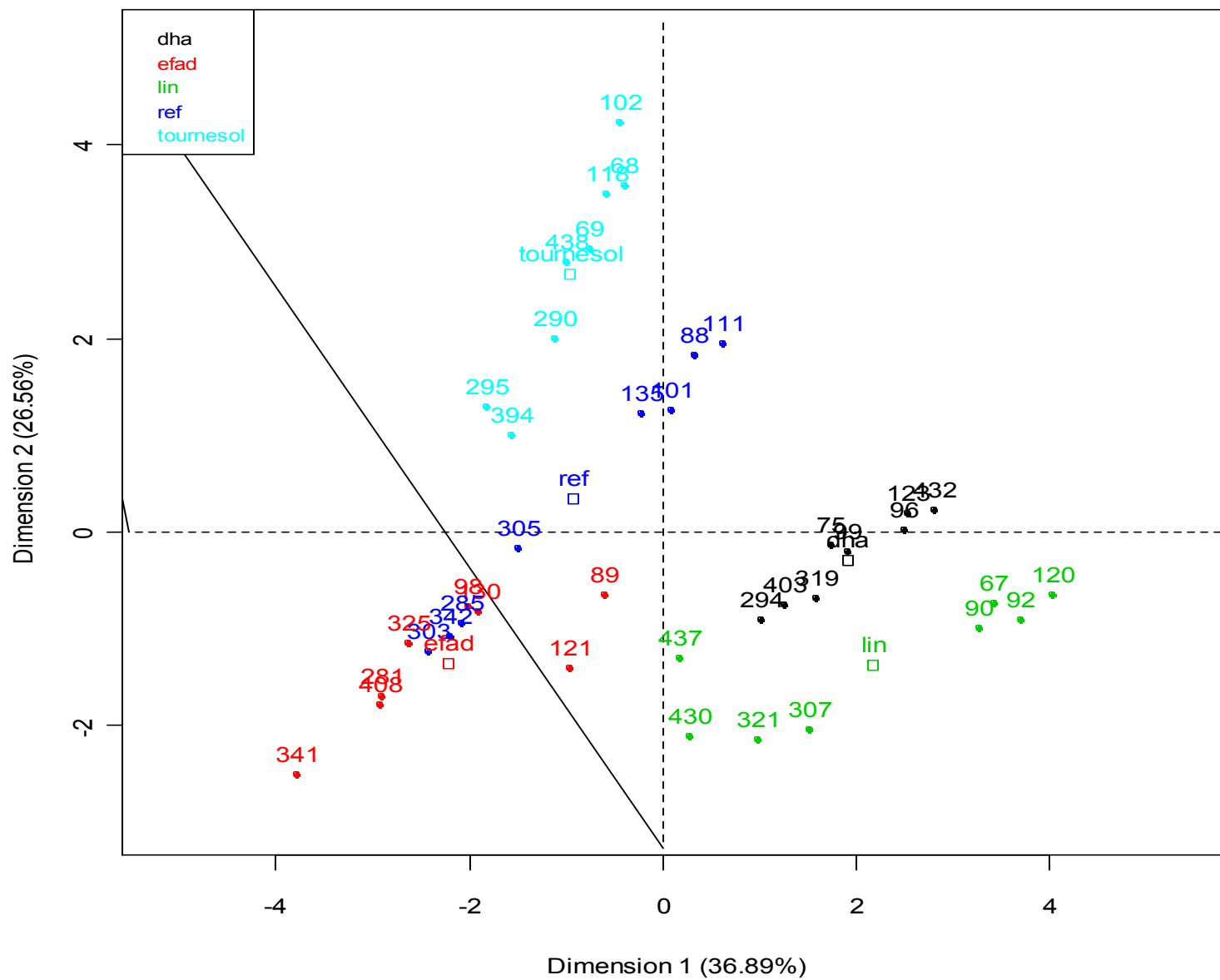
Individuals factor map (PCA)



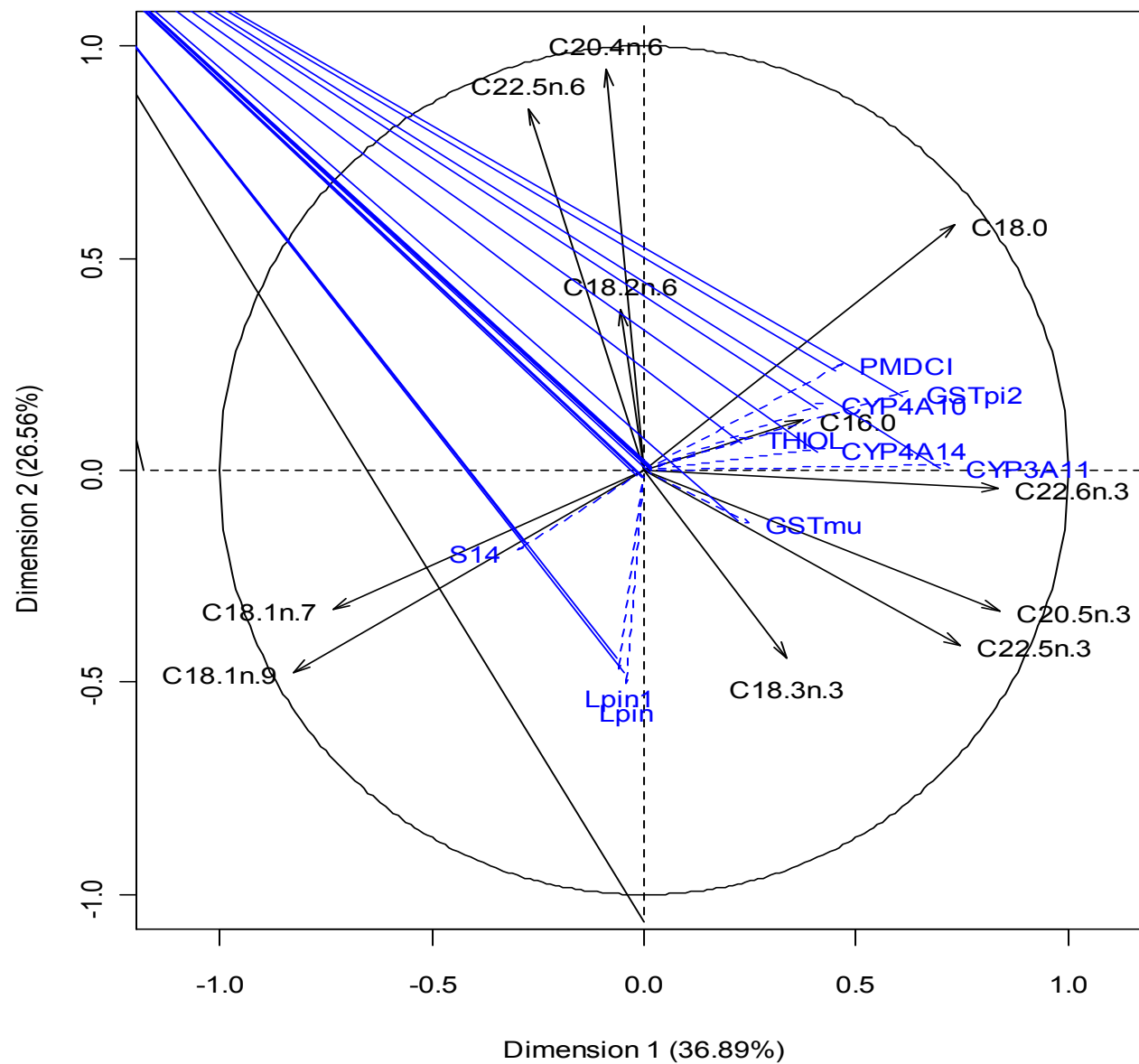
Individuals factor map (PCA)



Individuals factor map (PCA)



Variables factor map (PCA)



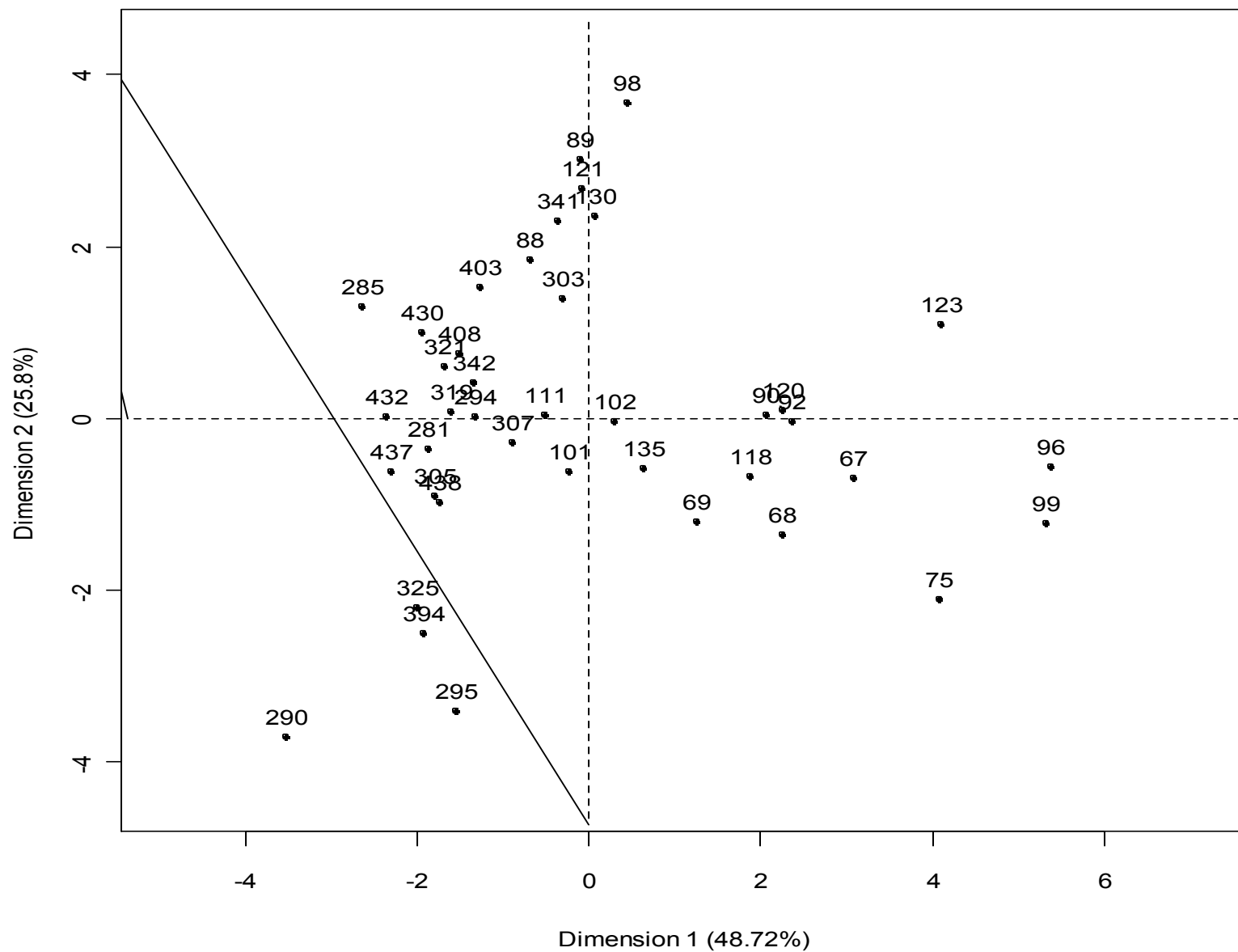
Les données

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	
1	Souris	Regime	Genotype	C14.0	C16.0	C18.0	C16.1n.9	C16.1n.7	C18.1n.9	X36b4	ACAT1	ACAT2	ACBP	ACC1	ACC2	ACO
2	67	lin	1	0.34	26.45	10.22	0.35	3.10	16.98	-0.42	-0.65	-0.84	-0.34	-1.29	-1.13	-0.93
3	68	tournesol	1	0.38	24.04	9.93	0.55	2.54	20.07	-0.44	-0.68	-0.91	-0.32	-1.23	-1.06	-0.99
4	69	tournesol	1	0.36	23.70	8.96	0.55	2.65	22.89	-0.48	-0.74	-1.1	-0.46	-1.3	-1.09	-1.06
5	75	dha	1	0.22	25.48	8.14	0.49	2.82	21.92	-0.45	-0.69	-0.65	-0.41	-1.26	-1.09	-0.93
6	88	ref	1	0.37	24.80	9.63	0.46	2.85	21.38	-0.42	-0.71	-0.54	-0.38	-1.21	-0.89	
7	89	efad	1	1.70	26.04	6.59	0.66	7.26	28.23	-0.43	-0.69	-0.8	-0.32	-1.13	-0.79	-0.93
8	90	lin	1	0.35	25.94	9.68	0.36	3.60	17.62	-0.53	-0.62	-1	-0.44	-1.22	-1	-0.94
9	92	lin	1	0.34	28.63	9.95	0.29	3.27	17.02	-0.49	-0.69	-0.91	-0.37	-1.29	-1.06	-1.05
10	96	dha	1	0.22	25.34	8.81	0.44	2.36	18.39	-0.36	-0.66	-0.74	-0.39	-1.15	-1.08	-0.88
11	98	efad	1	1.38	28.49	5.63	0.90	7.01	36.68	-0.5	-0.62	-0.79	-0.36	-1.21	-0.82	-0.92
12	99	dha	1	0.26	25.73	8.30	0.43	2.74	21.75	-0.4	-0.6	-0.55	-0.25	-1.22	-1.13	-0.81
13	101	ref	1	0.44	24.28	8.63	0.53	3.33	23.86	-0.52	-0.66	-0.66	-0.41	-1.28	-1.1	-0.95
14	102	tournesol	1	0.32	24.63	9.99	0.45	2.39	17.93	-0.52	-0.63	-0.99	-0.43	-1.24	-0.96	-0.96
15	111	ref	1	0.34	26.04	9.81	0.35	2.36	20.14	-0.47	-0.71	-0.44	-0.45	-1.44	-1.17	-1.02
16	118	tournesol	1	0.35	24.76	9.38	0.5	2.47	19.66	-0.42	-0.66	-0.88	-0.33	-1.24	-1.03	-0.92
17	120	lin	1	0.24	26.46	10.97	0.41	2.81	14.69	-0.58	-0.62	-0.85	-0.1	-1.33	-1.19	-0.91
18	121	efad	1	1.21	23.45	5.59	0.8	6.21	33.84	-0.46	-0.69	-0.45	-0.32	-1.21	-0.93	-1.06
19	123	dha	1	0.30	29.72	8.95	0.45	2.16	17.79	-0.36	-0.58	-0.71	-0.34	-1.2	-0.98	-0.92
20	130	efad	1	1.30	27.00	5.72	0.81	7.16	33.50	-0.35	-0.62	-0.56	-0.24	-1.2	-0.88	-0.95
21	135	ref	1	0.38	24.09	8.22	0.60	3.9	24.61	-0.44	-0.75	-0.7	-0.33	-1.25	-1.04	-0.99
22	281	efad	2	3.24	23.59	2.68	1.11	13.09	35.61	-0.48	-0.71	-0.63	-0.55	-1.27	-1.03	-0.88
23	285	ref	2	0.60	19.95	3.18	1.21	4.89	35.91	-0.5	-0.69	-0.86	-0.58	-1.31	-1.06	-0.88
24	290	tournesol	2	0.38	17.64	6.99	0.74	2.58	21.23	-0.54	-0.69	-1.02	-0.51	-1.32	-1.2	-0.96
25	294	dha	2	0.44	22.73	4.71	0.75	2.27	25.10	-0.39	-0.7	-0.83	-0.47	-1.27	-1.09	-0.91
26	295	tournesol	2	0.47	14.65	4.29	0.66	2.88	23.15	-0.54	-0.63	-0.86	-0.56	-1.35	-1.17	-0.88
27	303	ref	2	0.64	20.49	2.71	1.09	4.05	38.32	-0.35	-0.52	-0.74	-0.4	-1.07	-0.83	-0.73
28	305	ref	2	0.52	18.44	5.21	0.87	3.37	32.04	-0.46	-0.69	-0.53	-0.51	-1.33	-0.99	-0.9
29	307	lin	2	0.49	17.72	6.02	0.58	3.77	21.04	-0.42	-0.56	-0.86	-0.57	-1.23	-1.04	-0.75
30	319	dha	2	0.40	21.70	6.12	0.78	2.07	22.49	-0.51	-0.7	-0.68	-0.46	-1.34	-1.13	-0.94
31	321	lin	2	0.61	16.25	4.55	0.61	5.42	21.43	-0.47	-0.74	-0.88	-0.58	-1.3	-1.03	-0.83
32	325	efad	2	3.19	22.91	3.60	0.99	13.90	33.55	-0.54	-0.64	-0.39	-0.46	-1.3	-1.03	-0.85

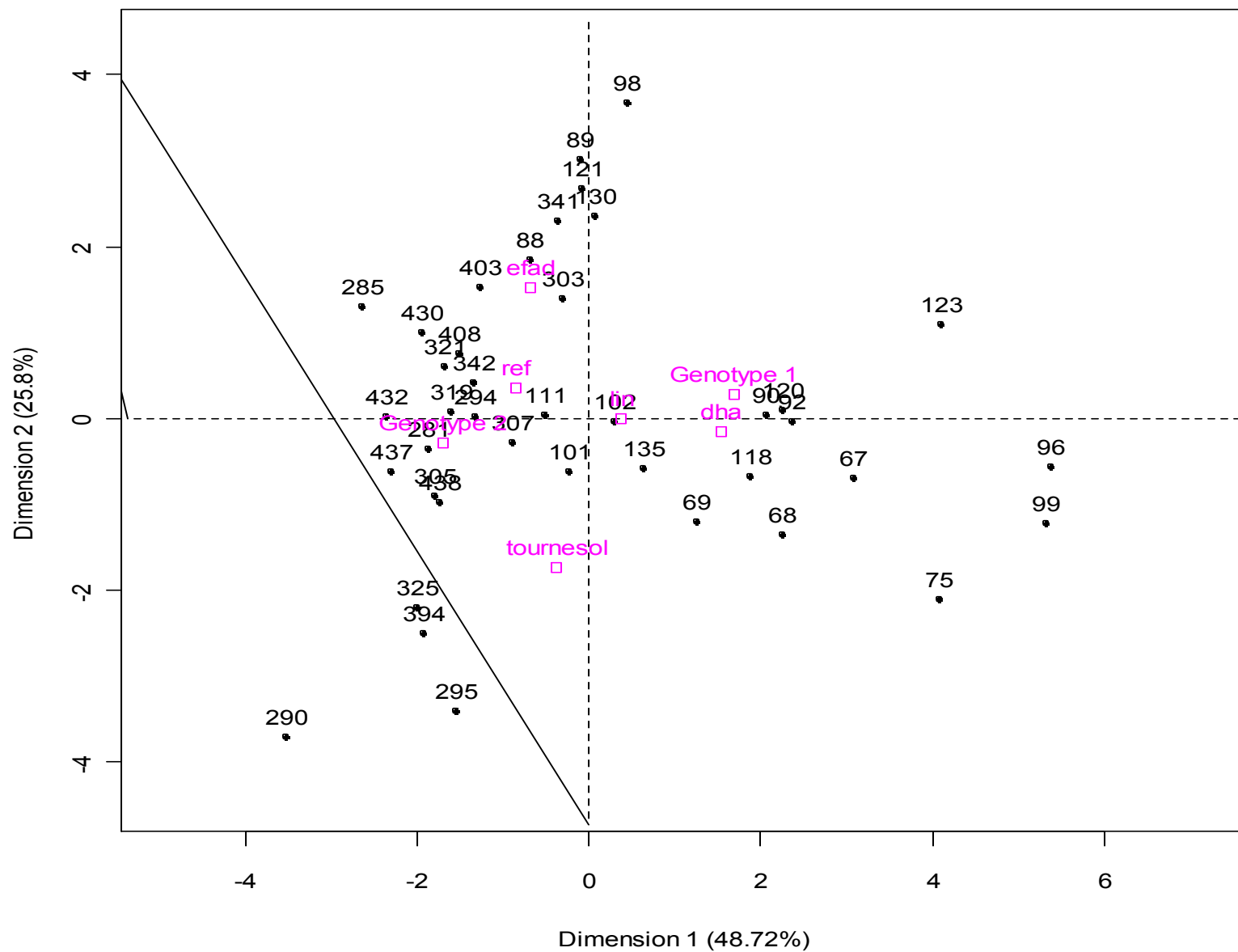
Les données

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	
1	Souris	Regime	Genotype	C14.0	C16.0	C18.0	C16.1n.9	C16.1n.7	C18.1n.9	X36b4	ACAT1	ACAT2	ACBP	ACC1	ACC2	ACO
2	67	lin	1	0.34	26.45	10.22	0.35	3.10	16.98	-0.42	-0.65	-0.84	-0.34	-1.29	-1.13	-0.93
3	68	tournesol	1	0.38	24.04	9.93	0.55	2.54	20.07	-0.44	-0.68	-0.91	-0.32	-1.23	-1.06	-0.99
4	69	tournesol	1	0.36	23.70	8.96	0.55	2.65	22.89	-0.48	-0.74	-1.1	-0.46	-1.3	-1.09	-1.06
5	75	dha	1	0.22	25.48	8.14	0.49	2.82	21.92	-0.45	-0.69	-0.65	-0.41	-1.26	-1.09	-0.93
6	88	ref	1	0.37	24.80	9.63	0.46	2.85	21.38	-0.42	-0.71	-0.54	-0.38	-1.21	-0.89	
7	89	efad	1	1.70	26.04	6.59	0.66	7.26	28.23	-0.43	-0.69	-0.8	-0.32	-1.13	-0.79	-0.93
8	90	lin	1	0.35	25.94	9.68	0.36	3.60	17.62	-0.53	-0.62	-1	-0.44	-1.22	-1	-0.94
9	92	lin	1	0.34	28.63	9.95	0.29	3.27	17.02	-0.49	-0.69	-0.91	-0.37	-1.29	-1.06	-1.05
10	96	dha	1	0.22	25.34	8.81	0.44	2.36	18.39	-0.36	-0.66	-0.74	-0.39	-1.15	-1.08	-0.88
11	98	efad	1	1.38	28.49	5.63	0.90	7.01	36.68	-0.5	-0.62	-0.79	-0.36	-1.21	-0.82	-0.92
12	99	dha	1	0.26	25.73	8.30	0.43	2.74	21.75	-0.4	-0.6	-0.55	-0.25	-1.22	-1.13	-0.81
13	101	ref	1	0.44	24.28	8.63	0.53	3.33	23.86	-0.52	-0.66	-0.66	-0.41	-1.28	-1.1	-0.95
14	102	tournesol	1	0.32	24.63	9.99	0.45	2.39	17.93	-0.52	-0.63	-0.99	-0.43	-1.24	-0.96	-0.96
15	111	ref	1	0.34	26.04	9.81	0.35	2.36	20.14	-0.47	-0.71	-0.44	-0.45	-1.44	-1.17	-1.02
16	118	tournesol	1	0.35	24.76	9.38	0.5	2.47	19.66	-0.42	-0.66	-0.88	-0.33	-1.24	-1.03	-0.92
17	120	lin	1	0.24	26.46	10.97	0.41	2.81	14.69	-0.58	-0.62	-0.85	-0.1	-1.33	-1.19	-0.91
18	121	efad	1	1.21	23.45	5.59	0.8	6.21	33.84	-0.46	-0.69	-0.45	-0.32	-1.21	-0.93	-1.06
19	123	dha	1	0.30	29.72	8.95	0.45	2.16	17.79	-0.36	-0.58	-0.71	-0.34	-1.2	-0.98	-0.92
20	130	efad	1	1.30	27.00	5.72	0.81	7.16	33.50	-0.35	-0.62	-0.56	-0.24	-1.2	-0.88	-0.95
21	135	ref	1	0.38	24.09	8.22	0.60	3.9	24.61	-0.44	-0.75	-0.7	-0.33	-1.26	-1.04	-0.99
22	281	efad	2	3.24	23.59	2.68	1.11	13.09	35.61	-0.48	-0.71	-0.63	-0.55	-1.27	-1.03	-0.88
23	285	ref	2	0.60	19.95	3.18	1.21	4.89	35.91	-0.5	-0.69	-0.86	-0.58	-1.31	-1.06	-0.88
24	290	tournesol	2	0.38	17.64	6.99	0.74	2.58	21.23	-0.54	-0.69	-1.02	-0.51	-1.32	-1.2	-0.96
25	294	dha	2	0.44	22.73	4.71	0.75	2.27	25.10	-0.39	-0.7	-0.83	-0.47	-1.27	-1.09	-0.91
26	295	tournesol	2	0.47	14.65	4.29	0.66	2.88	23.15	-0.54	-0.63	-0.86	-0.56	-1.35	-1.17	-0.88
27	303	ref	2	0.64	20.49	2.71	1.09	4.05	38.32	-0.35	-0.52	-0.74	-0.4	-1.07	-0.83	-0.73
28	305	ref	2	0.52	18.44	5.21	0.87	3.37	32.04	-0.46	-0.69	-0.53	-0.51	-1.33	-0.99	-0.9
29	307	lin	2	0.49	17.72	6.02	0.58	3.77	21.04	-0.42	-0.56	-0.86	-0.57	-1.23	-1.04	-0.75
30	319	dha	2	0.40	21.70	6.12	0.78	2.07	22.49	-0.51	-0.7	-0.68	-0.46	-1.34	-1.13	-0.94
31	321	lin	2	0.61	16.25	4.55	0.61	5.42	21.43	-0.47	-0.74	-0.88	-0.58	-1.3	-1.03	-0.83
32	325	efad	2	3.19	22.91	3.60	0.99	13.90	33.55	-0.54	-0.64	-0.39	-0.46	-1.3	-1.03	-0.85

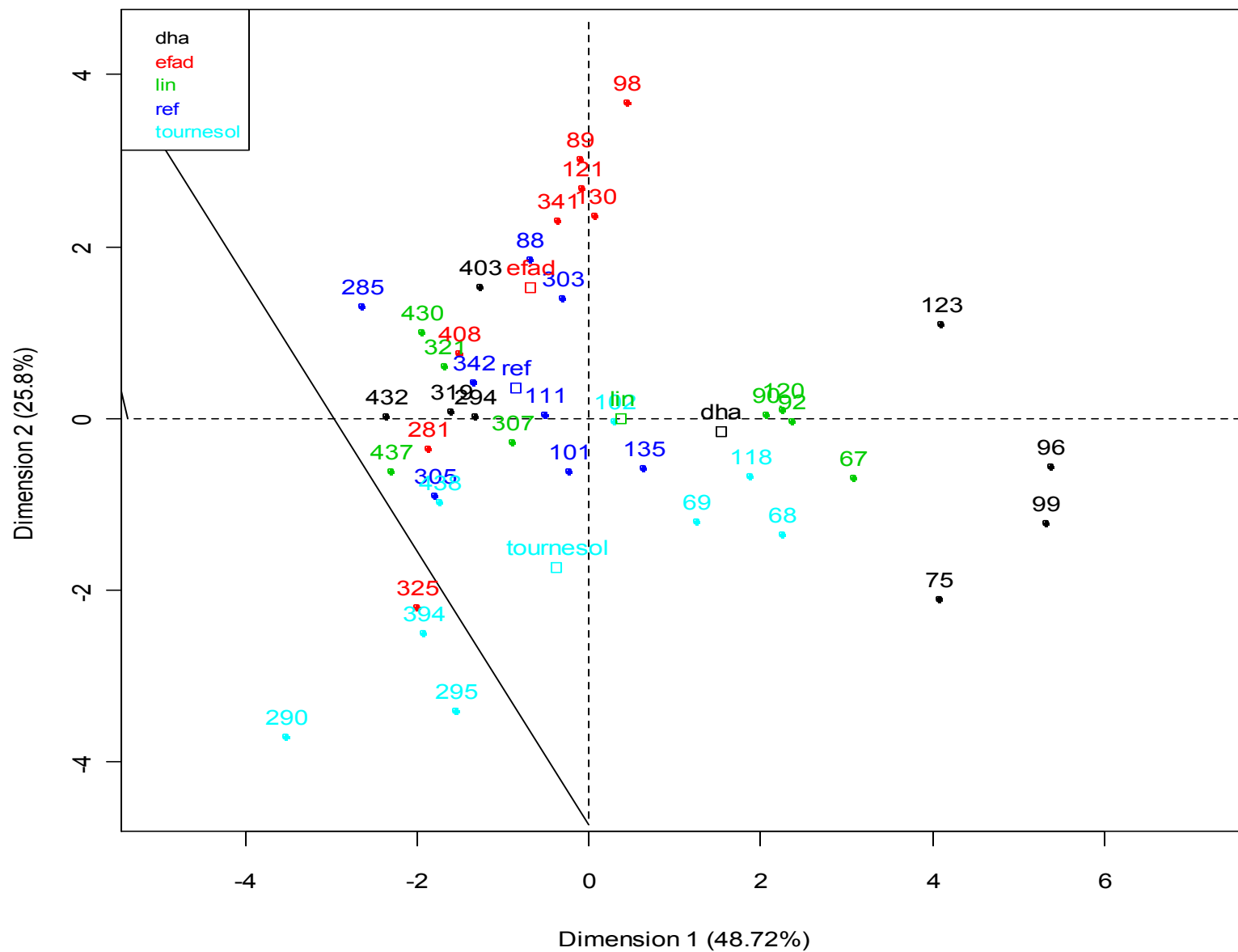
Individuals factor map (PCA)



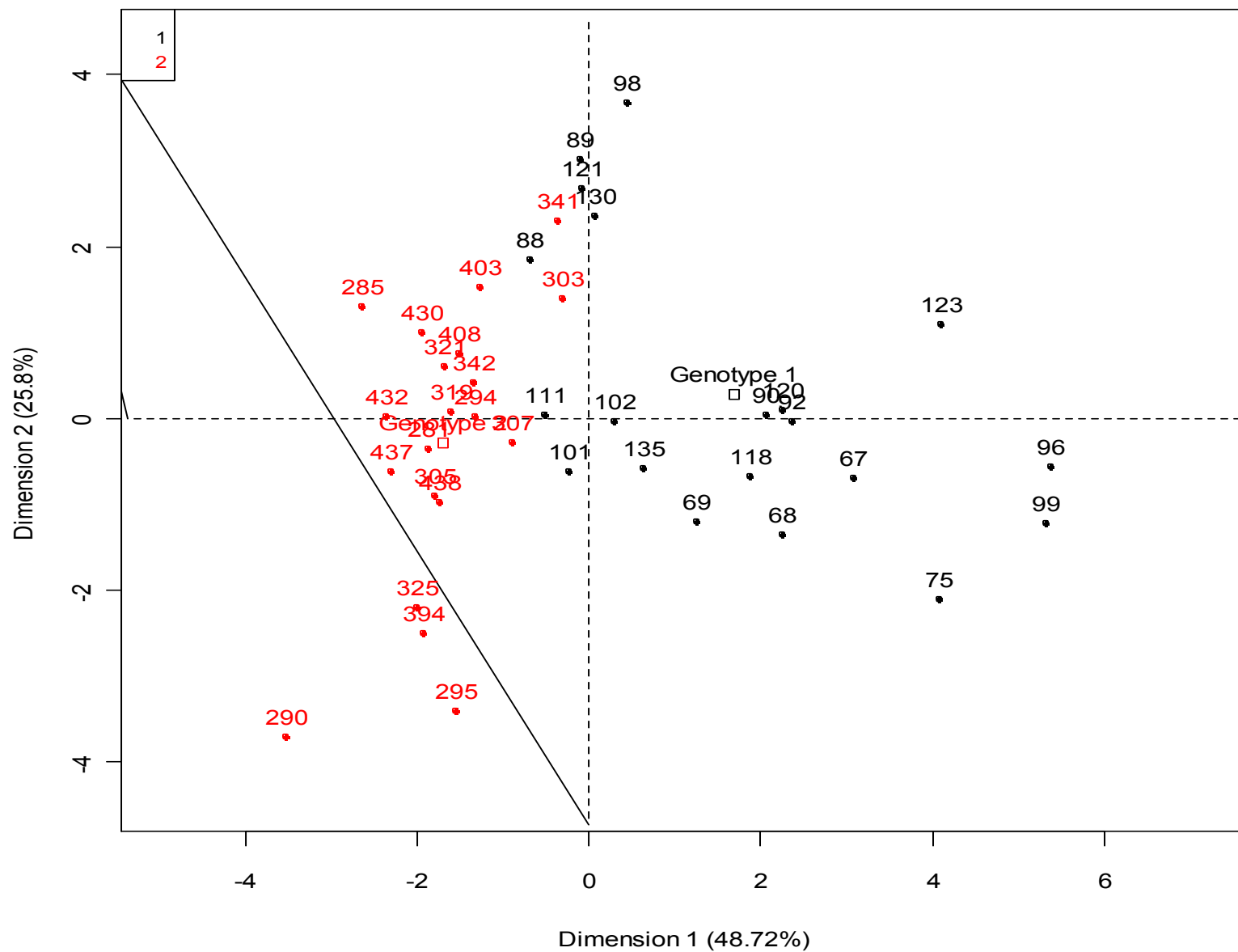
Individuals factor map (PCA)



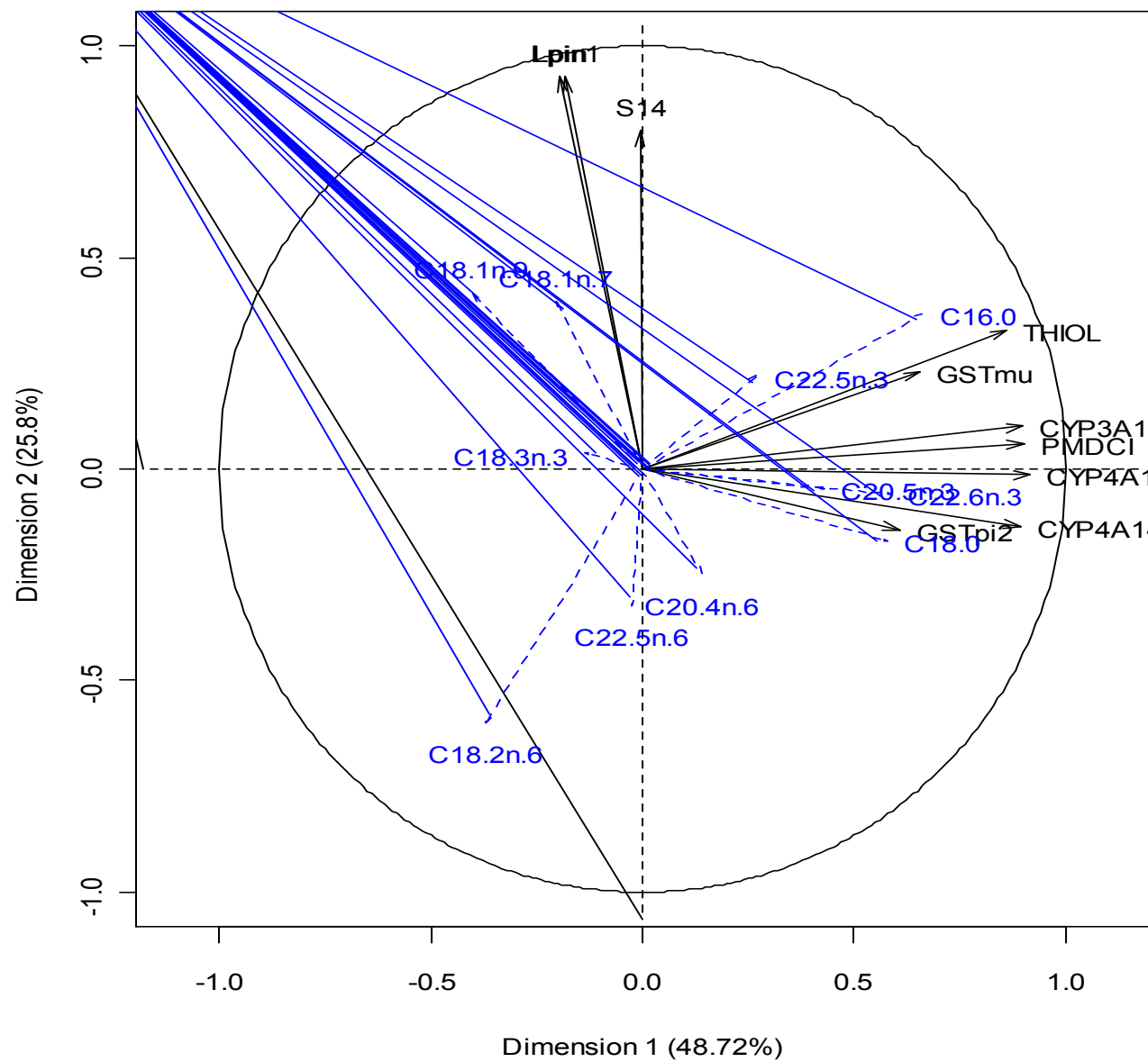
Individuals factor map (PCA)



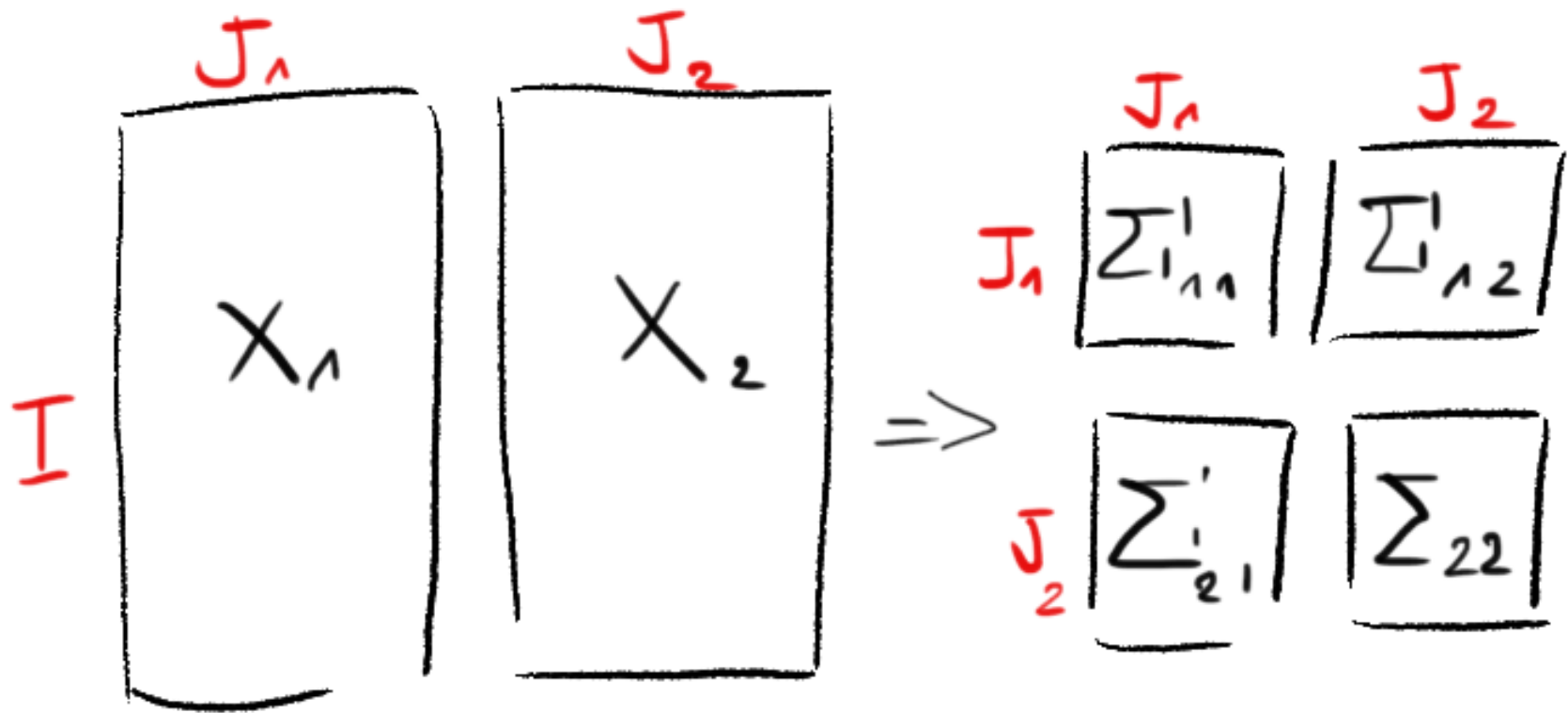
Individuals factor map (PCA)



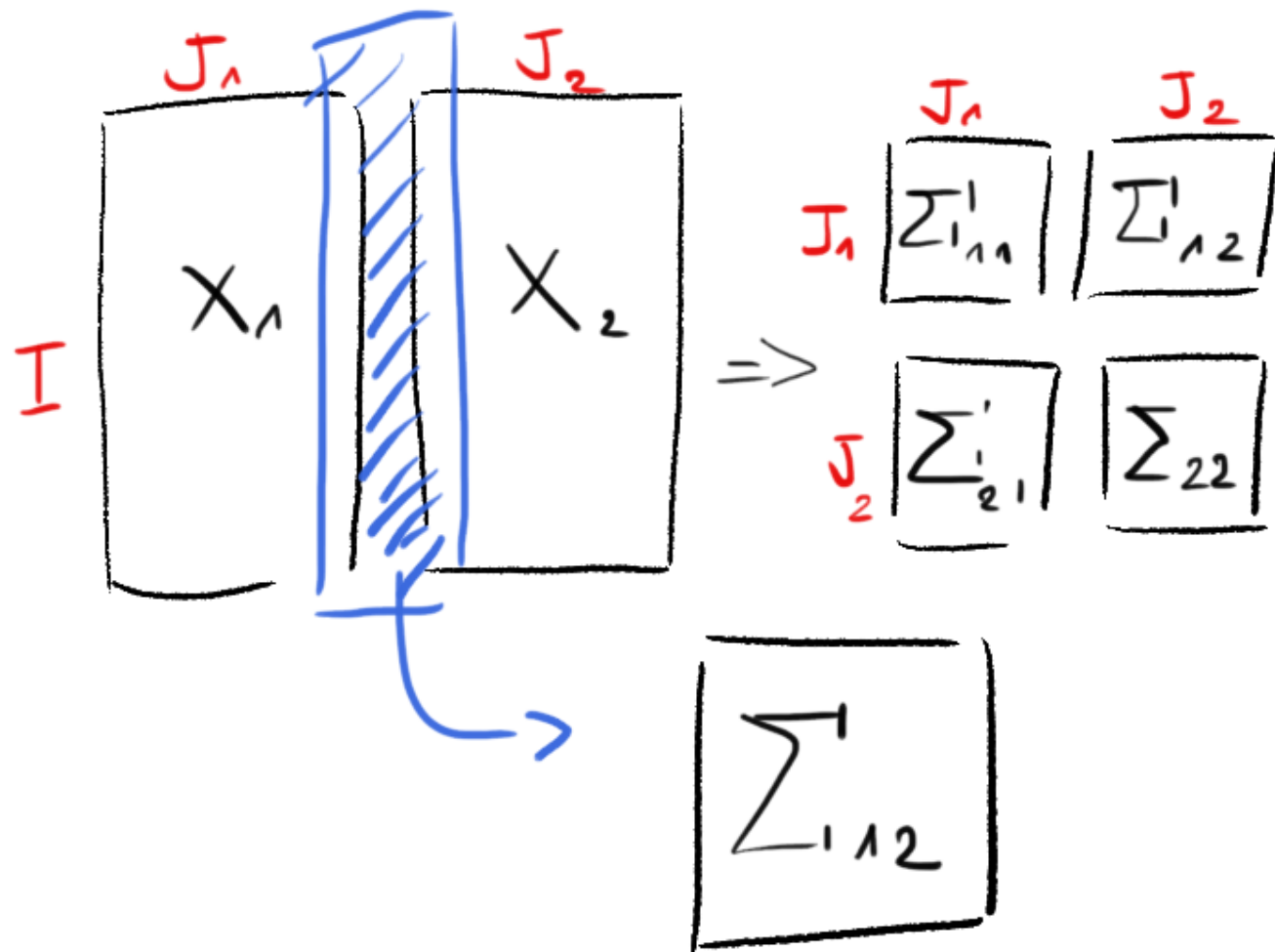
Variables factor map (PCA)

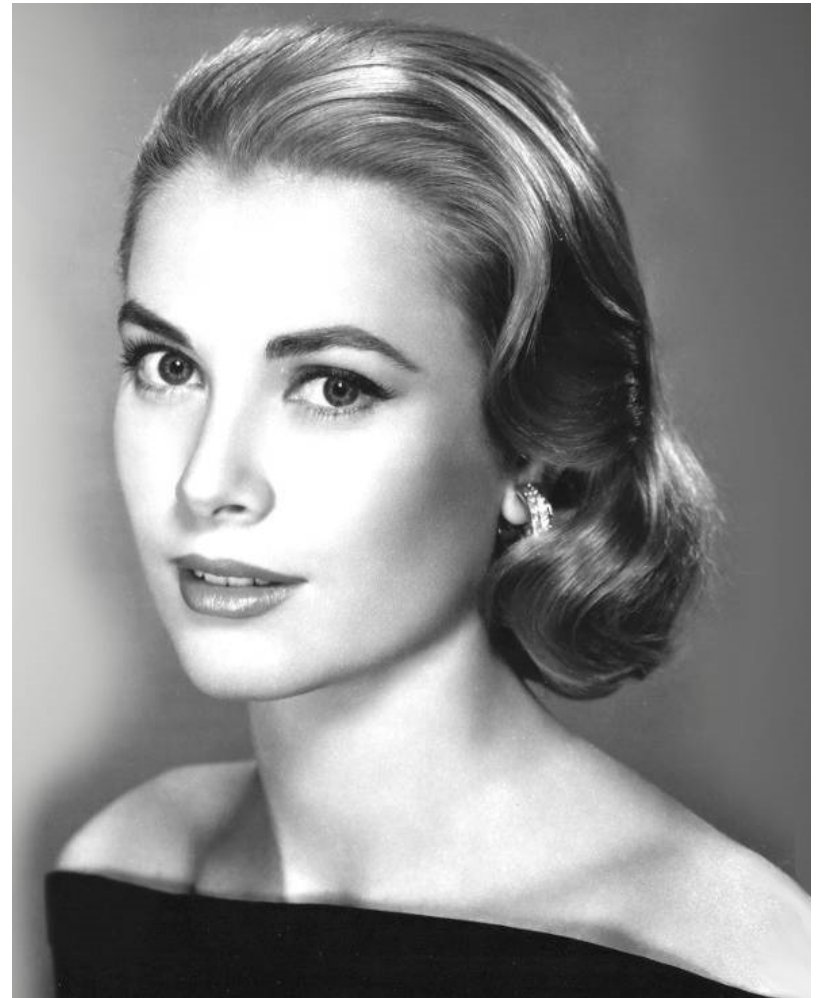
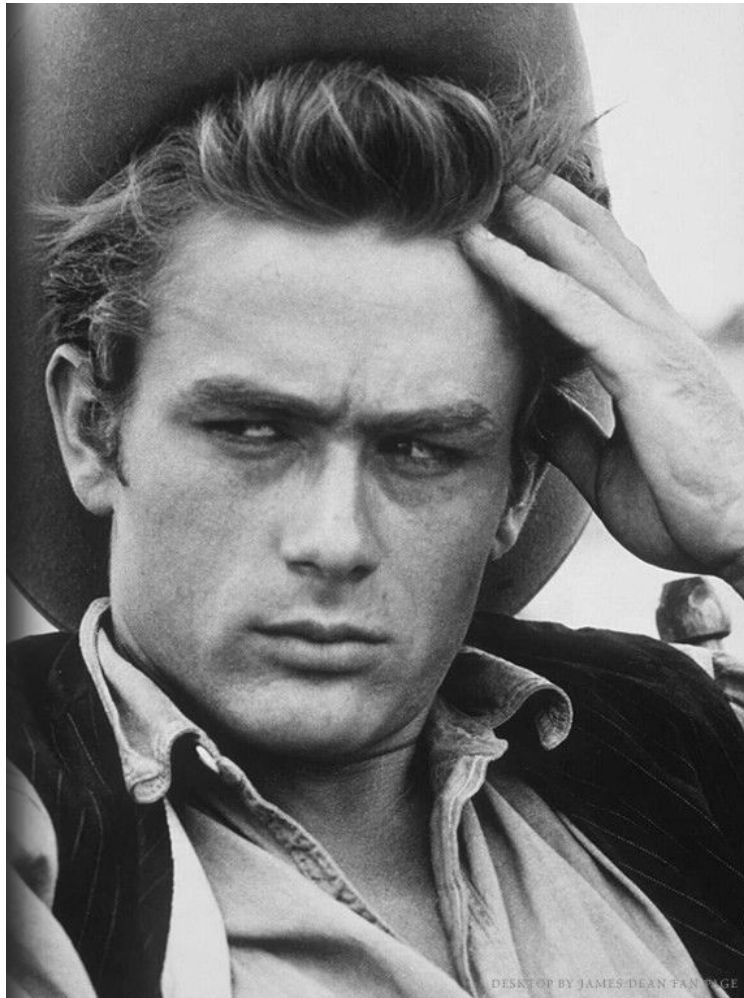


Les données



Les données







Qu' est ce qu' un canon?



Qu'est ce qu'un canon?

- Le mot **canon** vient du grec $\kappa \alpha \nu \acute{o} \nu$ / *kanôn* signifiant « règle, modèle », lui même emprunté à l'hébreu *qaneh* (« roseau, mesure, canne »)
- En mathématiques, **canonique** qualifie ce qui semble à tous comme le plus simple, le plus porteur de sens ou ce qui facilitera des manipulations ultérieures. Dans le cadre de la formalisation des mathématiques, la recherche et la création d'objets canoniques prend une grande importance

Qu'est ce que l'analyse canonique?

X_1



X_2



Qu'est ce que l'analyse canonique?

- Consiste à comprendre les combinaisons linéaires qui existent entre deux groupes de variables
- Lorsque n individus sont décrits par deux ensembles de variables, on cherche à examiner les liens existant entre ces deux ensembles afin de savoir s'ils décrivent ou non les mêmes propriétés
- On s'intéresse aux positions relatives de ces deux espaces de données en cherchant les éléments les plus proches
- La démarche de l'analyse canonique consiste à rechercher des couples de variables en corrélation maximale

cancor(lip,gen)

R Console

Fichier Edition Misc Packages Aide

```
> cancor(lip,gen)
```

```
$cor
```

```
[1] 0.96297273 0.93199442 0.91149643 0.85708380 0.78971594 0.71861893 0.60593887 0.40912187 0.24543555 0.04250940
```

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$xcoef
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C18.1n.9	0.028997123	0.0171655617	-0.032635011	-0.01450857	-0.018555194	-0.041183319	-0.013174087	0.040586602	0.08710232
C18.1n.7	0.032505732	-0.00171655617	0.032635011	0.01450857	0.018555194	0.041183319	0.013174087	-0.040586602	-0.08710232
C18.2n.6	0.011143241	-0.00171655617	0.032635011	0.01450857	0.018555194	0.041183319	0.013174087	-0.040586602	-0.08710232
C20.4n.6	0.016316003	0.00171655617	-0.032635011	-0.01450857	-0.018555194	-0.041183319	-0.013174087	0.040586602	0.08710232
C22.5n.6	0.013895923	-0.1994208277	-0.237792213	0.04828274	-0.294048565	-0.034069099	-0.278425025	-0.097912648	-0.01606464
C22.6n.3	-0.009625662	0.0180690151	-0.057893604	-0.01258168	0.010209536	-0.016871470	-0.040695824	0.018336510	0.07227701
C20.5n.3	0.001693435	0.0287109724	-0.052755724	0.11695136	0.028633355	-0.033946554	0.011660799	-0.006932460	0.11639351
C22.5n.3	0.080104739	0.0189714987	-0.078025488	-0.09597613	0.004368761	0.114483628	0.243505319	0.029838355	0.28063148
C16.0	0.025879989	0.0002305252	-0.014961055	-0.01606147	-0.087258413	-0.021124677	0.052003685	0.075732380	0.05434408
C18.0	0.053045462	0.0023552992	0.060777399	-0.15890538	-0.105767029	-0.003898920	-0.111955143	0.100838476	0.11642331
C18.3n.3	0.012796276	0.00171655617	-0.032635011	-0.01450857	-0.018555194	-0.041183319	-0.013174087	0.040586602	0.08710232

Attention : variables canoniques

```
$ycoef
```

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
PMDCI	0.51640610	0.6523181	1.0410813	-1.17646805	-0.23554143	0.96947711	-0.52053547	-0.16848881	0.1407219	-0.5615899
THIOL	0.63929635	0.3485394	-0.5578365	1.21794331	1.00912511	-0.40821774	0.12353419	-0.25882855	0.2587056	0.0627558
CYP3A11	-0.60991186	0.0407698	-0.2250082	0.26683169	-0.40367530	-0.01861773	0.53348063	-0.90329962	-0.4644879	0.3434860
CYP4A10	-0.05180081	-0.3360889	-0.1978164	0.19342476	-0.91569517	-0.05456395	-0.49015959	1.02698256	0.7043031	1.4347729
Lpin	0.26195541	0.2501206	-0.6088044	-0.13511715	-1.10231985	-0.27382711	-0.09176426	0.13063574	3.9408262	-1.7372312
Lpin1	-0.27203283	0.3351113	2.1529151	0.318	0.3644918	0.6715756	0.6348794	0.5592082	-1.3047358	
GSTmu	0.24643161	-0.5651113	2.1529151	0.318	0.3644918	0.6715756	0.6348794	0.5592082	-1.3047358	
GSTpi2	-0.25550623	0.3741113	2.1529151	0.318	0.3644918	0.6715756	0.6348794	0.5592082	-1.3047358	
S14	0.16336084	-0.3291935	0.1997579	0.06817508	-0.64894459	-0.01595339	0.56824837	0.05062431	-0.5990380	-0.6348794
CYP4A14	-0.30233566	0.1143903	-0.1328348	-0.33811760	0.30070528	-0.69227204	-0.18733677	-0.10210937	-0.5592082	-1.3047358

$G_1 = 0.51PMDCI + 0.63THIOL + \dots - 0.30CYP4A14$

```
$xcenter
```

```
C18.1n.9 C18.1n.7 C18.2n.6 C20.4n.6 C22.5n.6 C22.6n.3 C20.5n.3 C22.5n.3 C16.0 C18.0 C18.3n.3
25.27325 4.42600 15.27750 5.27925 0.43700 5.91400 1.78950 0.87175 23.02600 6.74700 2.88800
```

```
$ycenter
```

```
PMDCI THIOL CYP3A11 CYP4A10 Lpin Lpin1 GSTmu GSTpi2 S14 CYP4A14
-0.76725 -0.41100 -0.50825 -0.97975 -0.75325 -0.76475 -0.11900 0.22975 -0.80675 -0.99300
```

Qu' a-t-on envie de regarder?

- Les corrélations entre les acides gras et leurs composantes canoniques
- Les corrélations entre les expressions génétiques et leurs composantes canoniques
- Les corrélations entre les acides gras et les composantes canoniques « génétiques »
- Les corrélations entre les expressions génétiques et les composantes canoniques « lipidiques »

Qu' a-t-on envie de regarder?

- La part de variance des acides gras expliquée par les composantes canoniques
- La part de variance des expressions génétiques expliquée par les composantes canoniques

Qu' a-t-on envie de regarder?

- Le R^2 entre un acide gras et les composantes canoniques
- Le R^2 entre une expression génétique et les composantes canoniques

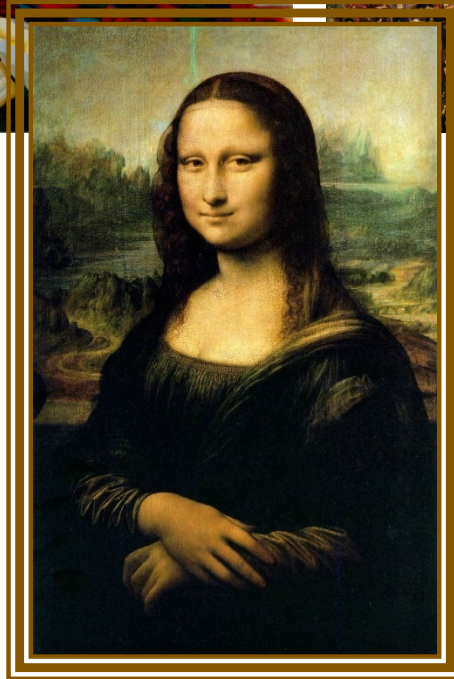
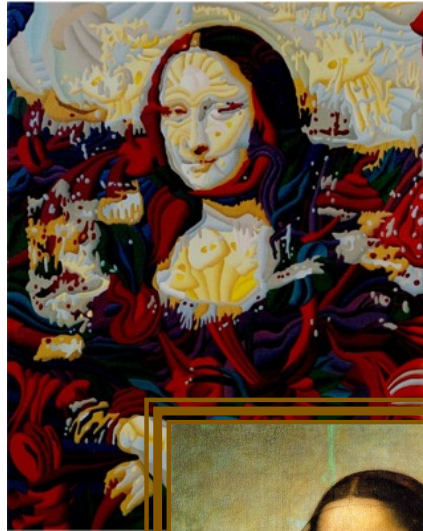
Qu' a-t-on envie de regarder?

$$G_1 = 0.51\text{PMDCI} + 0.63\text{THIOL} + \dots + 0.26\text{LPIN} - 0.27\text{LPIN1} + \dots - 0.30\text{CYP4A14}$$

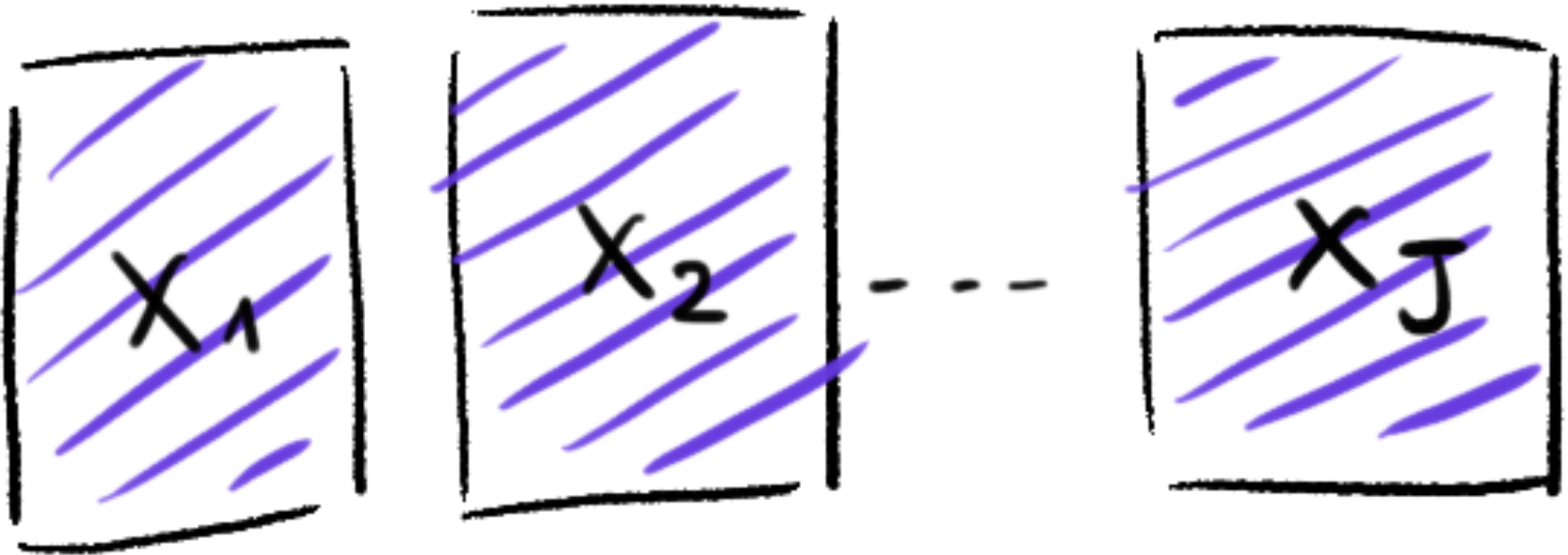
	PMDCI	THIOL	CYP3A11	CYP4A10	Lpin	Lpin1	GSTmu	GSTpi2	S14	CYP4A14
PMDCI	1.0000000	0.84318213	0.78800310	0.85333860	-0.15426020	-0.12132735	0.42444476	0.4422014	0.09117950	0.7509967
THIOL	0.8431821	1.00000000	0.73554530	0.79996380	0.07321187	0.09424437	0.56878570	0.3596621	0.33377479	0.6987517
CYP3A11	0.7880031	0.73554530	1.00000000	0.75508008	-0.01894254	-0.03396576	0.62005000	0.6041323	-0.03192741	0.7368760
CYP4A10	0.8533386	0.79996380	0.75508008	1.00000000	-0.22755111	-0.19530806	0.43563040	0.4159180	0.07638834	0.8853495
Lpin	-0.1542602	0.07321187	-0.01894254	-0.22755111	1.00000000	0.97166955	0.10963198	-0.1489248	0.57820562	-0.2886763
Lpin1	-0.1213273	0.09424437	-0.03396576	-0.19530806	0.97166955	1.00000000	0.06449885	-0.1234486	0.58591046	-0.2782659
GSTmu	0.4244448	0.56878570	0.62005000	0.43563040	0.10963198	0.06449885	1.00000000	0.4505130	0.08559840	0.5285176
GSTpi2	0.4422014	0.35966214	0.60413234	0.41591801	-0.14892482	-0.12344856	0.45051300	1.00000000	-0.27370381	0.4171278
S14	0.0911795	0.33377479	-0.03192741	0.07638834	0.57820562	0.58591046	0.08559840	-0.2737038	1.00000000	-0.1123210
CYP4A14	0.7509967	0.69875167	0.73687596	0.88534950	-0.28867628	-0.27826594	0.52851762	0.4171278	-0.11232101	1.0000000

$$r(\text{LPIN}, \text{LPIN1}) = 0.97$$

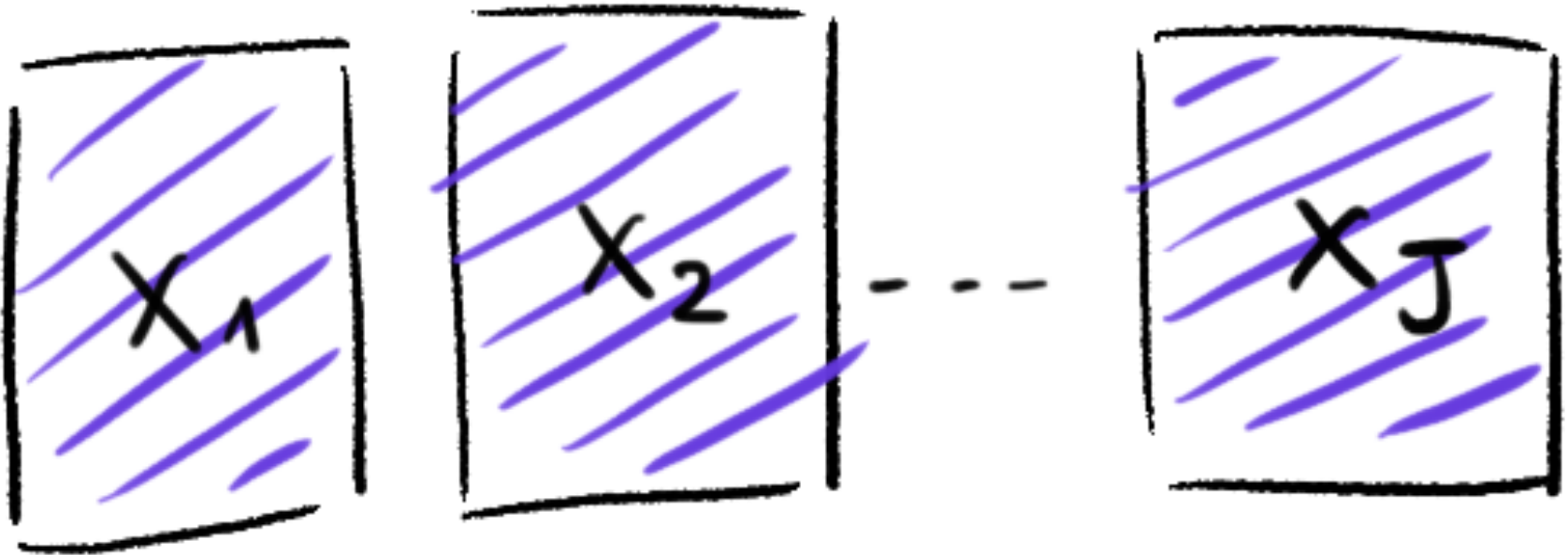
L'analyse canonique généralisée



L'analyse canonique généralisée

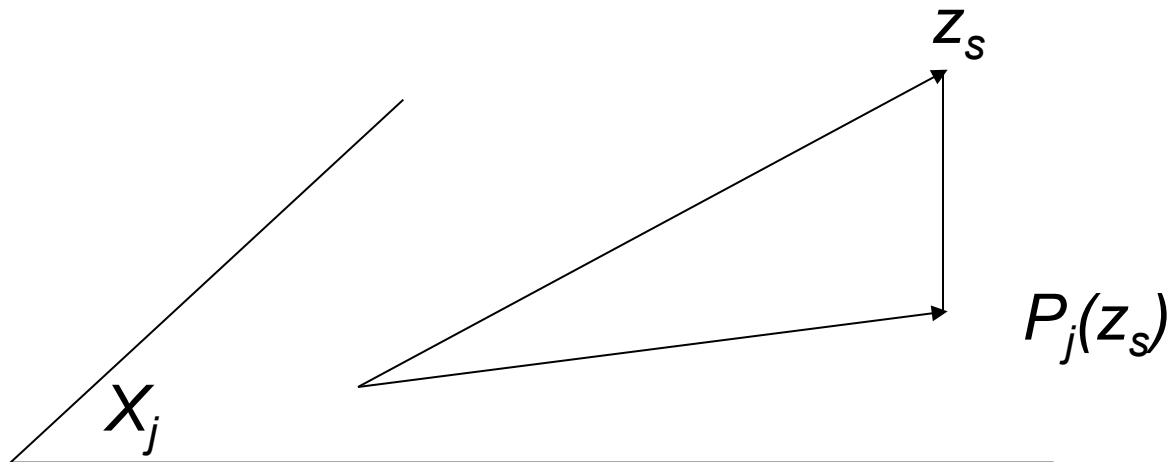


L'analyse canonique généralisée

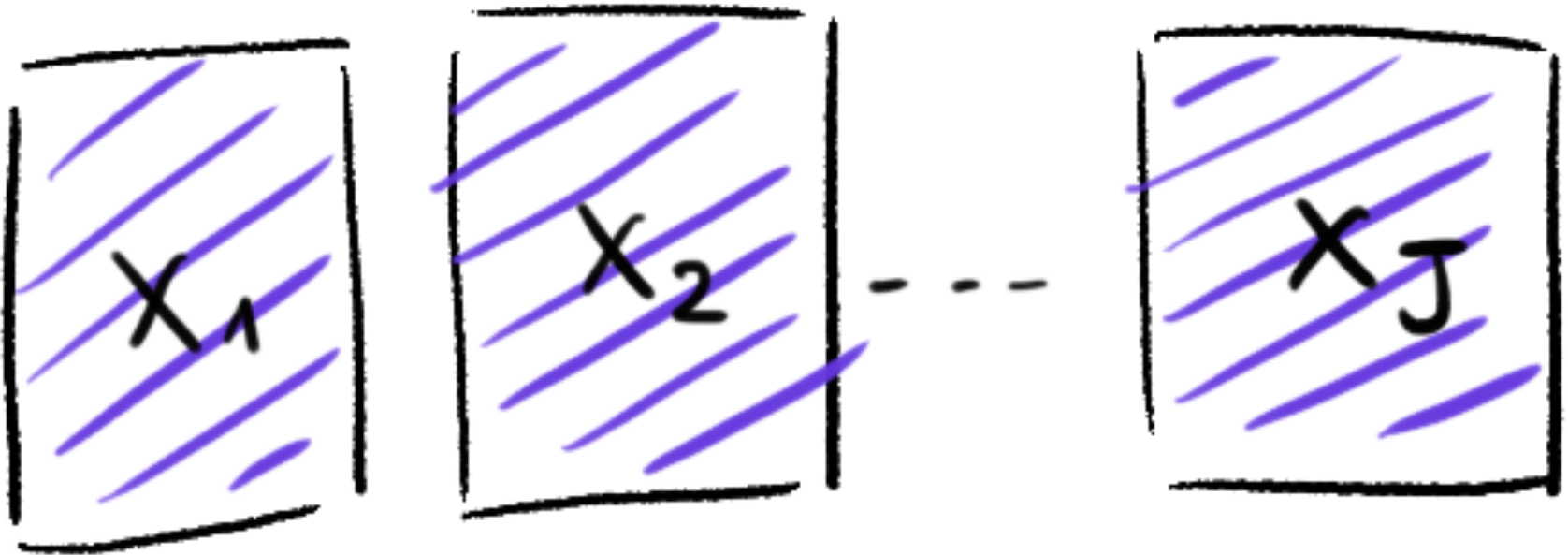


$$z_s / z_s \text{ maximise } \sum_j R^2(z_s, x_j)$$

Variables canoniques



L'analyse factorielle multiple



$$z_s / z_s \text{ maximise } \sum_j d_g(z_s, x_j)$$

Objectifs

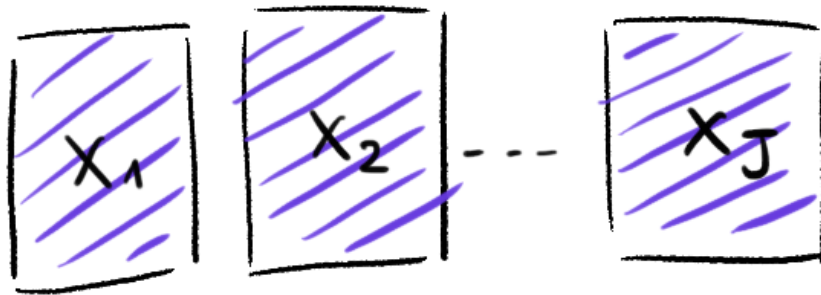
- ❑ Recherche de facteurs communs et représentant des directions de forte inertie
- ❑ Comparaison des principaux facteurs de variabilité
- ❑ Bilan des structures communes



Propriétés

- Elle équilibre l'influence de chacun des groupes
- Chaque variable du groupe j est pondérée par $1/\lambda_j$
- Aucun groupe ne peut engendrer à lui seul le premier axe
- Un groupe multidimensionnel contribue à un plus grand nombre d'axes qu'un groupe unidimensionnel

Propriétés



$$z_s / z_s \text{ maximise } \sum_j d_g(z_s, x_j)$$

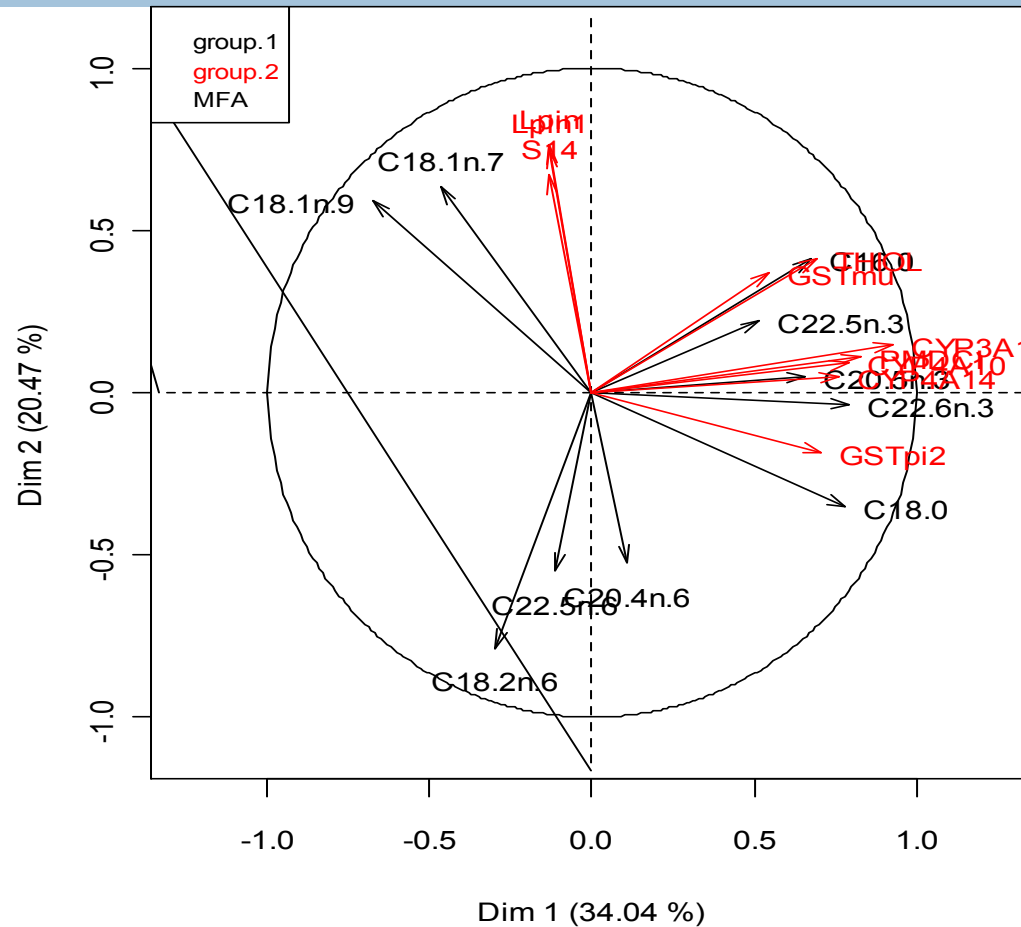
$$d_g(z, x_j) = \frac{1}{|x_j|} \sum_{k \in x_j} r^2(z, k)$$

$$d_g(z, x_j) = 1 \Leftrightarrow z = F_j$$

où F_j dirige le 1^{er} axe de $ACP(x_j)$

Représentation des variables

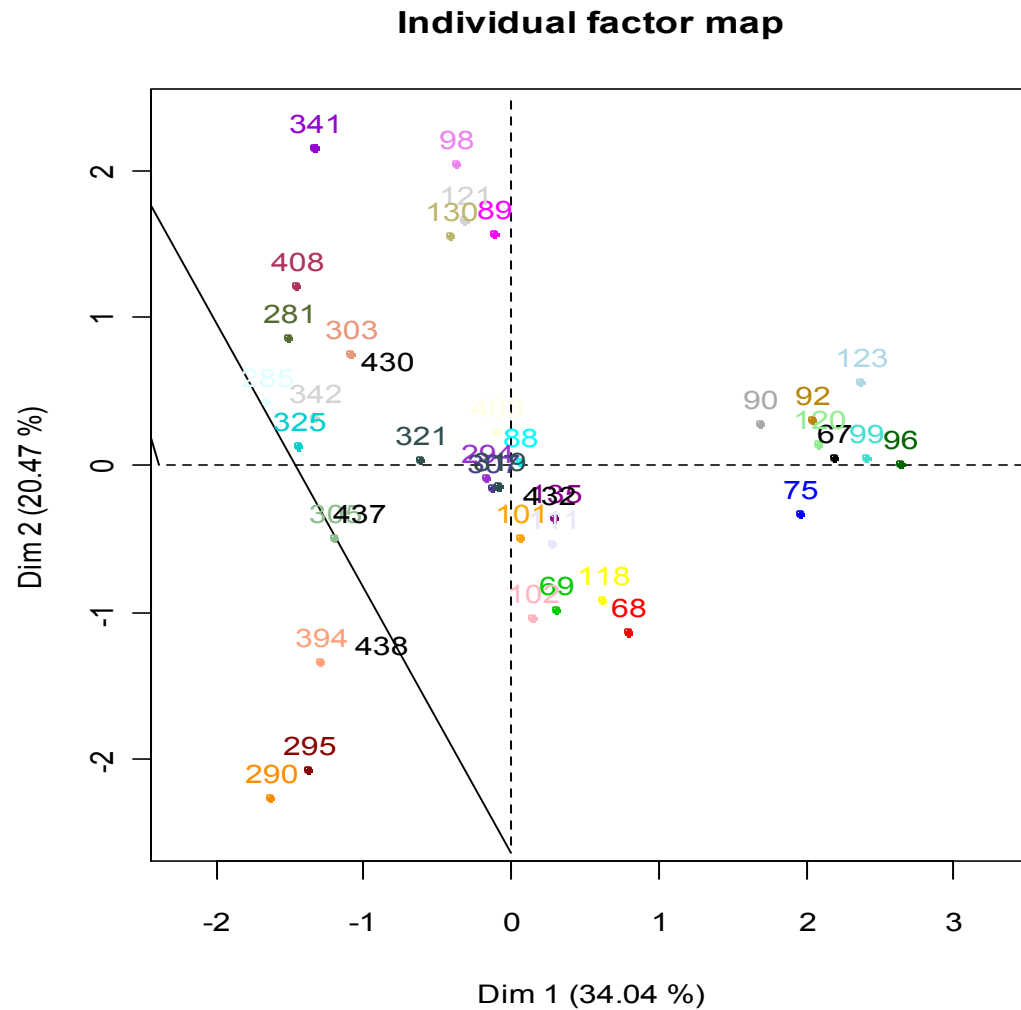
Correlation circle



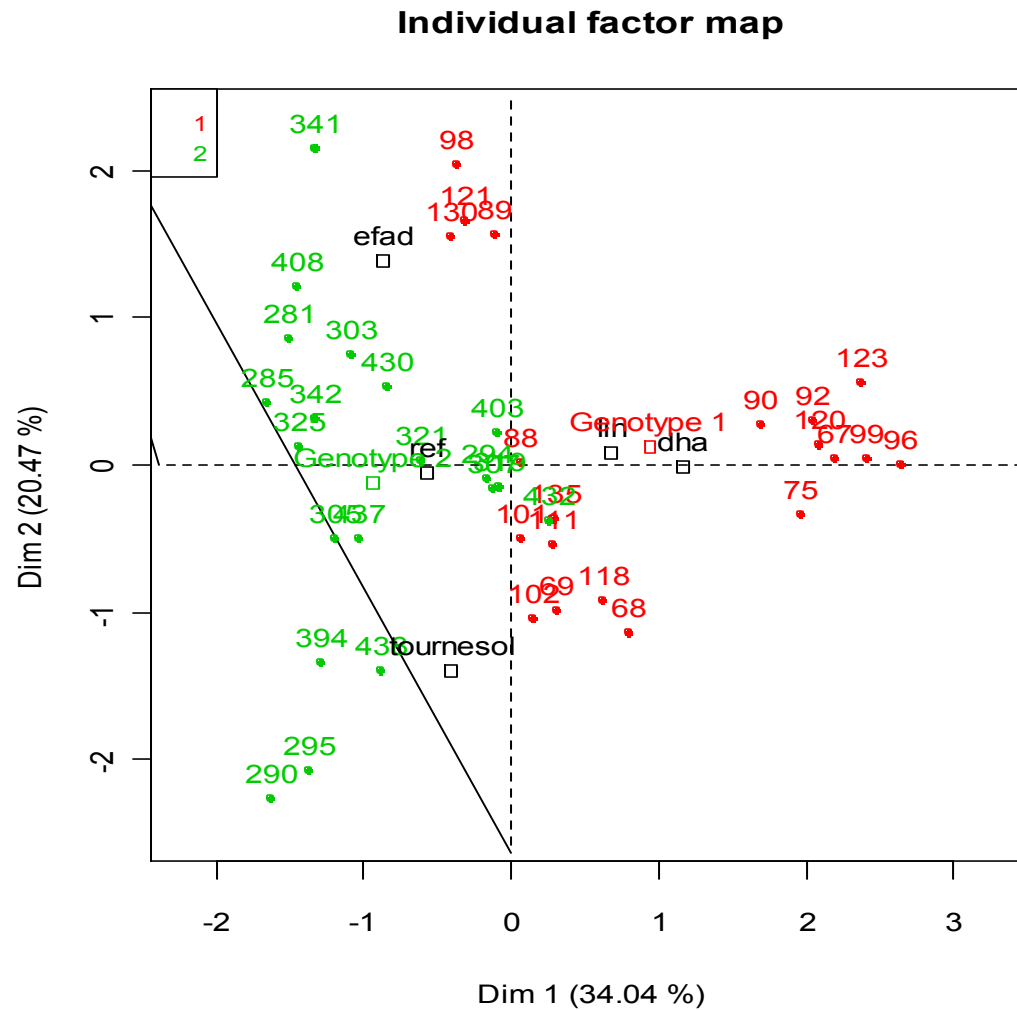
Représentation des individus

- Une représentation des individus caractérisés par l'ensemble des variables : **nuage des points moyens**

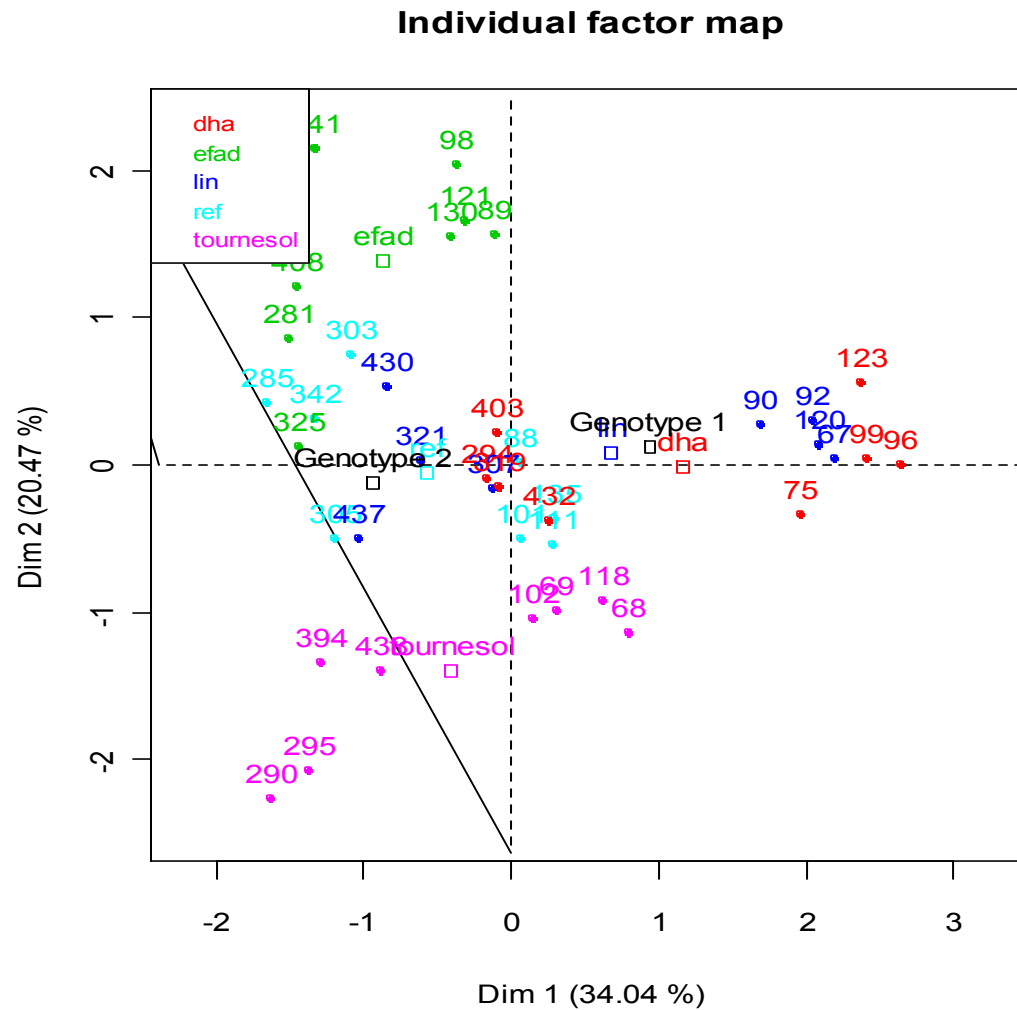
Représentation des individus



Représentation des individus



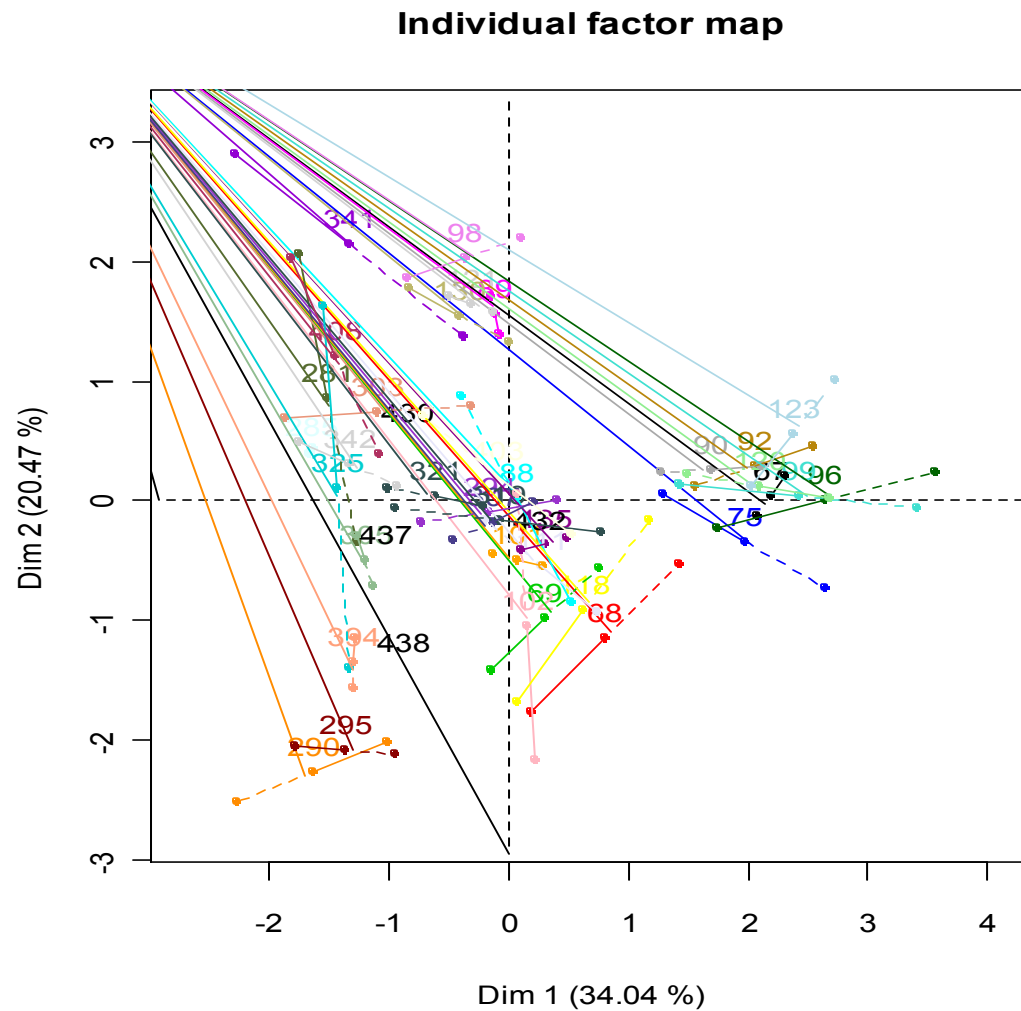
Représentation des individus



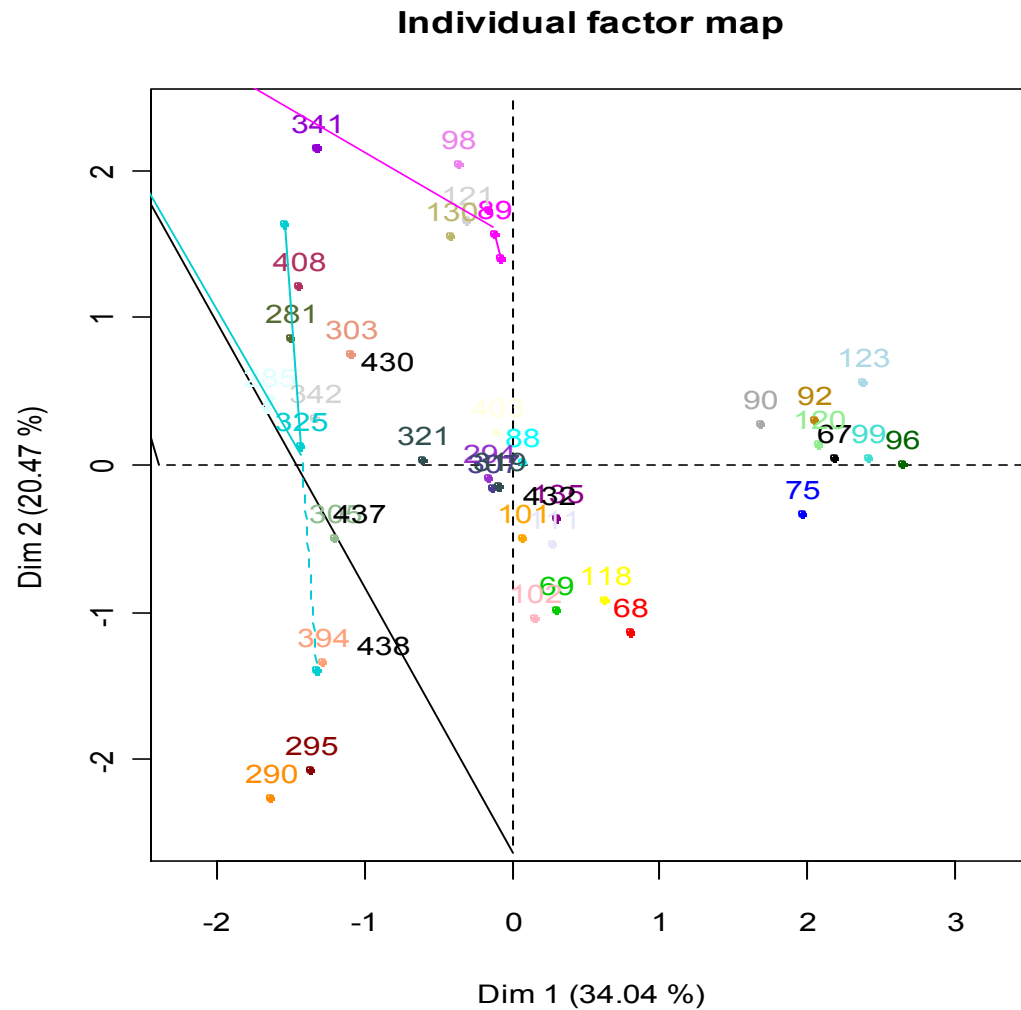
Représentation des individus

- Une représentation superposée des J nuages de points caractérisés chacun par un seul groupe de variables : **nuage des points partiels**

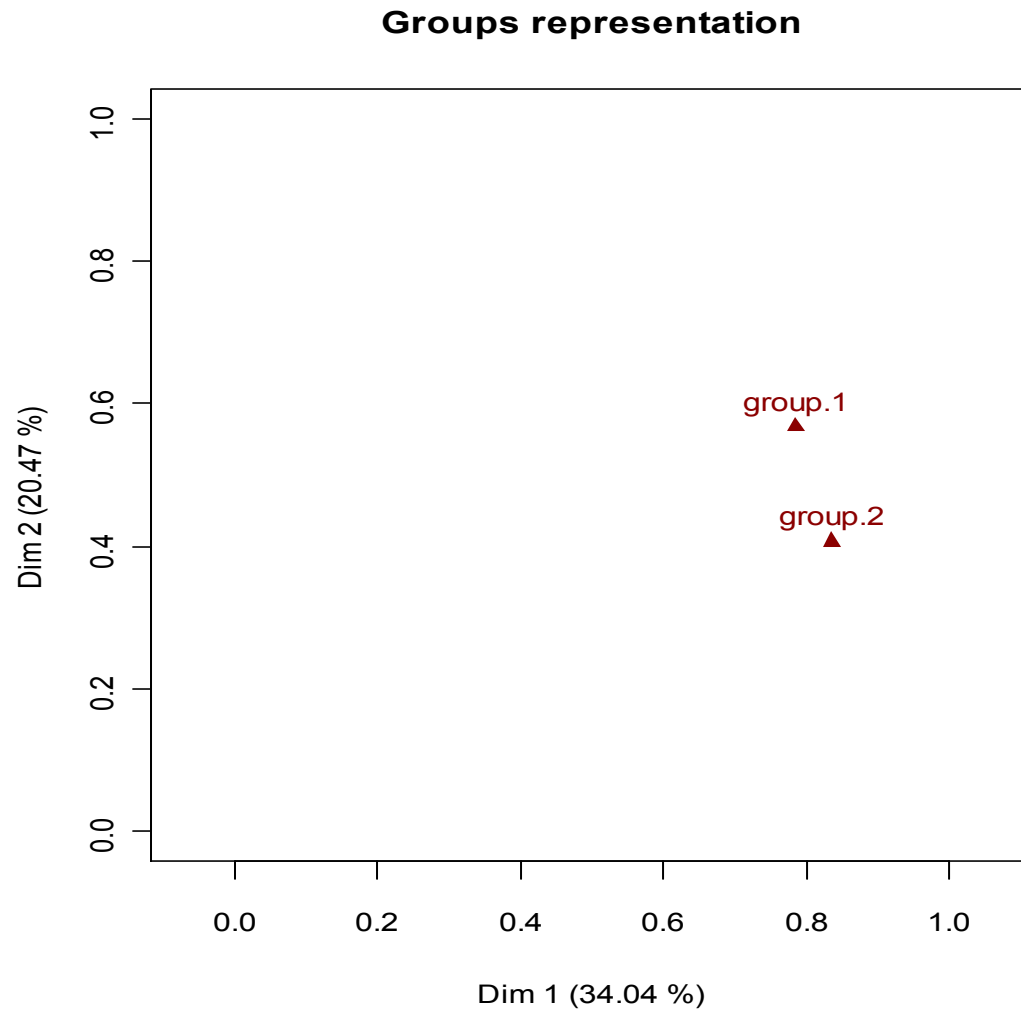
Représentation des individus partiels



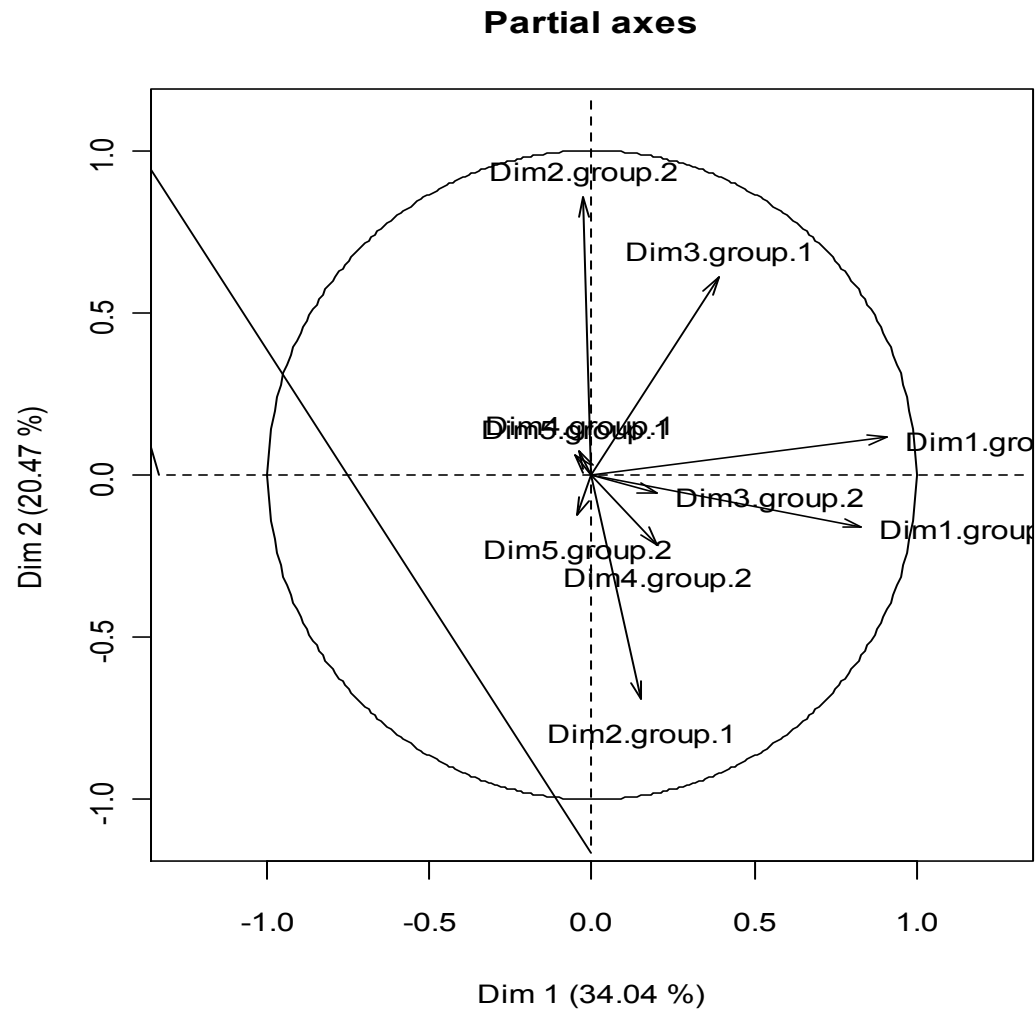
Représentation des individus



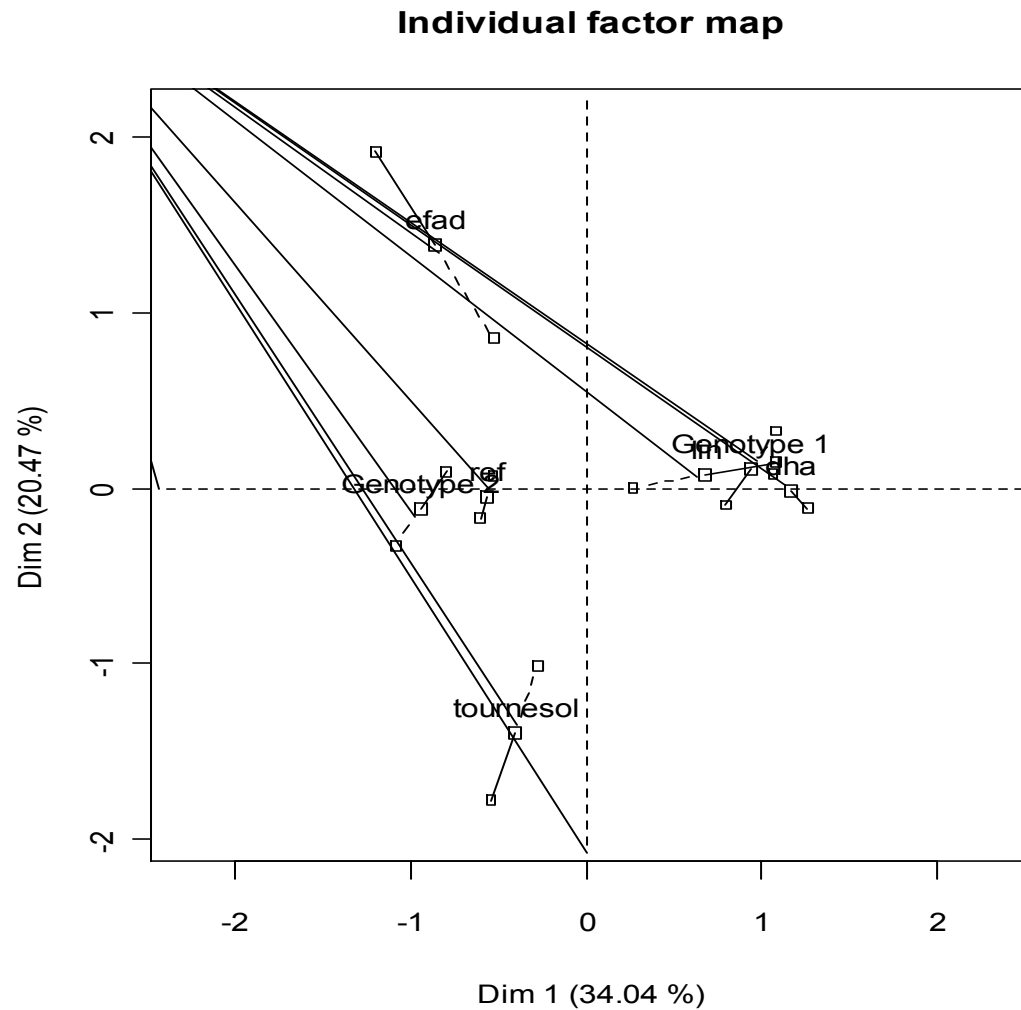
Représentation des groupes



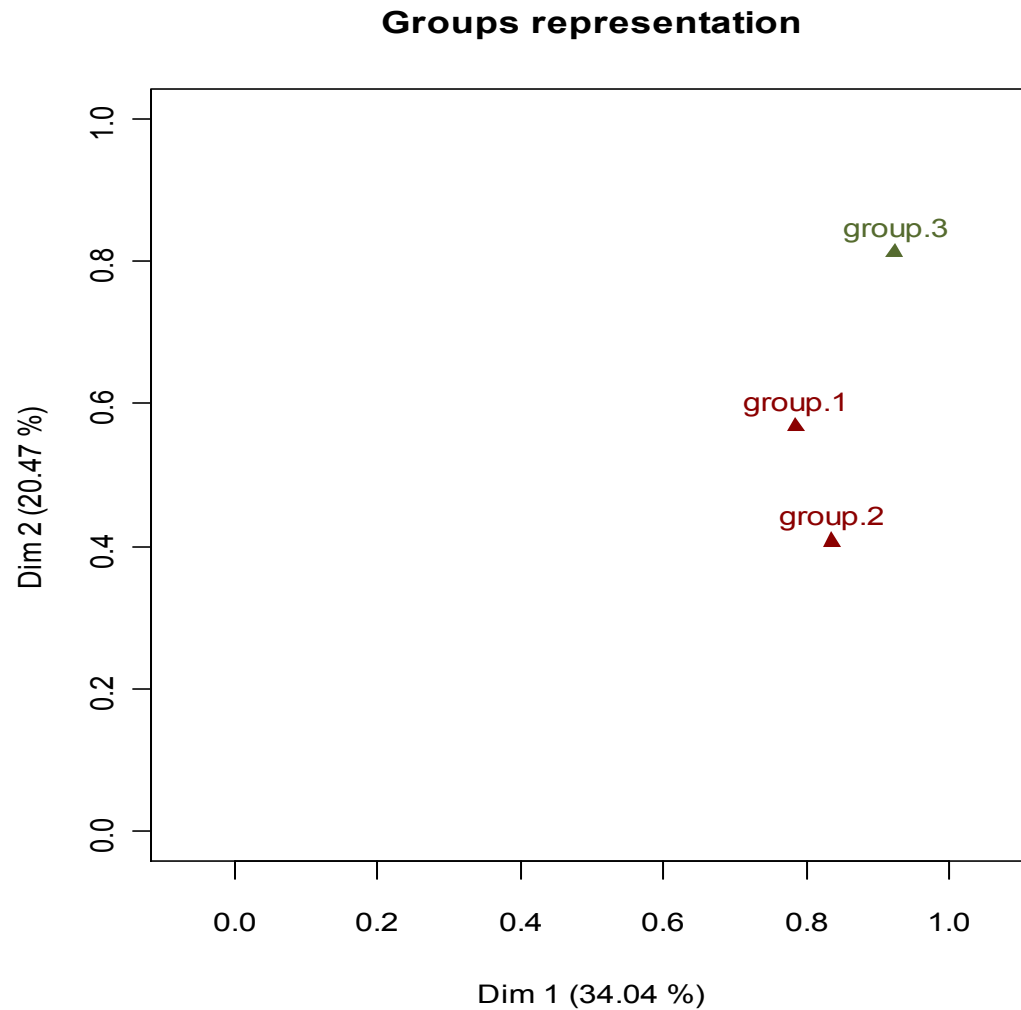
Bilan des structures communes



Gestion des variables illustratives



Gestion des groupes illustratifs



ADDING SUPPLEMENTARY INFORMATION IN AN “OMICS” FRAMEWORK

Bonus track

Annotations

Gene Ontology

- Cellular Component
- Molecular Function
- **Biological Process (BP)**

Genes could be grouped by GO BP terms

GO:0006928, cell motility

ANXA1
CALD1
EGFR
ENPP2
FN1
FPRL2
LSP1
MSN
PDPN
PLAUR
PRSS3
SAA2
SPINT2
TNFRSF12A
VEGF
WASF1
YARS

GO:0009966, regulation of
signal transduction

CASP1
EDG2
F2R
HCLS1
HMOX1
IGFBP3
IQSEC1
LYN
MALT1
TCF7L1
TNFAIP3
TRIO
VEGF
YWHAG
YWHAH

GO:0051276, chromosome
organization and biogenesis

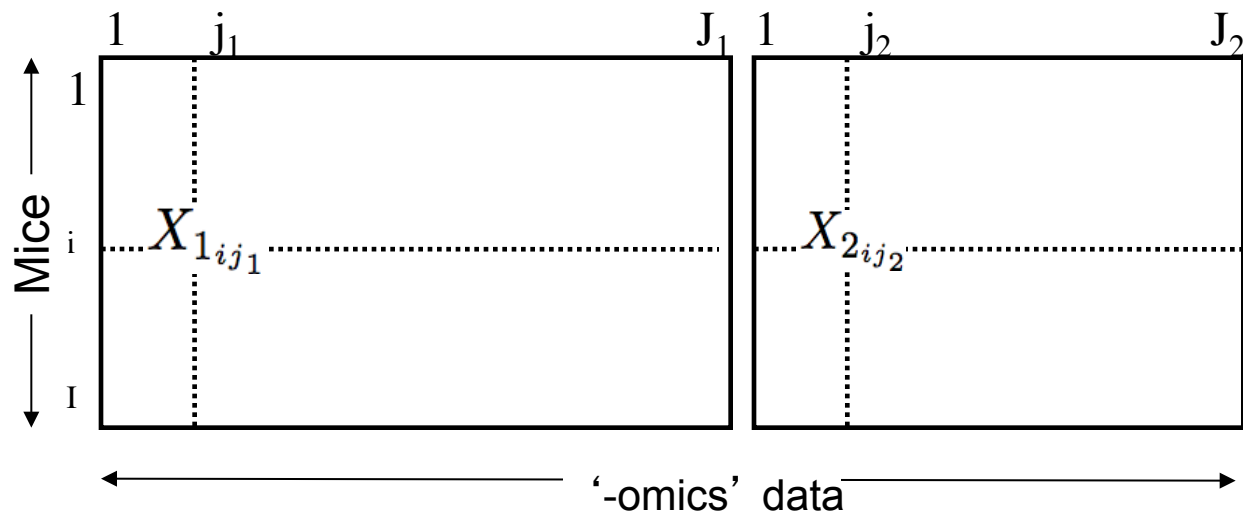
CBX6
NUSAP1
PCOLN3
PTTG1
SUV39H1
TCF7L1
TSPYL1

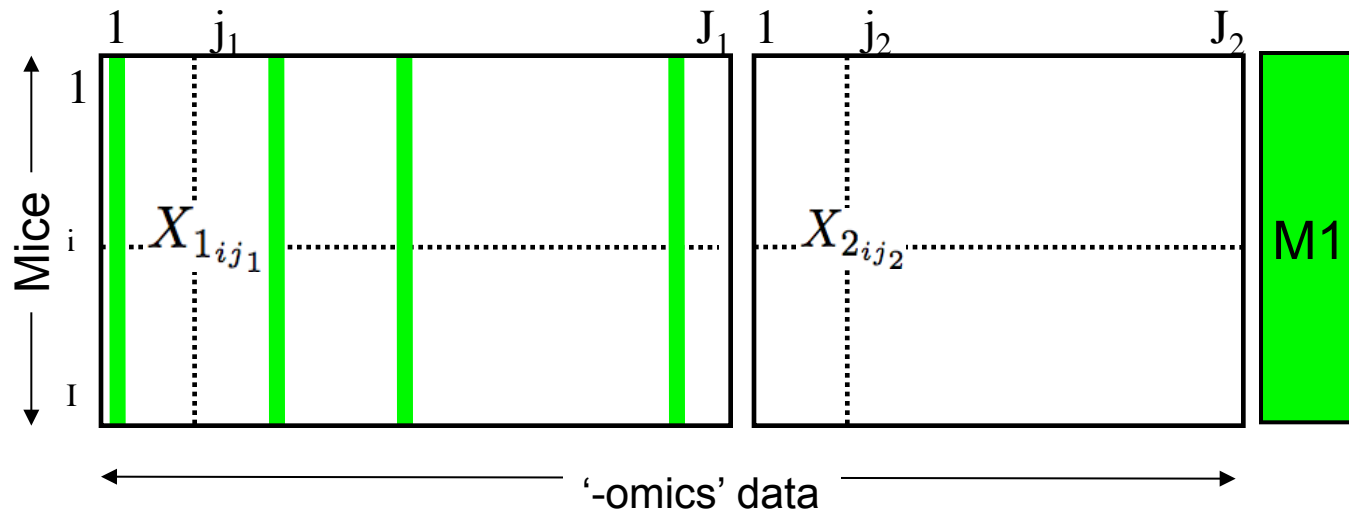
Annotations

HUGO_2_GO.pl 1.0 (2009)

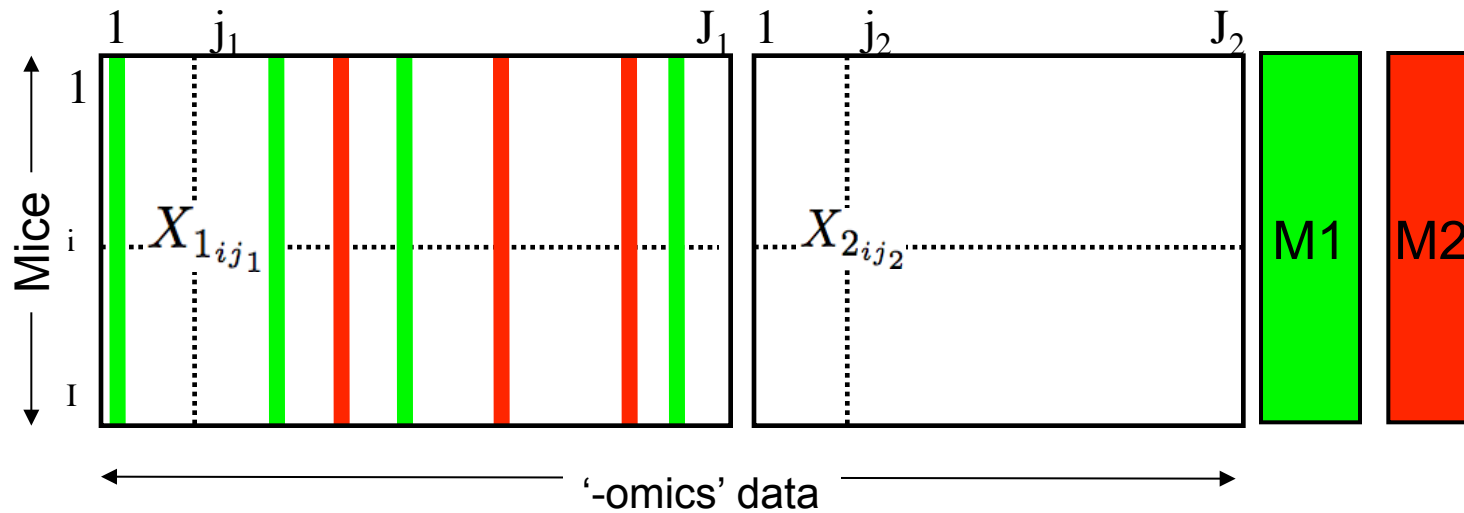
120 HUGO name read from file...

ACAT1	GO:0008152	metabolic process	P
ACAT1	GO:0006508	proteolysis	P
ACAT1	GO:0008203	cholesterol metabolic process	P
ACAT1	GO:0008150	biological_process	P
ACAT2	GO:0008152	metabolic process	P
ACAT2	GO:0006629	lipid metabolic process	P
ACAT2	GO:0006508	proteolysis	P
ACAT2	GO:0008150	biological_process	P
ACBP	GO:0006631	fatty acid metabolic process	P
ACC1	GO:0006606	protein import into nucleus	P
ACC1	GO:0008152	metabolic process	P
ACC1	GO:0006633	fatty acid biosynthetic process	P
ACC1	GO:0017001	antibiotic catabolic process	P
ACC1	GO:0009058	biosynthetic process	P
ACC1	GO:0006412	translation	P
ACC1	GO:0006417	regulation of translation	P
ACC1	GO:0006998	nuclear envelope organization	P
ACC1	GO:0008610	lipid biosynthetic process	P
ACC1	GO:0043284	biopolymer biosynthetic process	P
ACC2	GO:0006633	fatty acid biosynthetic process	P
ACC2	GO:0008152	metabolic process	P
ACC2	GO:0005975	carbohydrate metabolic process	P
ACC2	GO:0030245	cellulose catabolic process	P
ALDH3	GO:0008152	metabolic process	P
ALDH3	GO:0055114	oxidation reduction	P
AOX	GO:0007585	respiratory gaseous exchange	P
AOX	GO:0022900	electron transport chain	P
AOX	GO:0055114	oxidation reduction	P
AOX	GO:0006066	cellular alcohol metabolic process	P
AOX	GO:0006810	transport	P
BACT	GO:0009058	biosynthetic process	P
CACP	GO:0006508	proteolysis	P
CACP	GO:0030163	protein catabolic process	P
CAR1	GO:0019547	arginine catabolic process to ornithine	P
CAR1	GO:0000050	urea cycle	P
CAR1	GO:0006525	arginine metabolic process	P
CAR1	GO:0006950	response to stress	P
CAR1	GO:0009415	response to water	P

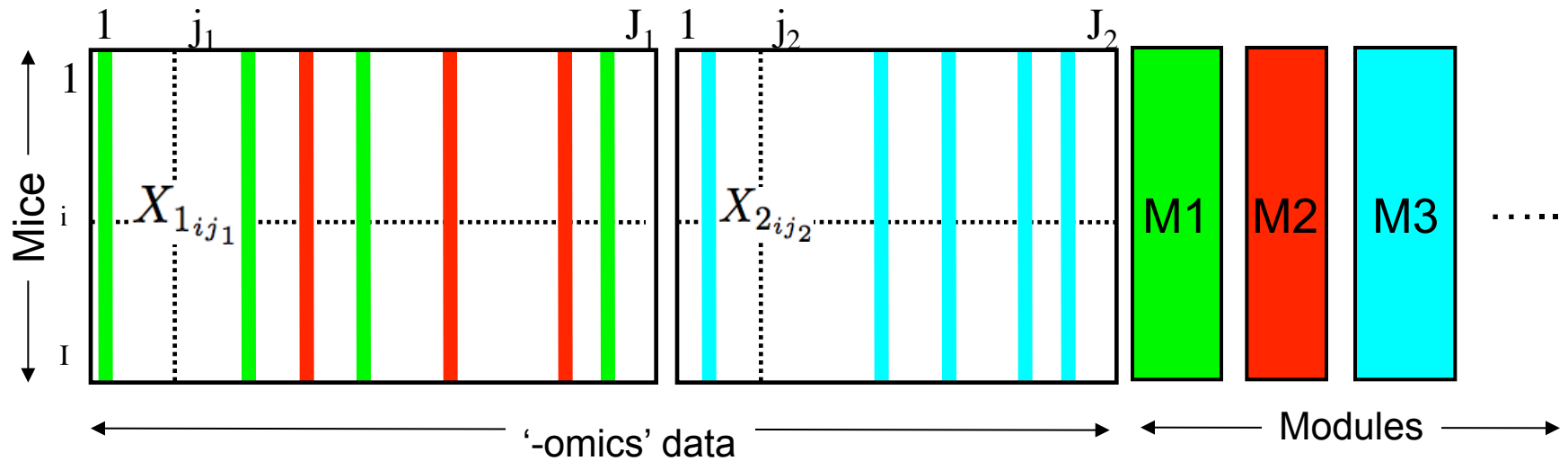




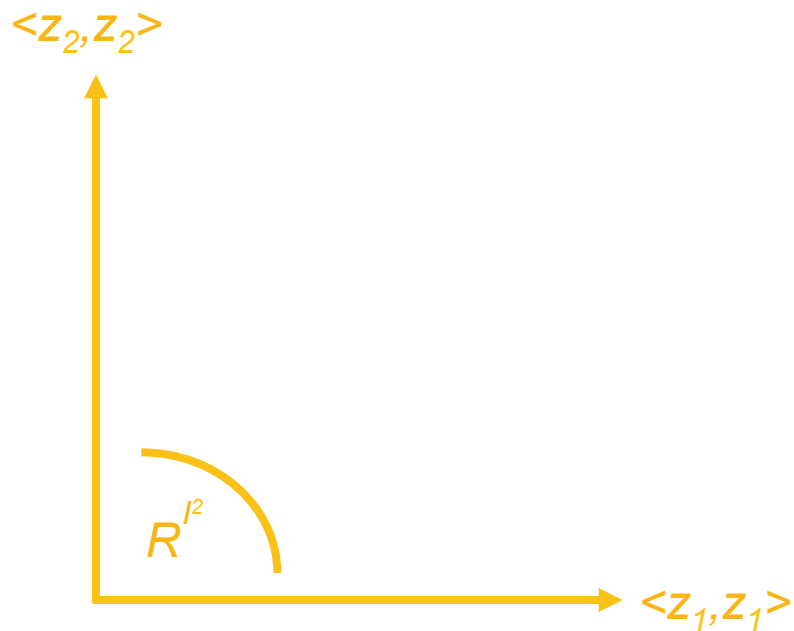
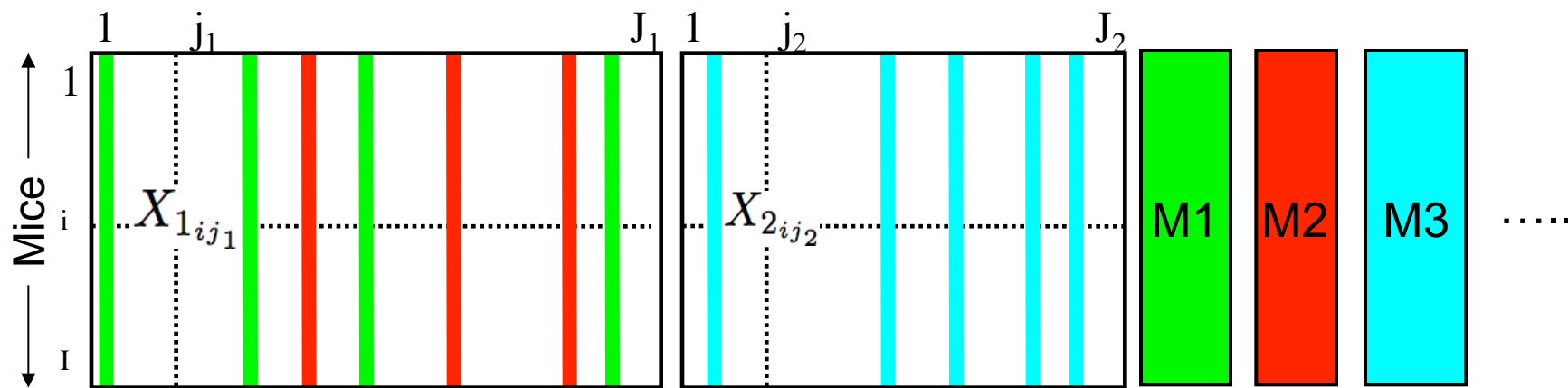
=> Integration of the modules as groups of supplementary variables

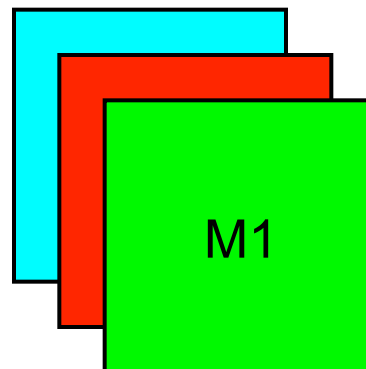
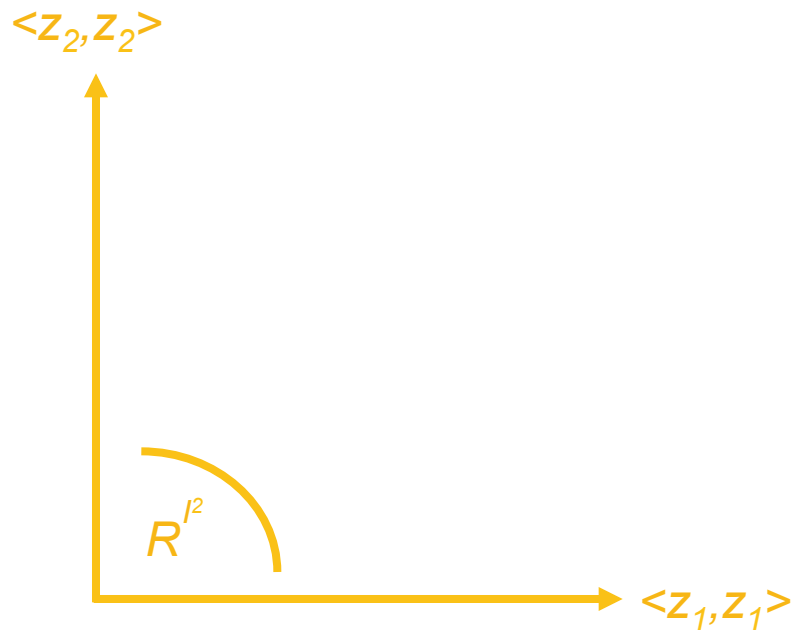
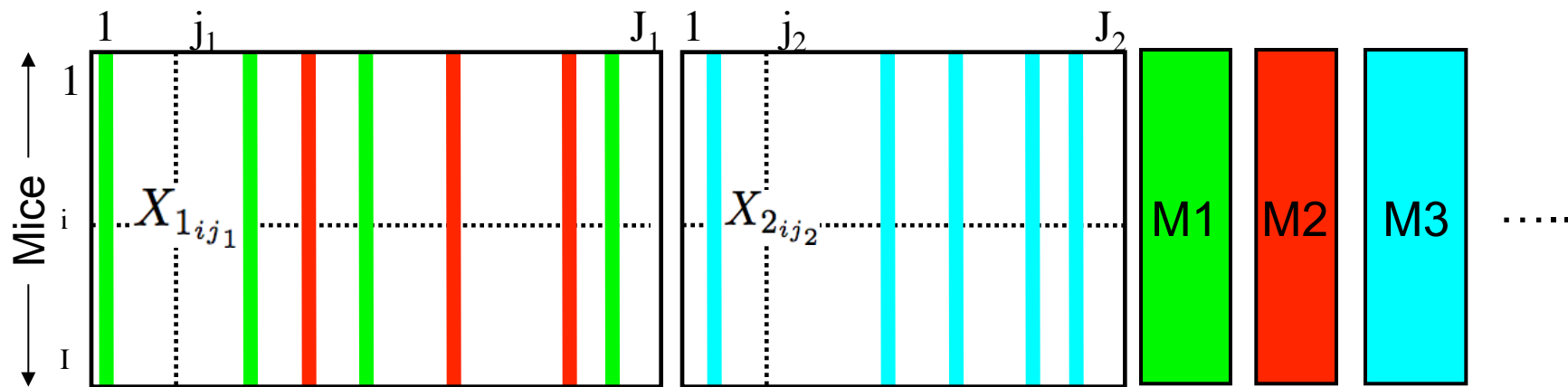


=> Integration of the modules as groups of supplementary variables

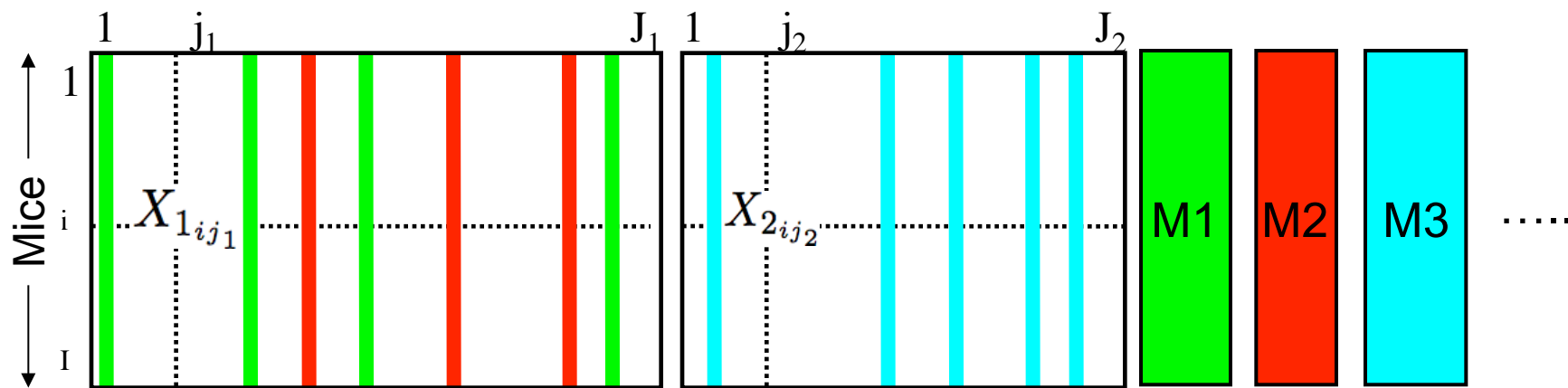


=> Integration of the modules as groups of supplementary variables





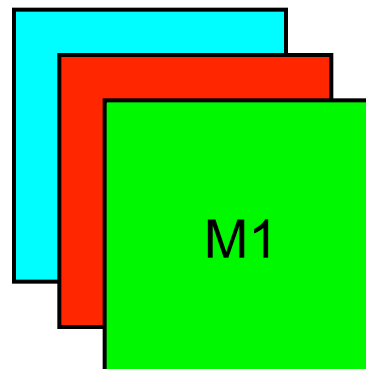
Scalar products matrices
between mice



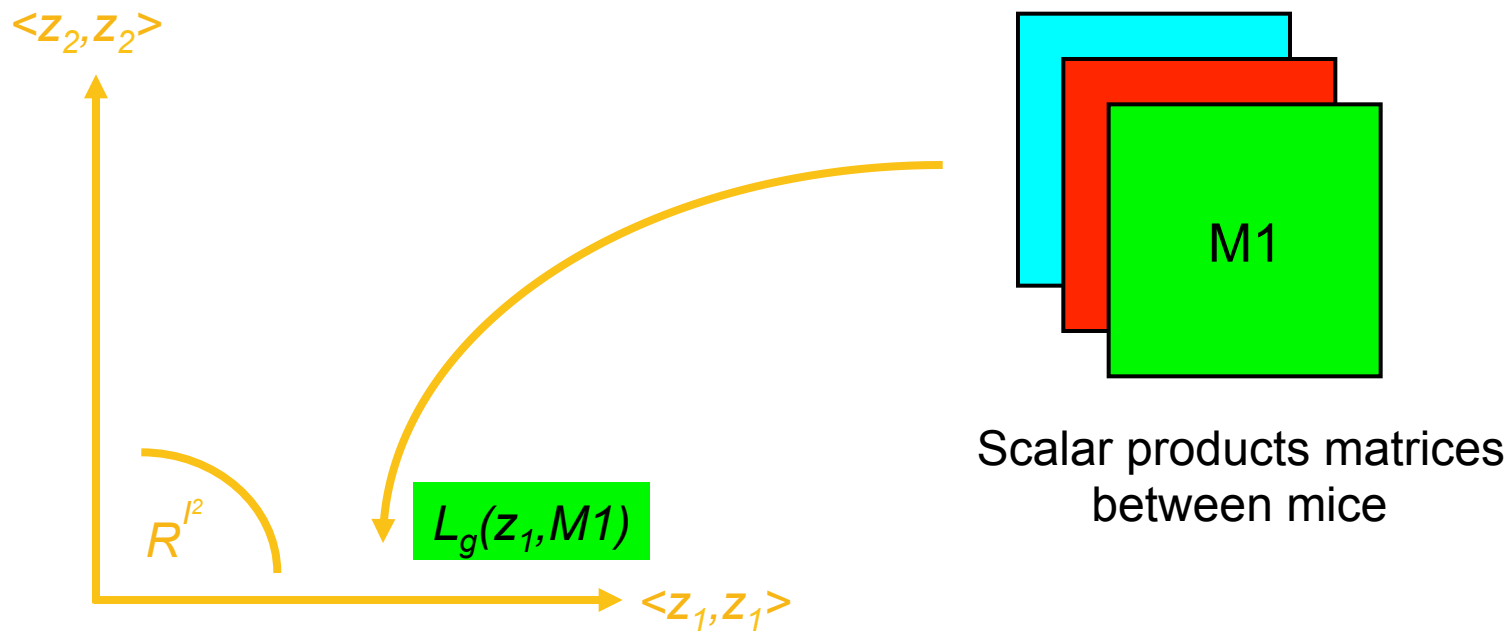
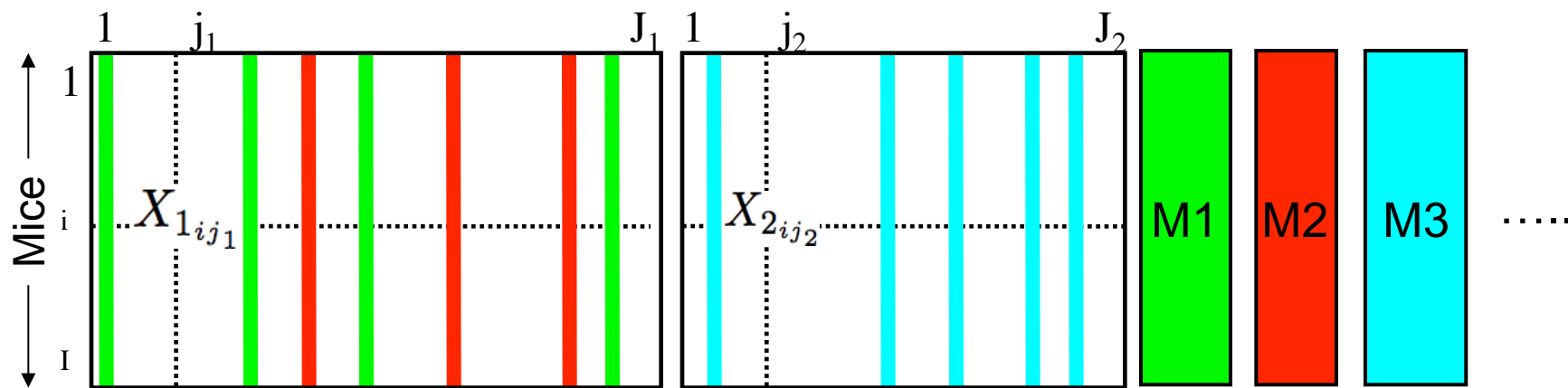
$\langle Z_2, Z_2 \rangle$



R^{I^2}



Scalar products matrices
between mice



“THANK YOU FOR BEING
HERE”

[http://www.ted.com/talks/
john_francis_walks_the_earth.html](http://www.ted.com/talks/john_francis_walks_the_earth.html)