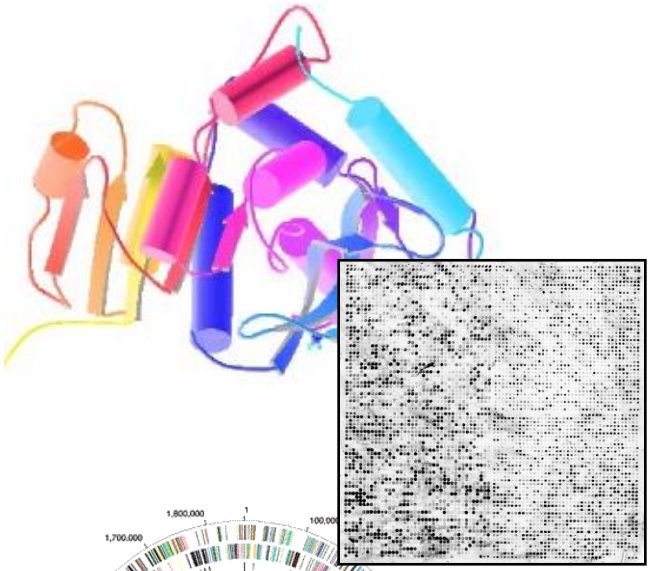
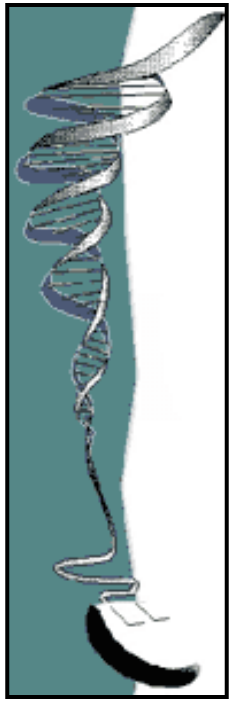
Biomed. Data Science:

Unsupervised Datamining -- SVD





Mark Gerstein, Yale University

gersteinlab.org/courses/452

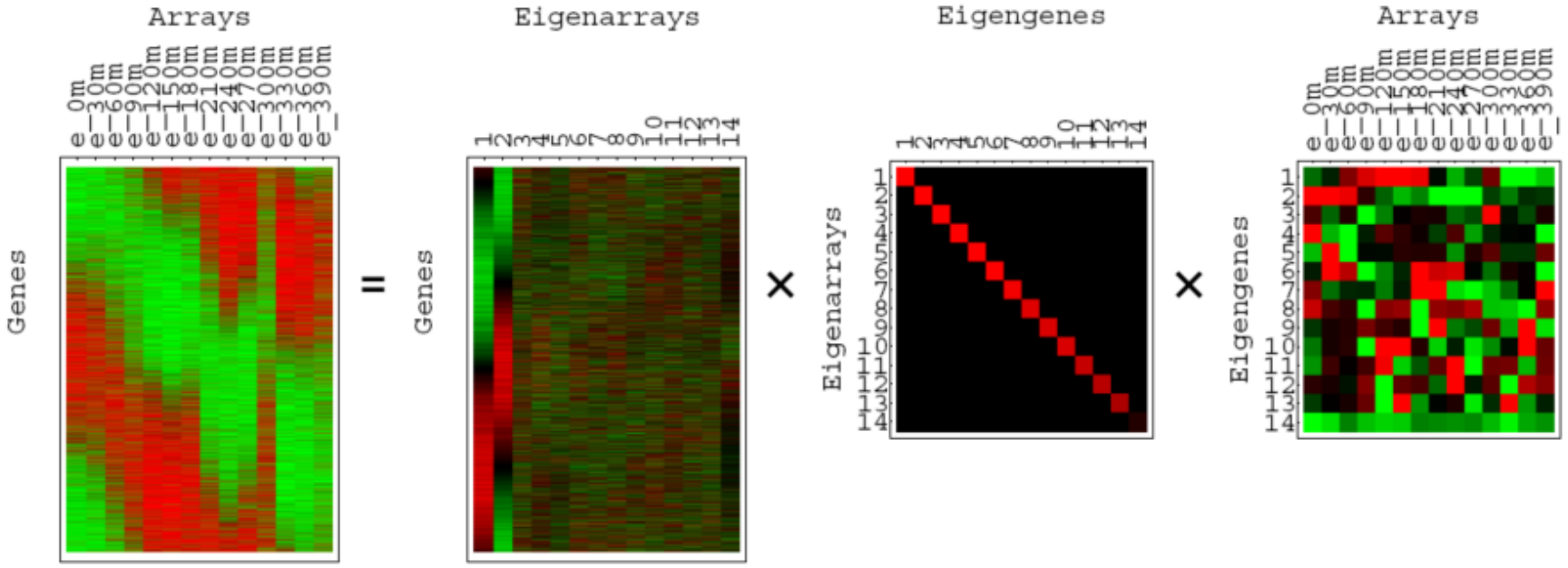
(Last edit in spring ’22, pack 22m9c, essentially the same as M9c from ‘21.)

Unsupervised Mining

SVD

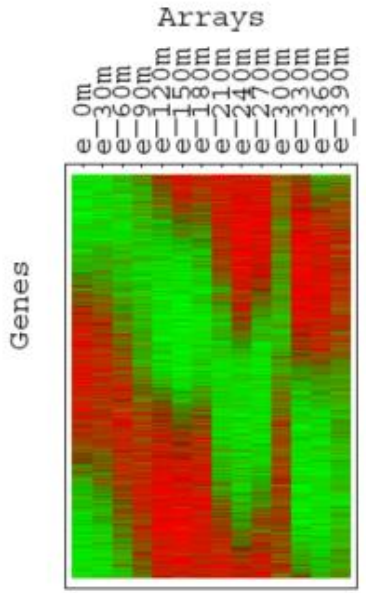
Puts together slides prepared by
Brandon Xia with images from
Alter et al. papers

SVD for microarray data (Alter et al, PNAS 2000)



$$A = USV^T$$

- A is any rectangular matrix (m ≥ n)
- Row space: vector subspace generated by the row vectors of A
- Column space: vector subspace generated by the column vectors of A
  - The dimension of the row & column space is the rank of the matrix A: r (≤ n)
- A is a linear transformation that maps vector x in row space into vector Ax in column space

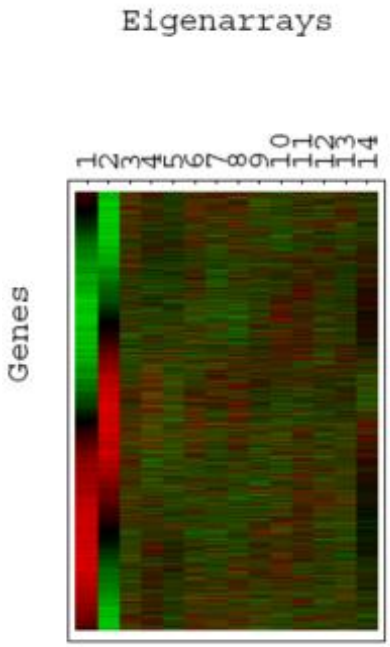


$A = USV^T$

- U is an "orthogonal" matrix (m ≥ n)
- Column vectors of U form an orthonormal basis for the column space of A: $U^T U = I$

$$U = \begin{pmatrix} | & | & & | \\ \mathbf{u}_1 & \mathbf{u}_2 & \cdots & \mathbf{u}_n \\ | & | & & | \end{pmatrix}$$

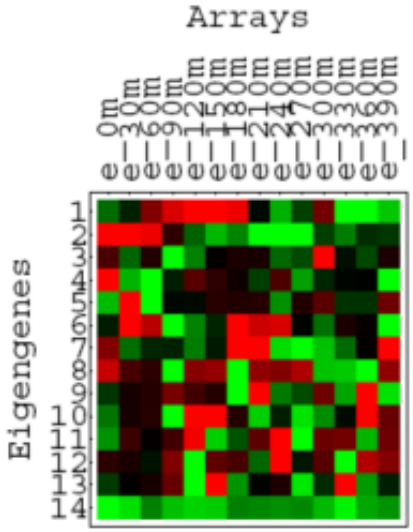
- $\boldsymbol{u}_1, \ldots, \boldsymbol{u}_n$ in U are eigenvectors of AA^T
  - $AA^T = USV^T VSU^T = US^2 U^T$
  - "Left singular vectors"



$A = USV^T$

- V is an orthogonal matrix (n by n)
- Column vectors of V form an orthonormal basis for the row space of A: $V^TV=VV^T=I$

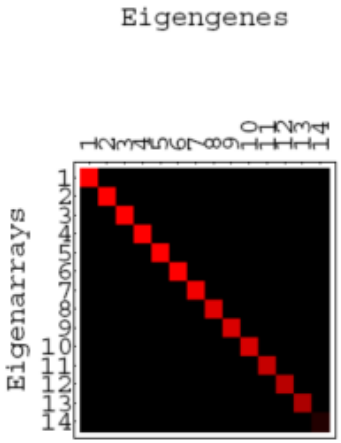
$$V = \begin{pmatrix} | & | & & | \\ \mathbf{v}_1 & \mathbf{v}_2 & \cdots & \mathbf{v}_n \\ | & | & & | \end{pmatrix}$$



- $\boldsymbol{v}_1, \ldots, \boldsymbol{v}_n$ in V are eigenvectors of A^TA
  - $A^TA = VSU^T\,USV^T = VS^2\,V^T$
  - "Right singular vectors"

$$A = USV^T$$

- S is a diagonal matrix (n by n) of non-negative singular values
- Typically sorted from largest to smallest
- Singular values are the non-negative square root of corresponding eigenvalues of A^TA and AA^T



$$AV = US$$

- Means each $A\boldsymbol{v}_i = s_i\boldsymbol{u}_i$
- Remember A is a linear map from row space to column space
- Here, A maps an orthonormal basis $\{\boldsymbol{v}_i\}$ in row space into an orthonormal basis $\{\boldsymbol{u}_i\}$ in column space
- Each component of u_i is the projection of a row of the data matrix A onto the vector v_i

SVD as sum of rank-1 matrices

- $A = USV^T$
- $A = s_1\boldsymbol{u}_1\boldsymbol{v}_1{}^T + s_2\boldsymbol{u}_2\boldsymbol{v}_2{}^T + \ldots + s_n\boldsymbol{u}_n\boldsymbol{v}_n{}^T$
- $s_1 \geq s_2 \geq \ldots \geq s_n \geq 0$
- What is the rank-r matrix $\hat{A}$ that best approximates A ?
  - Minimize $\sum_{i=1}^{m}\sum_{j=1}^{n}\left(\hat{A}_{ij} - A_{ij}\right)^2$
- $\hat{A} = s_1\boldsymbol{u}_1\boldsymbol{v}_1{}^T + s_2\boldsymbol{u}_2\boldsymbol{v}_2{}^T + \ldots + s_r\boldsymbol{u}_r\boldsymbol{v}_r{}^T$
- Very useful for matrix approximation

an outer product (uv^T) giving a matrix rather than the scalar of the inner product

LSQ approx. If r=1, this amounts to a line fit.

Examples of (almost) rank-1 matrices

- Steady states with fluctuations

$$\begin{pmatrix} 101 & 103 & 102 \\ 302 & 300 & 301 \\ 203 & 204 & 203 \\ 401 & 402 & 404 \end{pmatrix}$$

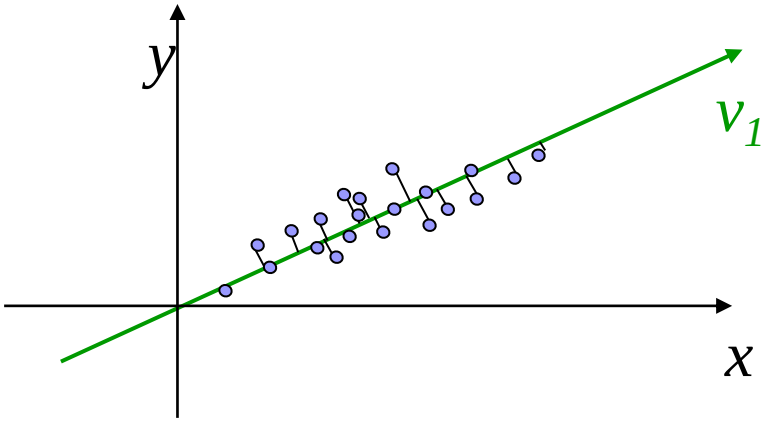
- Array artifacts?

$$\begin{pmatrix} 101 & 303 & 202 \\ 102 & 300 & 201 \\ 103 & 304 & 203 \\ 101 & 302 & 204 \end{pmatrix}$$

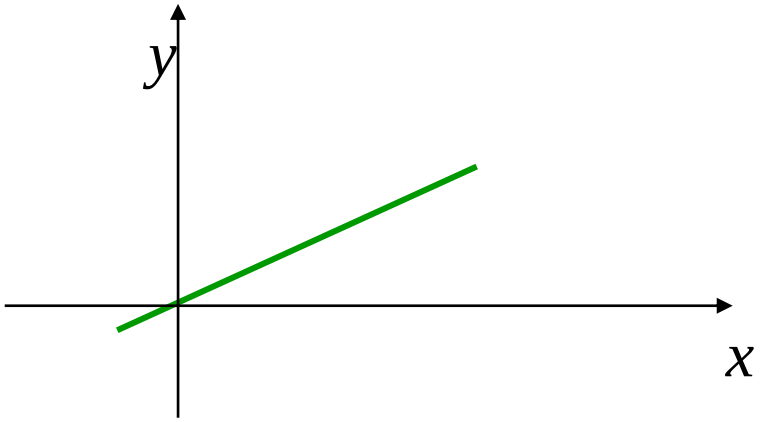
- Signals?

$$\begin{pmatrix} 1 & 2 & -1 \\ 2 & 4 & -2 \\ -1 & -2 & 1 \\ 0 & 0 & 0 \end{pmatrix}$$

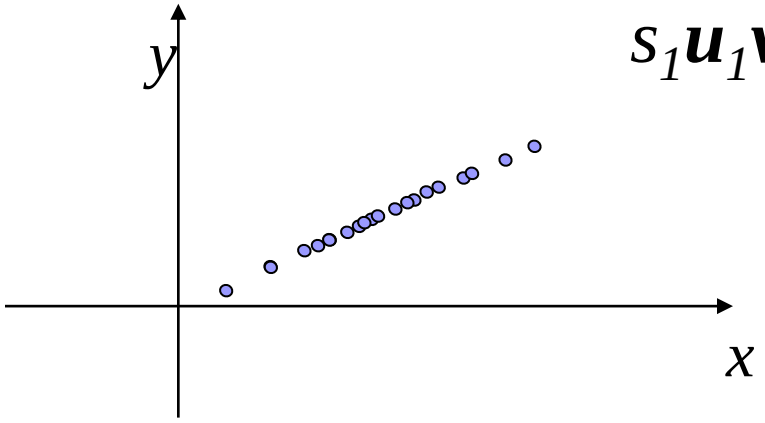
Geometry of SVD in row space



A



This line segment that goes through origin approximates the original data set

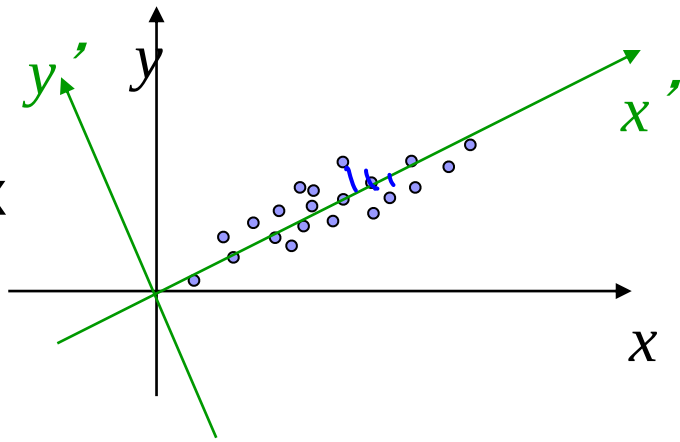


$s_1 \boldsymbol{u}_1 \boldsymbol{v}_1^T$

The projected data set approximates the original data set

Geometry of SVD in row space

- A as a collection of m row vectors (points) in the row space of A
- $s_1\boldsymbol{u}_1\boldsymbol{v}_1^T + s_2\boldsymbol{u}_2\boldsymbol{v}_2^T$ is the best rank-2 matrix approximation for A
- Geometrically: $\boldsymbol{v}_1$ and $\boldsymbol{v}_2$ are the directions of the best approximating rank-2 subspace that goes through origin
- $s_1\boldsymbol{u}_1$ and $s_2\boldsymbol{u}_2$ gives coordinates for row vectors in rank-2 subspace
- $\boldsymbol{v}_1$ and $\boldsymbol{v}_2$ gives coordinates for row space basis vectors in rank-2 subspace



$$A\,\mathbf{v_i} = s_i\mathbf{u_i}$$

$$I\,\mathbf{v_i} = \mathbf{v_i}$$

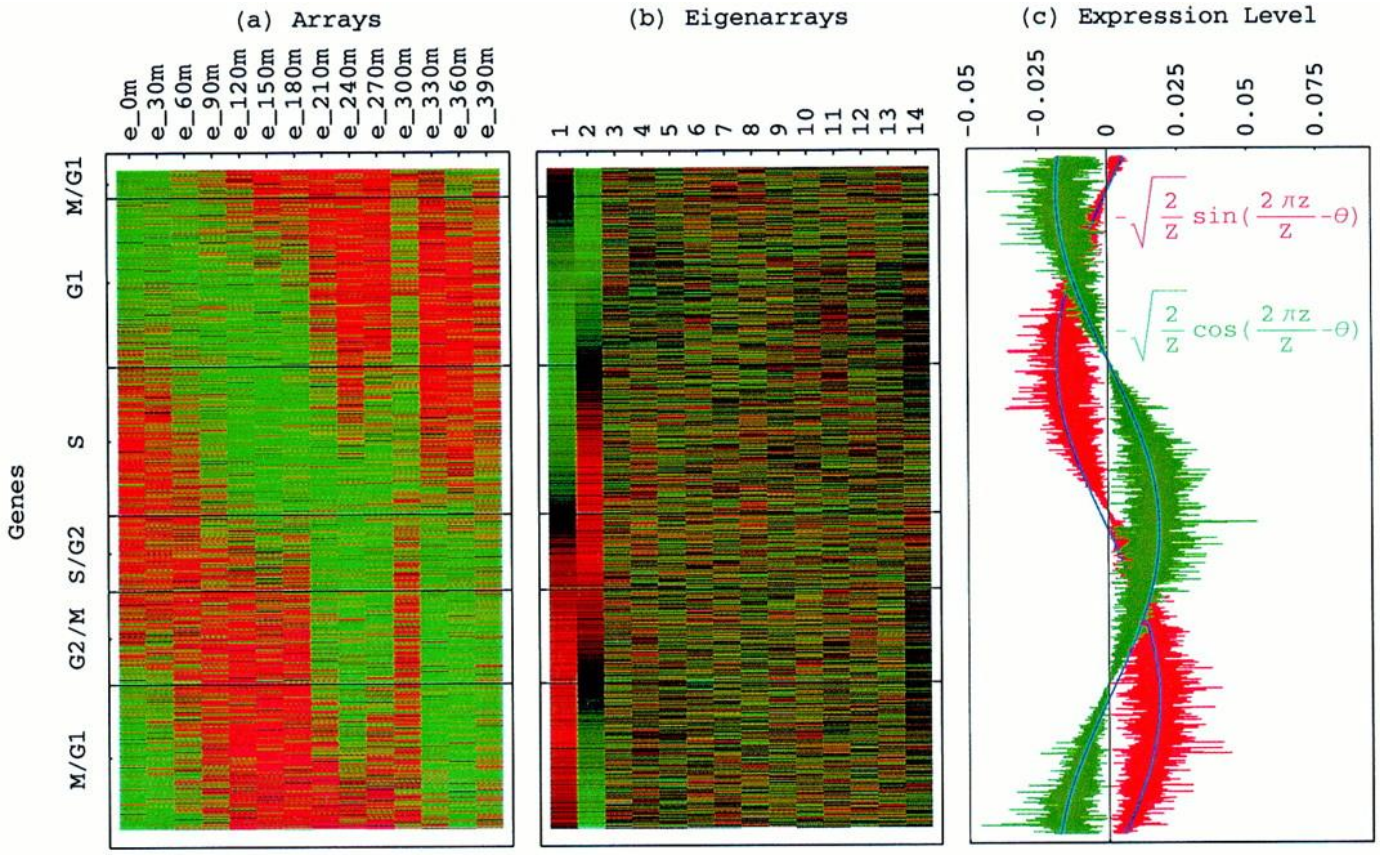
What about geometry of SVD in column space?

- $A = USV^T$
- $A^T = VSU^T$
- The column space of A becomes the row space of A^T
- The same as before, except that U and V are switched

Unsupervised Mining

Intuition on interpretation of SVD
in terms of genes and conditions

Genes sorted by correlation with top 2 eigengenes



Alter, Orly et al. (2000) Proc. Natl. Acad. Sci. USA 97, 10101-10106

Fig. 3. Genes sorted by relative correlation with $|\gamma_1\rangle_N$ and $|\gamma_2\rangle_N$ of normalized elutriation. (*a*) Normalized elutriation expression of the sorted 5,981 genes in the 14 arrays, showing traveling wave of expression. (*b*) Eigenarrays expression; the expression of $|\alpha_1\rangle_N$ and $|\alpha_2\rangle_N$, the eigenarrays corresponding to $|\gamma_1\rangle_N$ and $|\gamma_2\rangle_N$, displays the sorting. (*c*) Expression levels of $|\alpha_1\rangle_N$ (red) and $|\alpha_2\rangle_N$ (green) fit normalized sine and cosine functions of period $Z \equiv N - 1 = 5{,}980$ and phase $\theta \approx 2\pi/13$ (blue), respectively.

Normalized elutriation expression in the subspace associated with the cell cycle

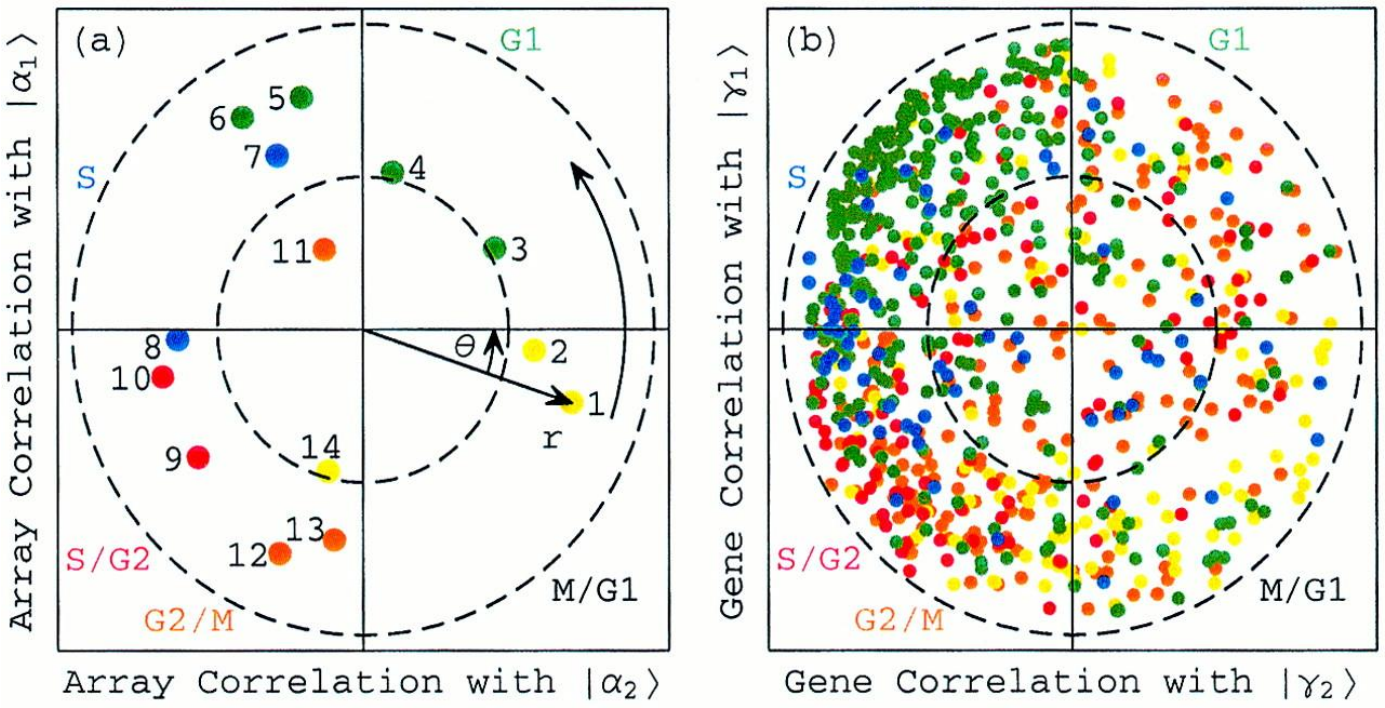


Fig. 2. Normalized elutriation expression in the subspace associated with the cell cycle. (*a*) Array correlation with $|\alpha_1\rangle_N$ along the *y*-axis vs. that with $|\alpha_2\rangle_N$ along the *x*-axis, color-coded according to the classification of the arrays into the five cell cycle stages, M/G_1 (yellow), G_1 (green), S (blue), S/G_2 (red), and G_2/M (orange). The dashed unit and half-unit circles outline 100% and 25% of overall normalized array expression in the $|\alpha_1\rangle_N$ and $|\alpha_2\rangle_N$ subspace. (*b*) Correlation of each gene with $|\gamma_1\rangle_N$ vs. that with $|\gamma_2\rangle_N$, for 784 cell cycle regulated genes, color-coded according to the classification by Spellman *et al.* (3).

Alter, Orly et al. (2000) Proc. Natl. Acad. Sci. USA 97, 10101-10106