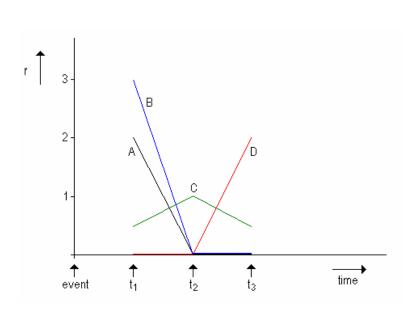
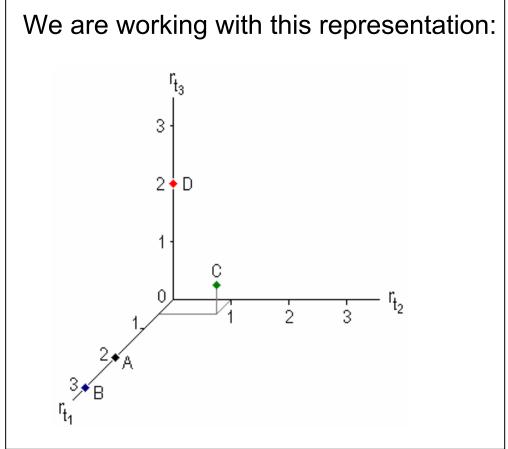
Some Mathematical Backgrounds

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gene	t ₁	t_2	t ₃
Α	2	0	0
В	3	0	0
С	0.5	1	0.5
D	0	0	2

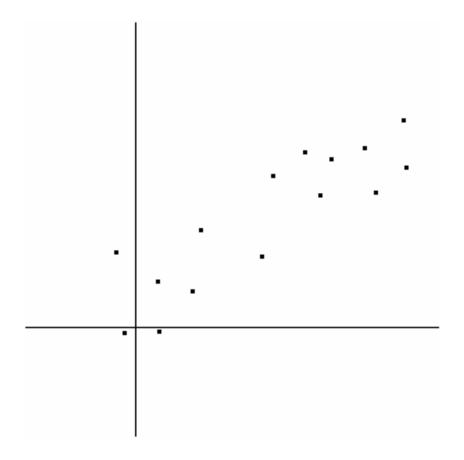
Principal Component Analysis (PCA):

Tool for screening data:

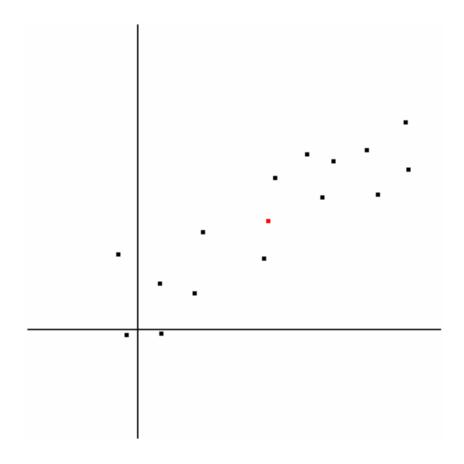
- are there strange or unusual aspects?
- do the data have a normal distribution?
- are there outliers?

Transformation of the data:

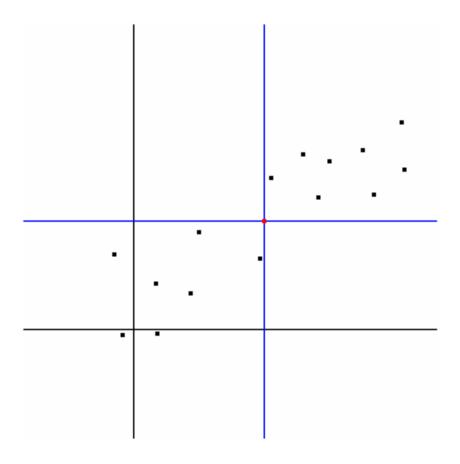
- into new set of variables (principal components)
- which are usually not interpretable
- first pc accounts for as much of the variability as possible
- and each succeeding pc as much of the remaining variability



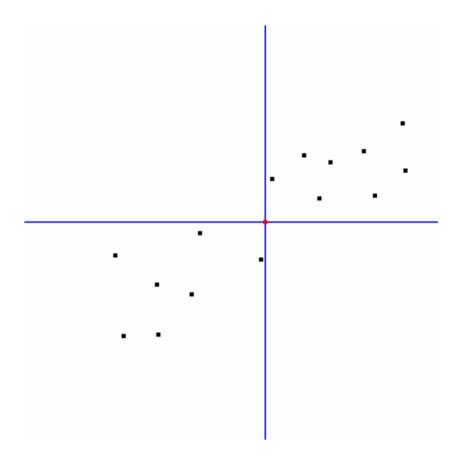
For a given data set ...



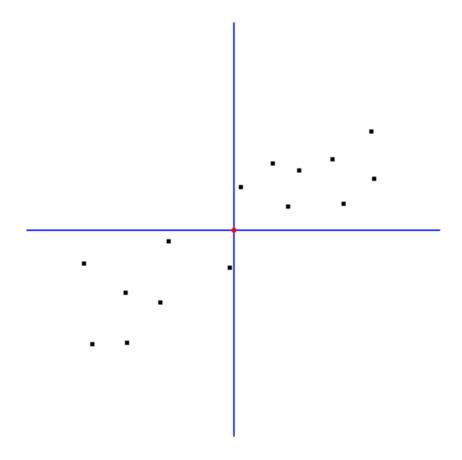
calculate the centroid (='mean in all directions') ...

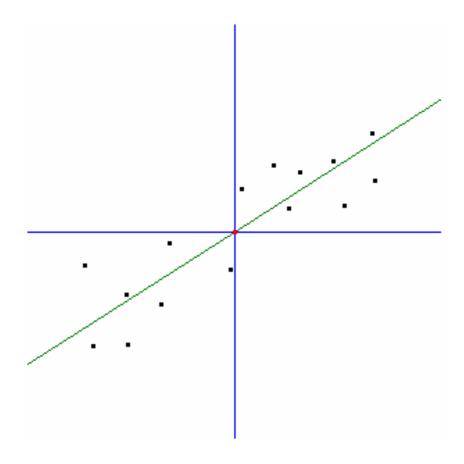


shift the grid to the centroid ...

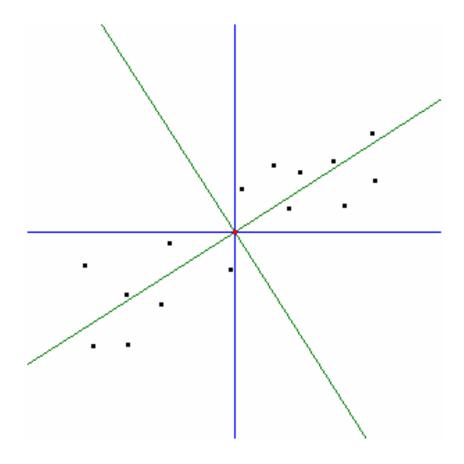


take this as our new coordinate system ...

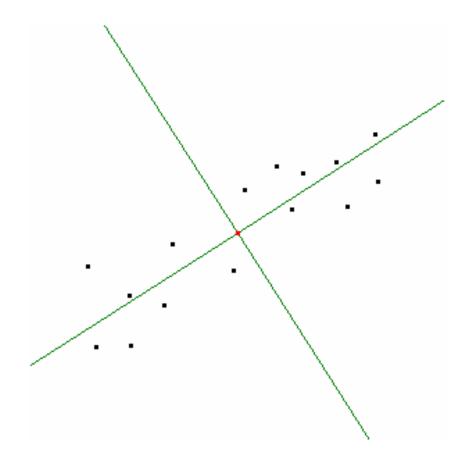




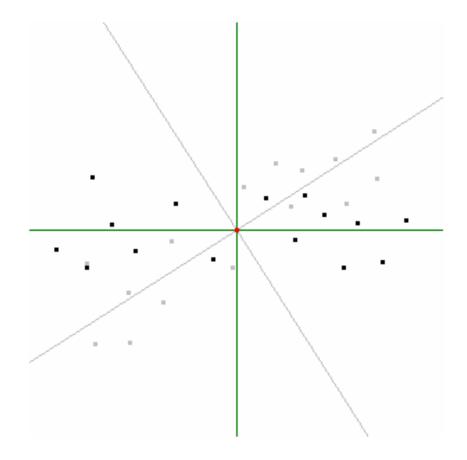
calculate the direction in which the variance is maximal ...



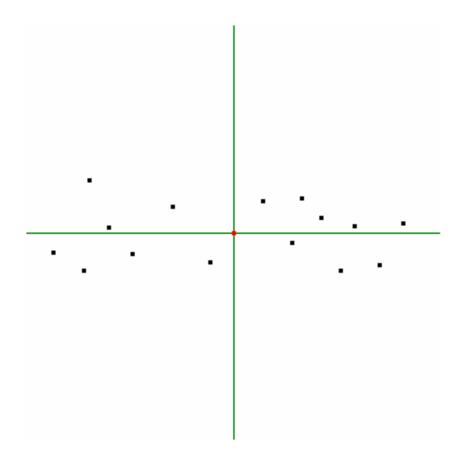
and repeat this for each next perpendicular axis ...



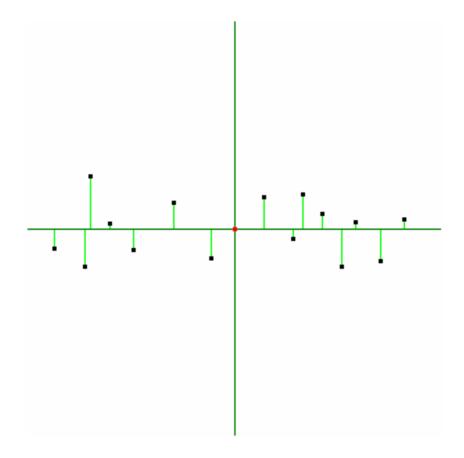
leaving us with a rotated grid ...



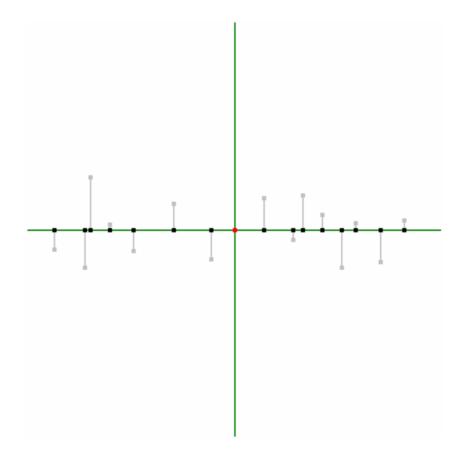
which we can rotate to a 'normal' position ...



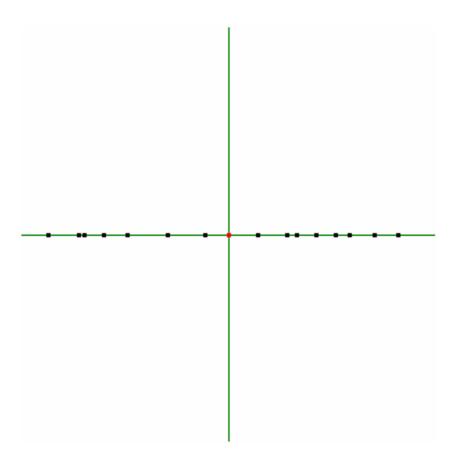
showing us maximal variance.



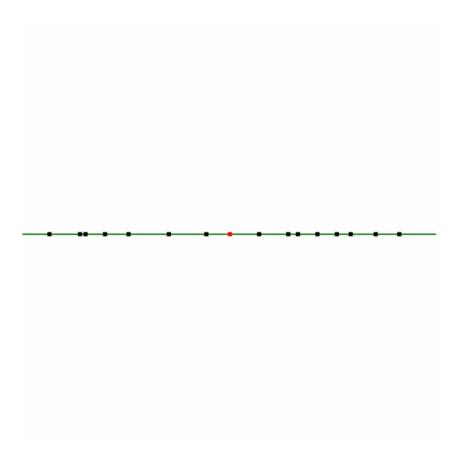
We can also use this to reduce the complexity of the data set ...



by eliminating a number of axis by projection of the points.

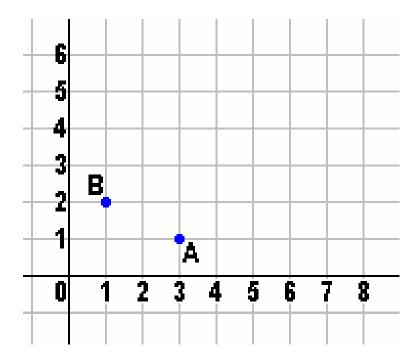


in this example moving from two ...

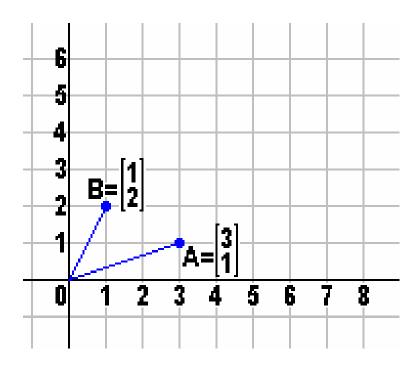


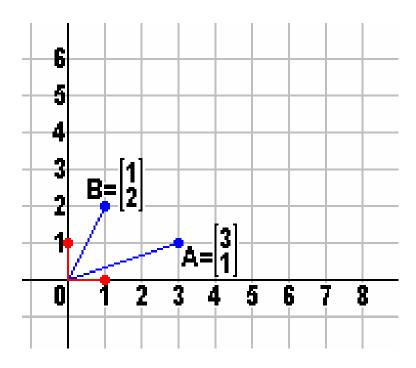
to one dimensional data points.

Now, what has happened?

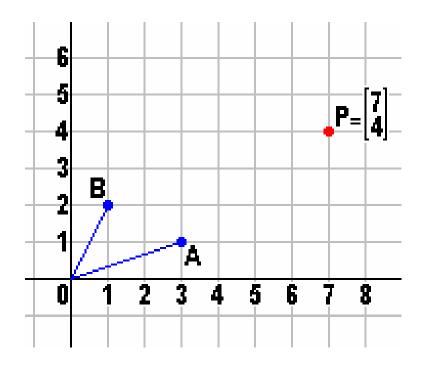


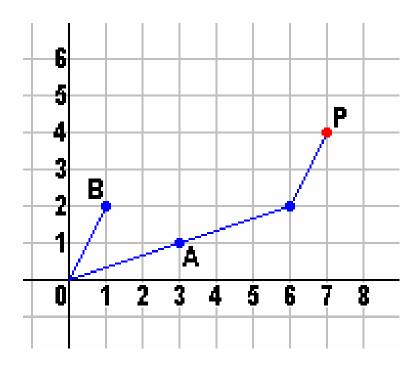
Remember the notations from linear algebra...



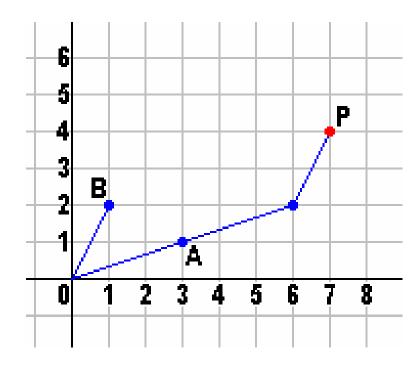


$$A = 3 \bullet \begin{bmatrix} 1 \\ 0 \end{bmatrix} + 1 \bullet \begin{bmatrix} 0 \\ 1 \end{bmatrix} = \begin{bmatrix} 3 \\ 0 \end{bmatrix} + \begin{bmatrix} 0 \\ 1 \end{bmatrix} = \begin{bmatrix} 3 \\ 1 \end{bmatrix}$$



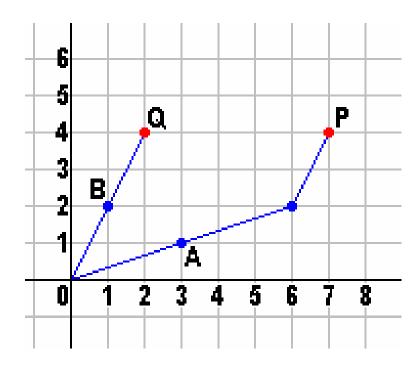


$$\mathbf{p} = 2 \bullet \mathbf{a} + 1 \bullet \mathbf{b}$$

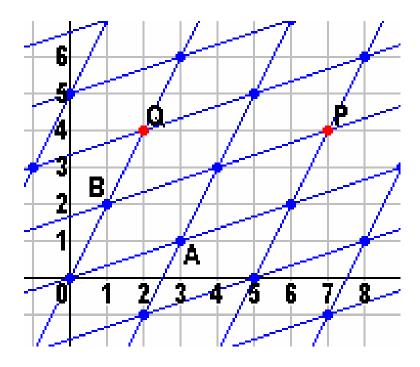


$$\mathbf{p} = 2 \bullet \mathbf{a} + 1 \bullet \mathbf{b}$$

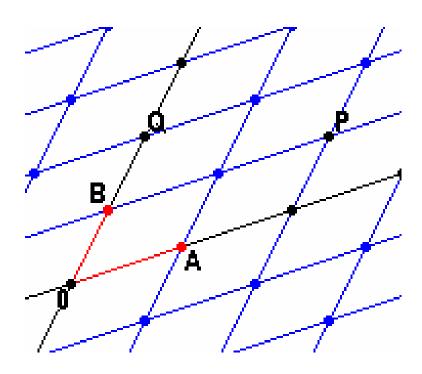
$$\mathbf{p} = 2 \bullet \begin{bmatrix} 3 \\ 1 \end{bmatrix} + 1 \bullet \begin{bmatrix} 1 \\ 2 \end{bmatrix} = \begin{bmatrix} 2 \bullet 3 + 1 \bullet 1 \\ 2 \bullet 1 + 1 \bullet 2 \end{bmatrix} = \begin{bmatrix} 7 \\ 4 \end{bmatrix}$$



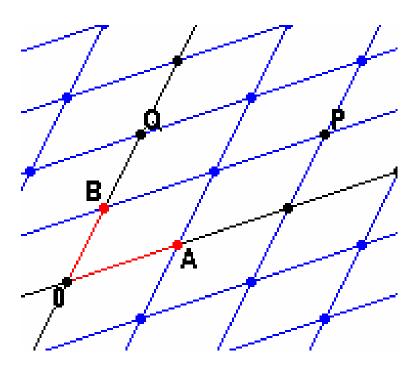
$$\mathbf{q} = 0 \bullet \mathbf{a} + 2 \bullet \mathbf{b}$$



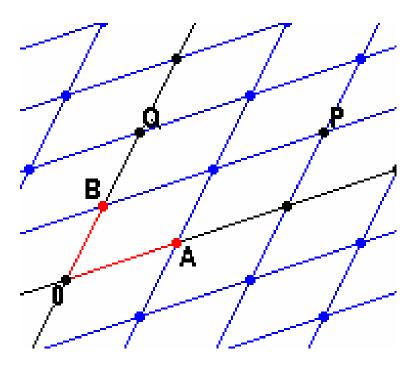
So, we can express each point in terms of A and B ...



which form another base for our grid.

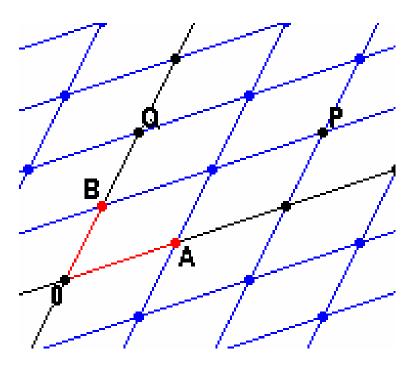


$$\mathbf{v}' = \begin{bmatrix} \mathbf{u} \\ \mathbf{w} \end{bmatrix} \rightarrow \mathbf{v} = \mathbf{u} \bullet \begin{bmatrix} 3 \\ 1 \end{bmatrix} + \mathbf{w} \bullet \begin{bmatrix} 1 \\ 2 \end{bmatrix} = \begin{bmatrix} 3 & 1 \\ 1 & 2 \end{bmatrix} \bullet \begin{bmatrix} \mathbf{u} \\ \mathbf{w} \end{bmatrix} = \begin{bmatrix} 3 \bullet \mathbf{u} + 1 \bullet \mathbf{w} \\ 1 \bullet \mathbf{u} + 2 \bullet \mathbf{w} \end{bmatrix}$$



$$\mathbf{v}' = \begin{bmatrix} \mathbf{u} \\ \mathbf{w} \end{bmatrix} \rightarrow \mathbf{v} = \mathbf{u} \bullet \begin{bmatrix} 3 \\ 1 \end{bmatrix} + \mathbf{w} \bullet \begin{bmatrix} 1 \\ 2 \end{bmatrix} = \begin{bmatrix} 3 & 1 \\ 1 & 2 \end{bmatrix} \bullet \begin{bmatrix} \mathbf{u} \\ \mathbf{w} \end{bmatrix} = \begin{bmatrix} 3 \bullet \mathbf{u} + 1 \bullet \mathbf{w} \\ 1 \bullet \mathbf{u} + 2 \bullet \mathbf{w} \end{bmatrix}$$

$$\mathbf{v} = \mathbf{A} \bullet \mathbf{v}'$$

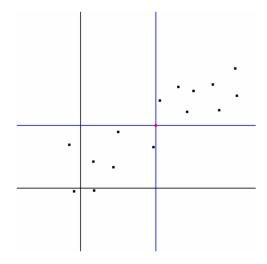


$$\mathbf{v}' = \begin{bmatrix} \mathbf{u} \\ \mathbf{w} \end{bmatrix} \rightarrow \mathbf{v} = \mathbf{u} \bullet \begin{bmatrix} 3 \\ 1 \end{bmatrix} + \mathbf{w} \bullet \begin{bmatrix} 1 \\ 2 \end{bmatrix} = \begin{bmatrix} 3 & 1 \\ 1 & 2 \end{bmatrix} \bullet \begin{bmatrix} \mathbf{u} \\ \mathbf{w} \end{bmatrix} = \begin{bmatrix} 3 \bullet \mathbf{u} + 1 \bullet \mathbf{w} \\ 1 \bullet \mathbf{u} + 2 \bullet \mathbf{w} \end{bmatrix}$$

$$\mathbf{v} = \mathbf{A} \bullet \mathbf{v}'$$
 $\mathbf{v}' = \mathbf{A}^{-1} \bullet \mathbf{v}'$



PCA step 1: moving the grid



	x = time1	y = time2
gene A	4	2
gene B	0	1
gene C	8	7
gene D	2	2
gene E	6	3

\sim
2
1
7
2
3

 $\mu_2 = 3$

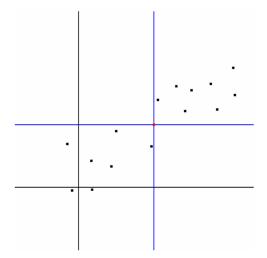
	x- μ ₁	y- μ ₂
gene A	4-4	2-3
gene B	0-4	1-3
gene C	8-4	7-3
gene D	2-4	2-3
gene E	6-4	3-3

 $\mu_2 = 3$

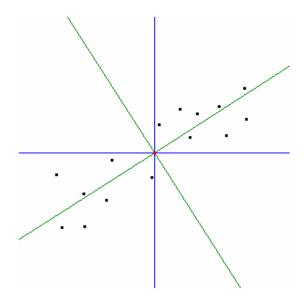
x- μ ₁	y-μ ₂
0	-1
-4	-2
4	4
-2	-1
2	0
	0 -4 4 -2

 $\mu_2 = 3$

x'=x-μ ₁	y'=y-μ ₂
0	-1
-4	-2
4	4
-2	-1
2	0
	0 -4 4 -2



PCA step 2: rotating the grid, based on variance



$$\begin{split} \sigma_p^2 &= \frac{\sum_{i=1}^n (p_i - \mu)^2}{n} = \frac{\sum_i p_i^2}{n} - \left(\frac{\sum_i p_i}{n}\right)^2 \quad \text{variance} \\ \sigma_p^2 &= E(p^2) - [E(p)]^2 \\ p &= x + y: \\ \sigma_p^2 &= E((x+y)^2) - [E(x+y)]^2 \\ &= E(x^2) + 2E(xy) + E(y^2) - [E(x) + E(y)]^2 \\ &= E(x^2) + 2E(xy) + E(y^2) - [E(x)]^2 - 2E(x)E(y) - [E(y)]^2 \\ &= E(x^2) - [E(x)]^2 + E(y^2) - [E(y)]^2 + 2E(xy) - 2E(x)E(y) \\ &= \sigma_x^2 + \sigma_y^2 + 2\sigma_{x,y}^2 \\ \sigma_{x,y}^2 &= E(xy) - E(x)E(y) \quad \text{covariance} \end{split}$$

$$\sigma^2_{x,y} = E(xy) - E(x)E(y)$$
 covariance

,,			
	$x_1 (=x')$	x ₂ (=y')	
gene A	0	-1	
gene B	-4	-2	
gene C	4	4	•
gene D	-2	-1	• •
gene E	2	0	• •

$$\sigma^2_{x1,x2} = E(x_1x_2) = (0+8+16+2+0)/5 = 5.2$$

 $\sigma^2_{x2,x1} = \sigma^2_{x1,x2} = 5.2$
 $\sigma^2_{x1,x1} = E(x_1x_1) = (0+16+16+4+4)/5 = 8$
 $\sigma^2_{x2,x2} = E(x_2x_2) = (1+4+16+1+0)/5 = 4.4$

$$\sigma_{1,2}^{2} = \sigma_{x1,x2}^{2} = 5.2$$

$$\sigma_{2,1}^{2} = \sigma_{1,2}^{2} = 5.2$$

$$\sigma_{1,1}^{2} = 8$$

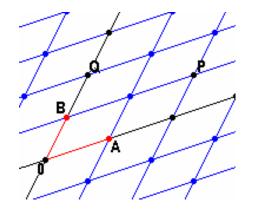
$$\sigma_{2,2}^{2} = 4.4$$

Covariance Matrix:
$$C = \begin{bmatrix} \sigma_{1,1}^2 & \sigma_{1,2}^2 & ... & \sigma_{1,m}^2 \\ \sigma_{2,1}^2 & \sigma_{2,2}^2 & ... & \sigma_{2,m}^2 \\ ... & ... & ... \\ \sigma_{m,1}^2 & \sigma_{m,2}^2 & ... & \sigma_{m,m}^2 \end{bmatrix}$$

$$C = \begin{bmatrix} \sigma_{1,1}^2 & \sigma_{1,2}^2 \\ \sigma_{2,1}^2 & \sigma_{2,2}^2 \end{bmatrix} = \begin{bmatrix} 8 & 5.2 \\ 5.2 & 4.4 \end{bmatrix}$$

$$C = \begin{bmatrix} \sigma_{1,1}^2 & \sigma_{1,2}^2 \\ \sigma_{2,1}^2 & \sigma_{2,2}^2 \end{bmatrix} = \begin{bmatrix} 8 & 5.2 \\ 5.2 & 4.4 \end{bmatrix}$$

$$\sigma_{p}^{2} = \sigma_{x}^{2} + \sigma_{y}^{2} + 2\sigma_{x,y}^{2} \longrightarrow \sigma_{p}^{2} = \sigma_{x}^{2} + \sigma_{y}^{2}$$



$$\mathbf{p} = \begin{bmatrix} 3 & 1 \\ 1 & 2 \end{bmatrix} \bullet \mathbf{p'} = \mathbf{A} \bullet \mathbf{p'}$$

$$C = \begin{bmatrix} \sigma_{1,1}^2 & \sigma_{1,2}^2 \\ \sigma_{2,1}^2 & \sigma_{2,2}^2 \end{bmatrix} = \begin{bmatrix} 8 & 5.2 \\ 5.2 & 4.4 \end{bmatrix}$$

$$\sigma_{p}^{2} = \sigma_{x}^{2} + \sigma_{y}^{2} + 2\sigma_{x,y}^{2} \longrightarrow \sigma_{p}^{2} = \sigma_{x}^{2} + \sigma_{y}^{2}$$

$$\mathbf{p} = \mathbf{X} \bullet \mathbf{p'}$$

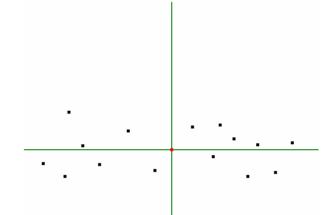
$$C = \begin{bmatrix} \sigma_{1,1}^2 & \sigma_{1,2}^2 \\ \sigma_{2,1}^2 & \sigma_{2,2}^2 \end{bmatrix} \rightarrow C' = \begin{bmatrix} e'_1 & 0 \\ 0 & e'_2 \end{bmatrix}$$

$$I = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \rightarrow X = \begin{bmatrix} ev_{1,1} & ev_{1,2} \\ ev_{2,1} & ev_{2,2} \end{bmatrix}$$

$$\sigma^2_{p'} = \sigma^2_{x'} + \sigma^2_{y'}$$

$$C' = \begin{bmatrix} e'_1 & 0 \\ 0 & e'_2 \end{bmatrix}$$

$$X = \begin{bmatrix} ev_{1,1} & ev_{1,2} \\ ev_{2,1} & ev_{2,2} \end{bmatrix} = \begin{bmatrix} 1' & 0' \\ 0' & 1' \end{bmatrix}$$



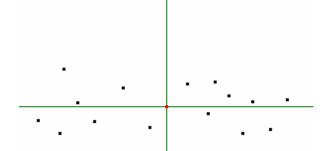
for each **v'** on x'-axis: $\mathbf{v'} = \begin{bmatrix} \mathbf{v'} \\ 0 \end{bmatrix}$

$$cov(\mathbf{v'}) = C' \bullet \mathbf{v'} = \begin{bmatrix} e'_1 & 0 \\ 0 & e'_2 \end{bmatrix} \bullet \begin{bmatrix} v' \\ 0 \end{bmatrix} = \begin{bmatrix} v' \bullet e'_1 \\ 0 \end{bmatrix} = e'_1 \bullet \begin{bmatrix} v' \\ 0 \end{bmatrix} = e'_1 \bullet \mathbf{v'}$$

$$C' \bullet v' = \lambda_1 \bullet v'$$

$$v_1'$$
 on x-axis: $C' \bullet v_1' = \lambda_1 \bullet v_1'$

$$\mathbf{v_2}'$$
 on y-axis: $\mathbf{C'} \bullet \mathbf{v_2}' = \lambda_2 \bullet \mathbf{v_2}'$



$$\lambda_i$$
 = eigenvalue of C'

$$v_i$$
 = eigenvector corresponding to λ_i

The value of λ_i corresponds to the variance on the x_i -axis

$$C = \begin{bmatrix} \sigma_{1,1}^2 & \sigma_{1,2}^2 \\ \sigma_{2,1}^2 & \sigma_{2,2}^2 \end{bmatrix} = \begin{bmatrix} 8 & 5.2 \\ 5.2 & 4.4 \end{bmatrix}$$

$$\sigma_{p}^{2} = \sigma_{x}^{2} + \sigma_{y}^{2} + 2\sigma_{x,y}^{2} \longrightarrow \sigma_{p}^{2} = \sigma_{x}^{2} + \sigma_{y}^{2}$$

$$\mathbf{p} = \mathbf{X} \bullet \mathbf{p'}$$

$$C = \begin{bmatrix} \sigma_{1,1}^2 & \sigma_{1,2}^2 \\ \sigma_{2,1}^2 & \sigma_{2,2}^2 \end{bmatrix} \rightarrow C' = \begin{bmatrix} e'_1 & 0 \\ 0 & e'_2 \end{bmatrix}$$

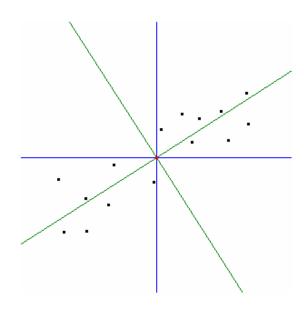
$$I = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \rightarrow X = \begin{bmatrix} ev_{1,1} & ev_{1,2} \\ ev_{2,1} & ev_{2,2} \end{bmatrix}$$

$$C = \begin{bmatrix} \sigma_{1,1}^2 & \sigma_{1,2}^2 \\ \sigma_{2,1}^2 & \sigma_{2,2}^2 \end{bmatrix} = \begin{bmatrix} 8 & 5.2 \\ 5.2 & 4.4 \end{bmatrix} \qquad X = \begin{bmatrix} ev_{1,1} & ev_{1,2} \\ ev_{2,1} & ev_{2,2} \end{bmatrix}$$

We have to solve: $\mathbf{C} \bullet \mathbf{x} = \lambda \bullet \mathbf{x}$ for all λ and \mathbf{x} (with $|\mathbf{x}_i| \equiv 1$)

$$\begin{bmatrix} 8 & 5.2 \\ 5.2 & 4.4 \end{bmatrix} \bullet \mathbf{x} = \lambda \bullet \mathbf{x} = \lambda \bullet \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \bullet \mathbf{x} = \begin{bmatrix} \lambda & 0 \\ 0 & \lambda \end{bmatrix} \bullet \mathbf{x}$$

$$\Leftrightarrow \begin{bmatrix} 8 - \lambda & 5.2 \\ 5.2 & 4.4 - \lambda \end{bmatrix} \bullet \mathbf{x} = 0 \Leftrightarrow \begin{cases} 8\mathbf{x}_1 - \lambda \mathbf{x}_1 + 5.2\mathbf{x}_2 = 0 \\ 5.2\mathbf{x}_1 + 4.4\mathbf{x}_2 - \lambda \mathbf{x}_2 = 0 \\ \mathbf{x}_1^2 + \mathbf{x}_2^2 = 1 \end{cases}$$



$$\lambda_1 \approx 73.59$$

$$\mathbf{x}_1 \approx \begin{bmatrix} 0.8428 \\ 0.5383 \end{bmatrix}$$

$$\lambda_2 \approx 4.33$$

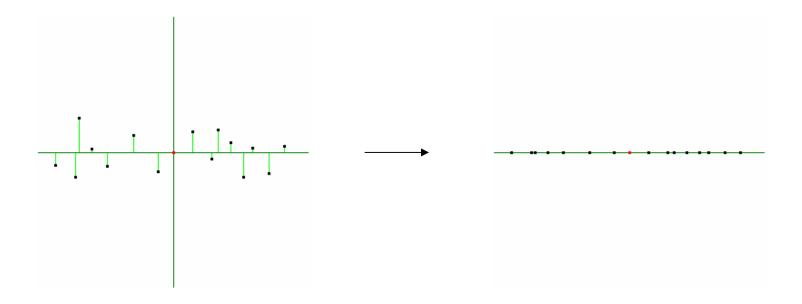
$$\mathbf{x}_2 \approx \begin{vmatrix} -0.5383 \\ 0.8428 \end{vmatrix}$$

$$\sigma^2_{p'} = \sigma^2_{x'} + \sigma^2_{y'}$$

 $\lambda_1 \approx 73.59 \cong 94.44\%$ of the total variance

 $\lambda_2 \approx 4.33 \cong 5.56\%$ of the total variance

PCA step 3: reducing complexity



Reducing complexity = removing dimensions:

$$\mathbf{v} = \begin{bmatrix} v_1 \\ v_2 \end{bmatrix} \rightarrow \mathbf{v'} = \begin{bmatrix} v_1 \\ 0 \end{bmatrix} \cong \begin{bmatrix} v_1 \end{bmatrix}$$

PCA: an example:

8 arrays, 1120 genes

covariation	n:							Eigenvalue:	%-variance:	som%-variance:
0.082	0.085	0.067	0.085	0.065	0.049	0.053	0.035	0.7788:	78.2862%	78.2862%
0.085	0.137	0.106	0.132	0.089	0.070	0.066	0.056	0.0830:	8.3442%	86.6304%
0.067	0.106	0.132	0.166	0.104	0.085	0.074	0.058	0.0588:	5.9087%	92.5391%
0.085	0.132	0.166	0.261	0.161	0.133	0.111	0.087	0.0238:	2.3914%	94.9306%
0.065	0.089	0.104	0.161	0.138	0.098	0.098	0.072	0.0153:	1.5408%	96.4713%
0.049	0.070	0.085	0.133	0.098	0.094	0.076	0.056	0.0149:	1.4954%	97.9667%
0.053	0.066	0.074	0.111	0.098	0.076	0.091	0.060	0.0119:	1.1925%	99.1592%
0.035	0.056	0.058	0.087	0.072	0.056	0.060	0.061	0.0084:	0.8408%	100.0000%
mean:										
0.041	0.010	-0.035	-0.006	0.031	-0.025	0.030	-0.028			
Eigenvalue										
0.7788	0.0830	0.0588	0.0238	0.0153	0.0149	0.0119	0.0084			
_	ors (matrix X):									
0.2372	-0.5089	0.3112	-0.5889	-0.0258	-0.0140	0.3536	-0.3395			
0.3437	-0.6736	0.0588	0.3954	0.1540	-0.2464	-0.2782	0.3265			
0.3780	-0.1457	-0.3817	0.1185	-0.2134	0.7361	-0.1585	-0.2521			
0.5482	0.2153	-0.5569	-0.1363	-0.0477	-0.3681	0.3816	0.2025			
0.3882	0.2877	0.2753	-0.1770	-0.4124	-0.2872	-0.6085	-0.1911			
0.3121	0.2596	0.0977	-0.1033	0.8603	0.1105	-0.1866	-0.1668			
0.2905	0.2158	0.5081	-0.0343	-0.1130	0.3924	0.2214	0.6277			
0.2230	0.1517	0.3168	0.6489	-0.0699	-0.1143	0.4155	-0.4640			

Jacobi max error: 0.00000016

Jacobi iterations: 4

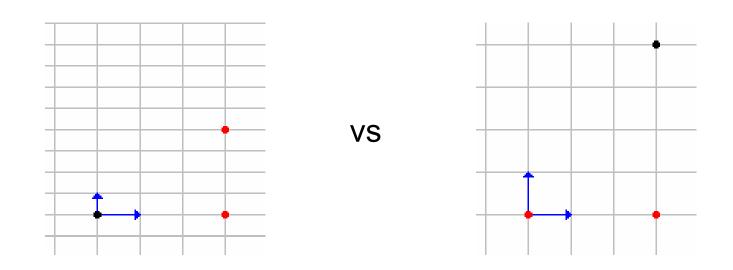
PCA and clustering

PCA and clustering:

- we are able to reduce the dimensionality of the data set, and
- identify variables with strong relationships with a component
- PCA helps to evaluate the quality of a given clustering
- all distances between data points remain the same

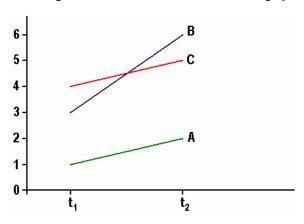
Demand: variables have to be "on an equal footing": should be measured in the same (or comparable) units

Transformation of axis with different factors can change a clustering:

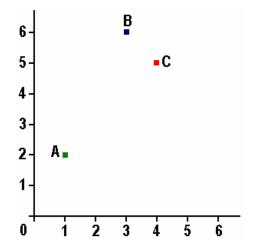


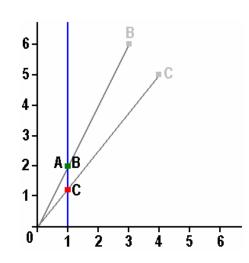
so think what you are doing!

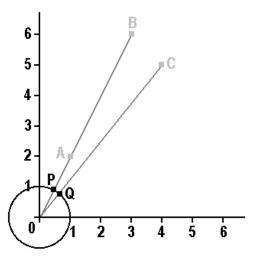
just like other types of transformations:



gene A gene B gene C



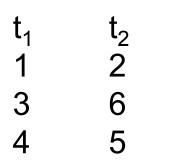


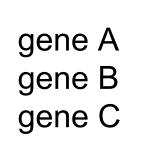


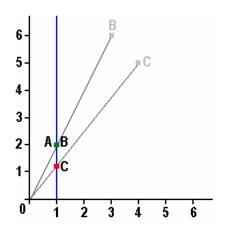
raw signals: **C** = {{A}, {B,C}} ratio s_{t2}/s_{t1} : **C** = {{A,B}, {C}} normalized s_{t2}/s_{t1} : **C** = {{A,B}, {C}}

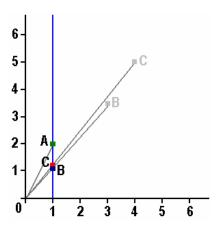
do not guess missing values:

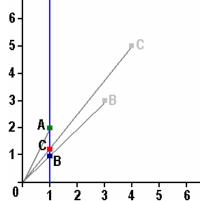
gene A gene B gene C

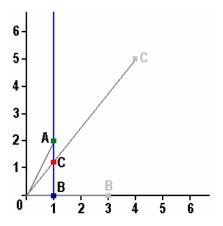












ratio
$$s_{t2}/s_{t1}$$
:
C = {{A,B}, {C}}

$$B_2 = \mu_{t2} = 3.5$$
 $B_2 = \mu_B = 3$ $C = \{\{A\}, \{B,C\}\}$

$$B_2=0$$
: **C** = {{A,C}, {B}}

Each clustering result needs further evaluation (visualisation, etc).

The only quality measure of a clustering is its usefulness in practice.