NEW RANDOM AND NON-RANDOM ALGEBRAIC MATRIX METHODS FOR BIOLOGICAL SYSTEMS

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FOR: INTERNATIONAL WORKSHOP ON MATHEMATICAL PHYSICS OF COMPLEX NETWORKS

MAX PLANCK INSTITUTE FOR PHYSICS OF COMPLEX SYSTEMS DRESDEN

MAY 14TH - 18TH 2012

BIOLOGICAL SYSTEMS PRESENT A VARIED AND COMPLEX FIELD FOR ANALYSIS AND DEVELOPMENT INTO A MATHEMATICAL METHODOLOGY. THIS IS BECAUSE THERE ARE MANY INDEPENDENT AND YET COMPLIMENTARY FACTORS IN BIOLOGICAL SYSTEMS WHICH MAY APPEAR SIMPLE TO QUANTIFY AND DEFINE ON FIRST APPEARANCE BUT ON CLOSER EXAMINATION SHOW A COMPLEXITY BASED ON MANY INTERLINKING CHEMICAL AND PHYSICAL REACTIONS.

THEREFORE ANY MATHEMATICAL SYSTEM ATTEMPTING TO ORDER SUCH A SYSTEM HAS TO TRY TO FIT MANY VARIABLES INTO ITS REPRESENTATION.

IN THIS TALK WE WILL EXAMINE IF IN A PARTICULAR ARBITRARY BIOLOGICAL SYSTEM SOME VARIABLES WHICH ARE VERY RELEVANT TO THE SYSTEMS FUNCTIONING CAN BE PUT INTO A MATRIX SYSTEM WHICH WOULD ENABLE PROJECTIONS OF DIFFERENT PHYSICAL STATES OF THE SYSTEM.

BIOLOGICAL SYSTEM VARIABLES ----> ARBITRARY CHOICE ----> MATHEMATICAL MATRIX

WE TAKE AS OUR EXAMPLE BIOLOGICAL SYSTEM A MILIEU OF THE MICROBIOLOGICAL SYSTEM OF CLOSTRIDIA FELSINEUM ON THE SUBTRATE OF PHOSPHORYLATED PECTIN. WHAT WE SEE IN THE FOLLOWING THREE SEM PHOTOGRAPHS ARE THE EXISTENCE OF THE CLOSTRIDIA FELSINEUM ENTITY IN DIFFERENT STAGES OF DEVELOPMENT.

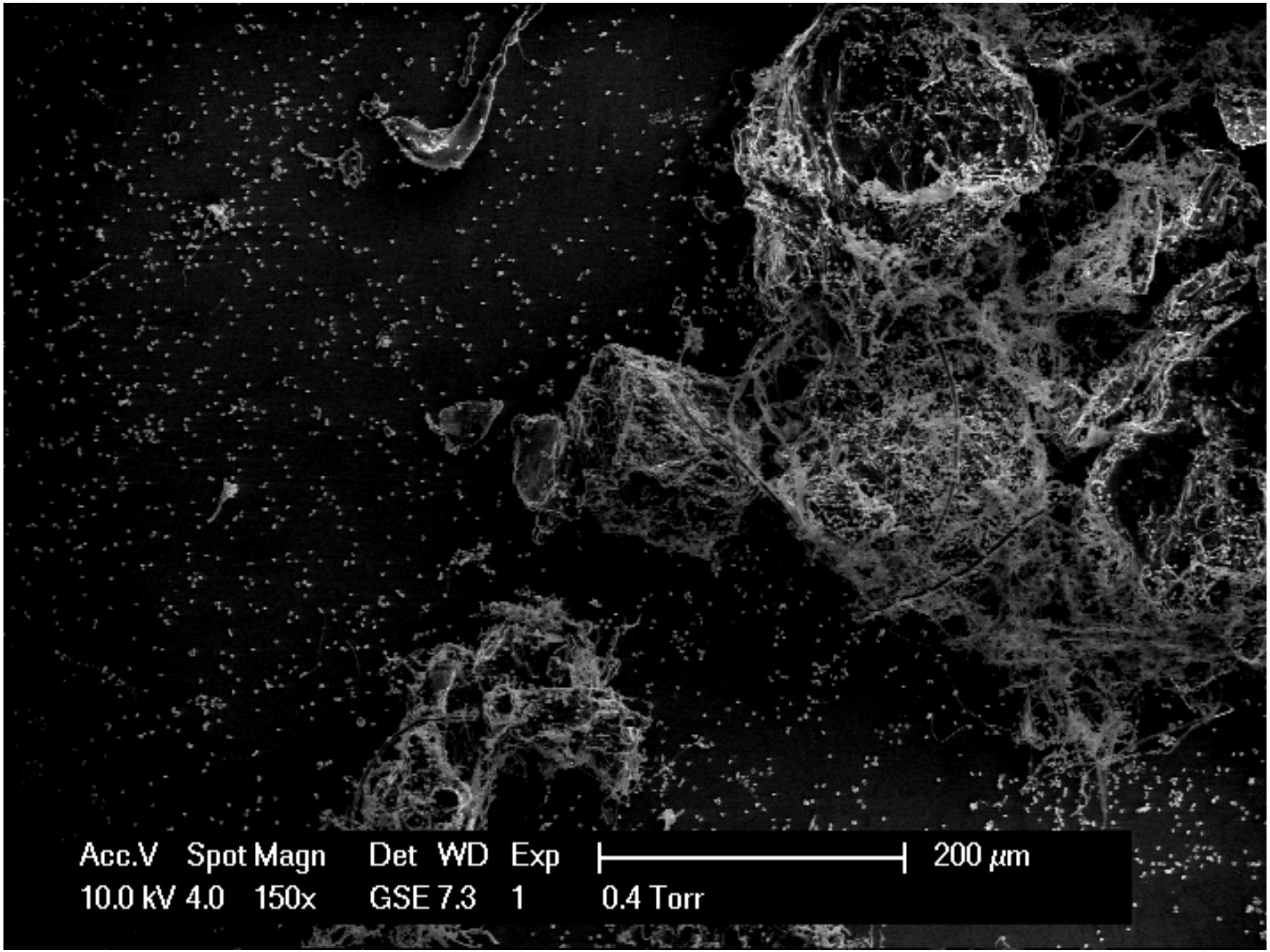
1) COMPARATIVELY LONG NUCLEIC ACID AND PHOSPHOLIPID FILAMENTS AND STRANDS
2) NUMEROUS INDIVIDUAL SPORES AND STAGES OF SPORULATION
3) RESIDUAL INITIAL GROWTH ON THE SUBSTRATE

WHICH OF THESE THREE VARIABLES SHOULD WE CHOOSE TO DEVELOP INTO OUR MATRIX REPRESENTATION?

FILAMENTS AND STRANDS

SPORULATION AND SPORES

ORIGINAL GROWTH ON SUBSTRATE ????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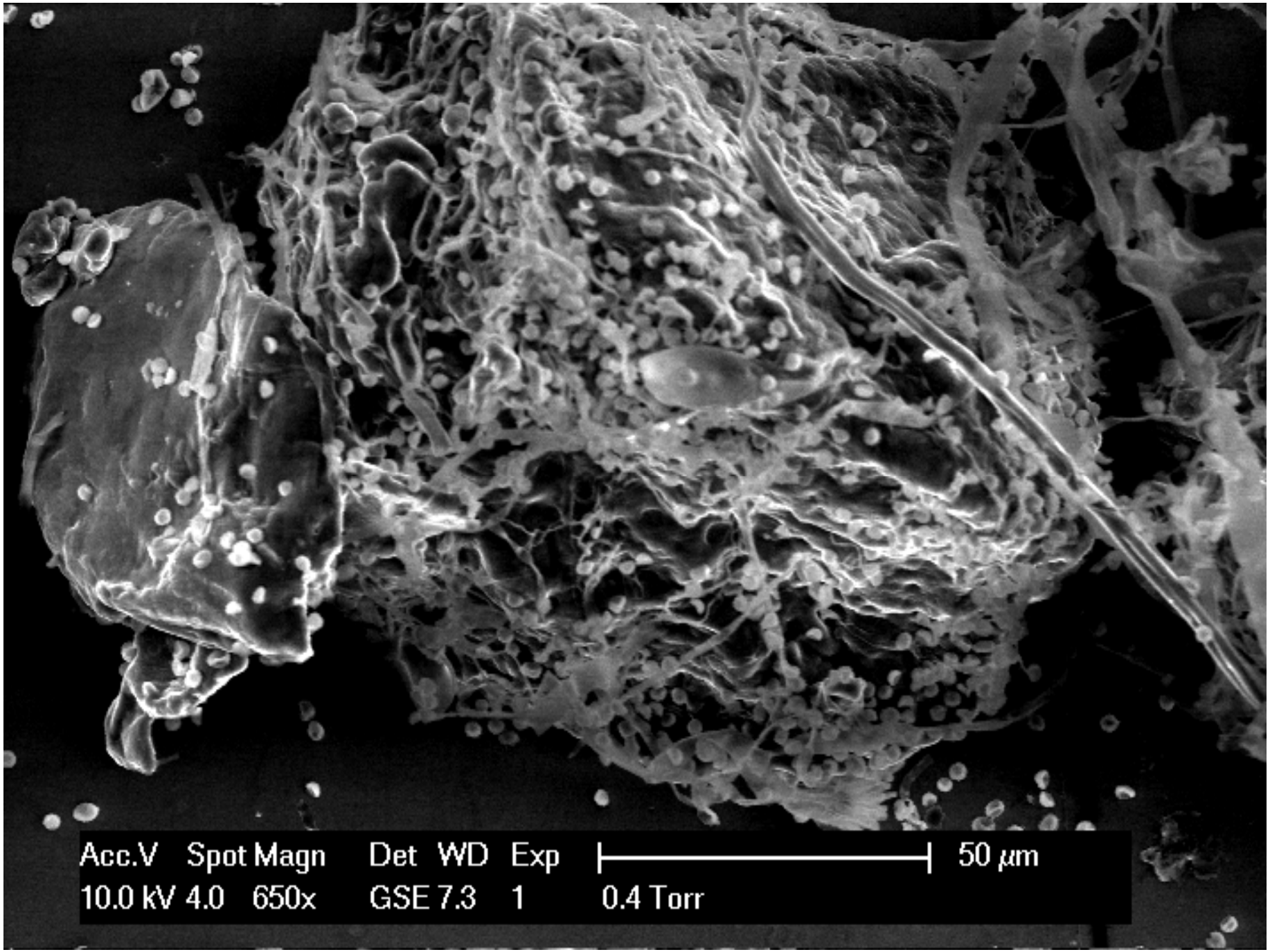
200 µm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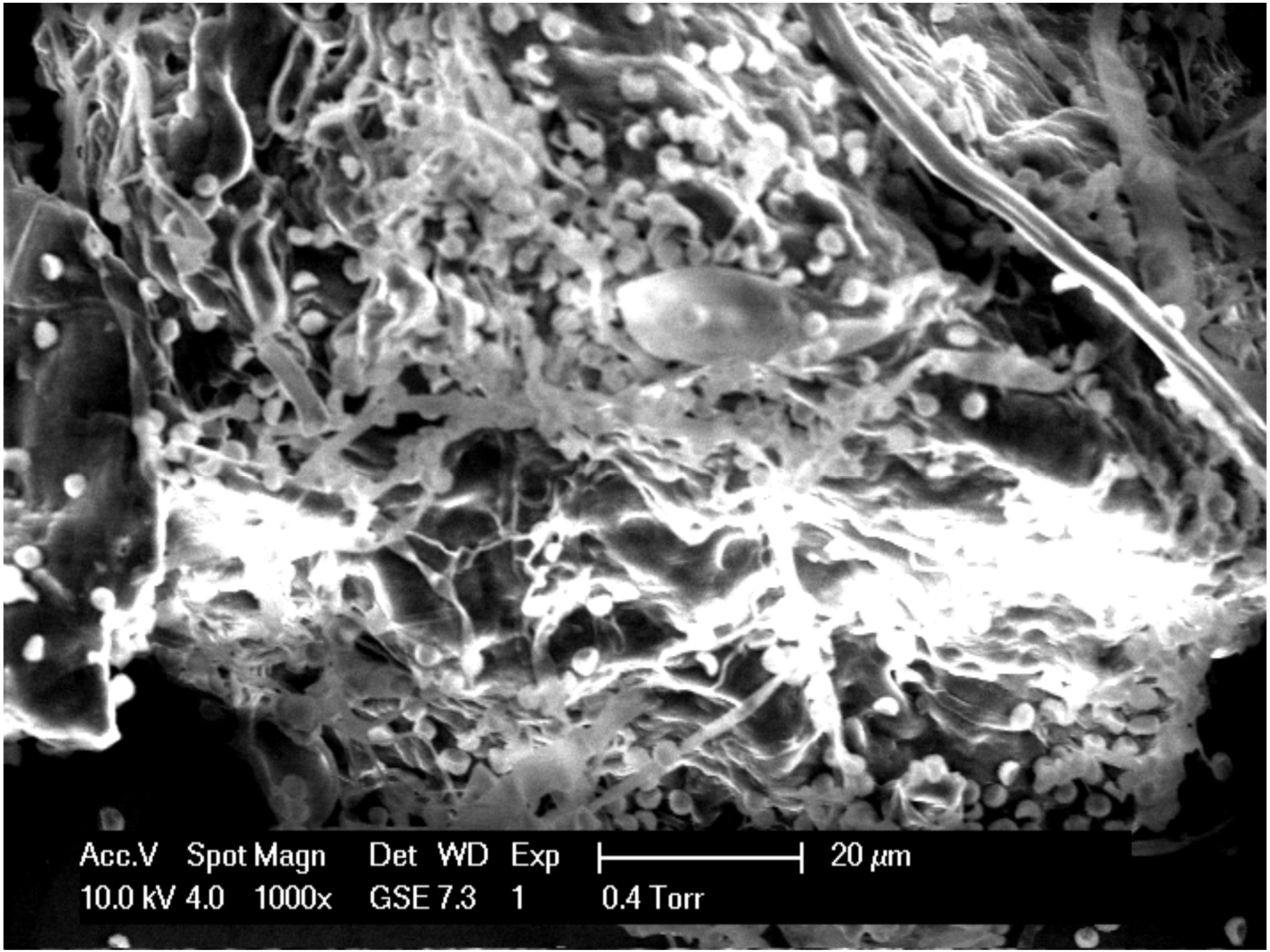
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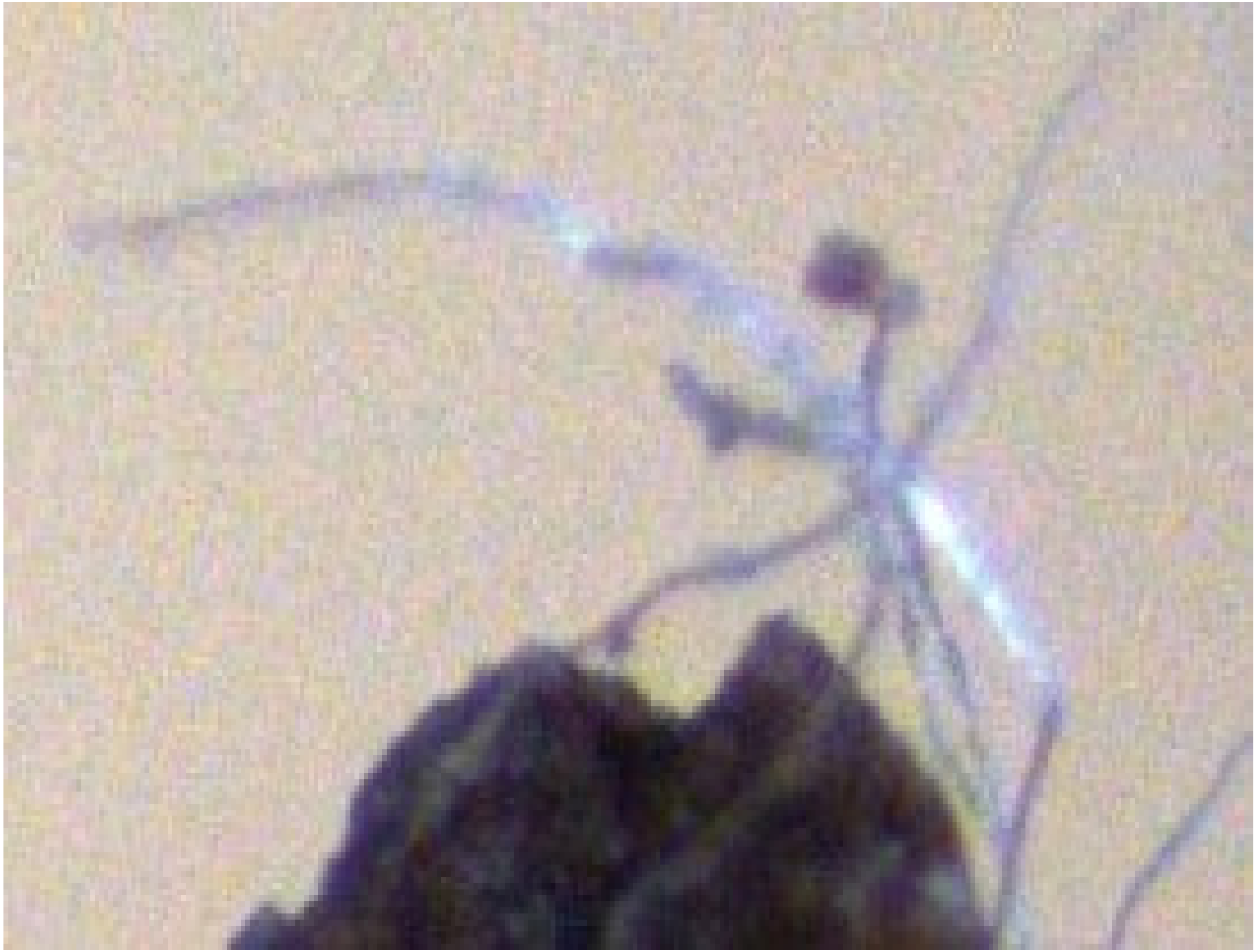
0.4 Torr


100Pix


100pix



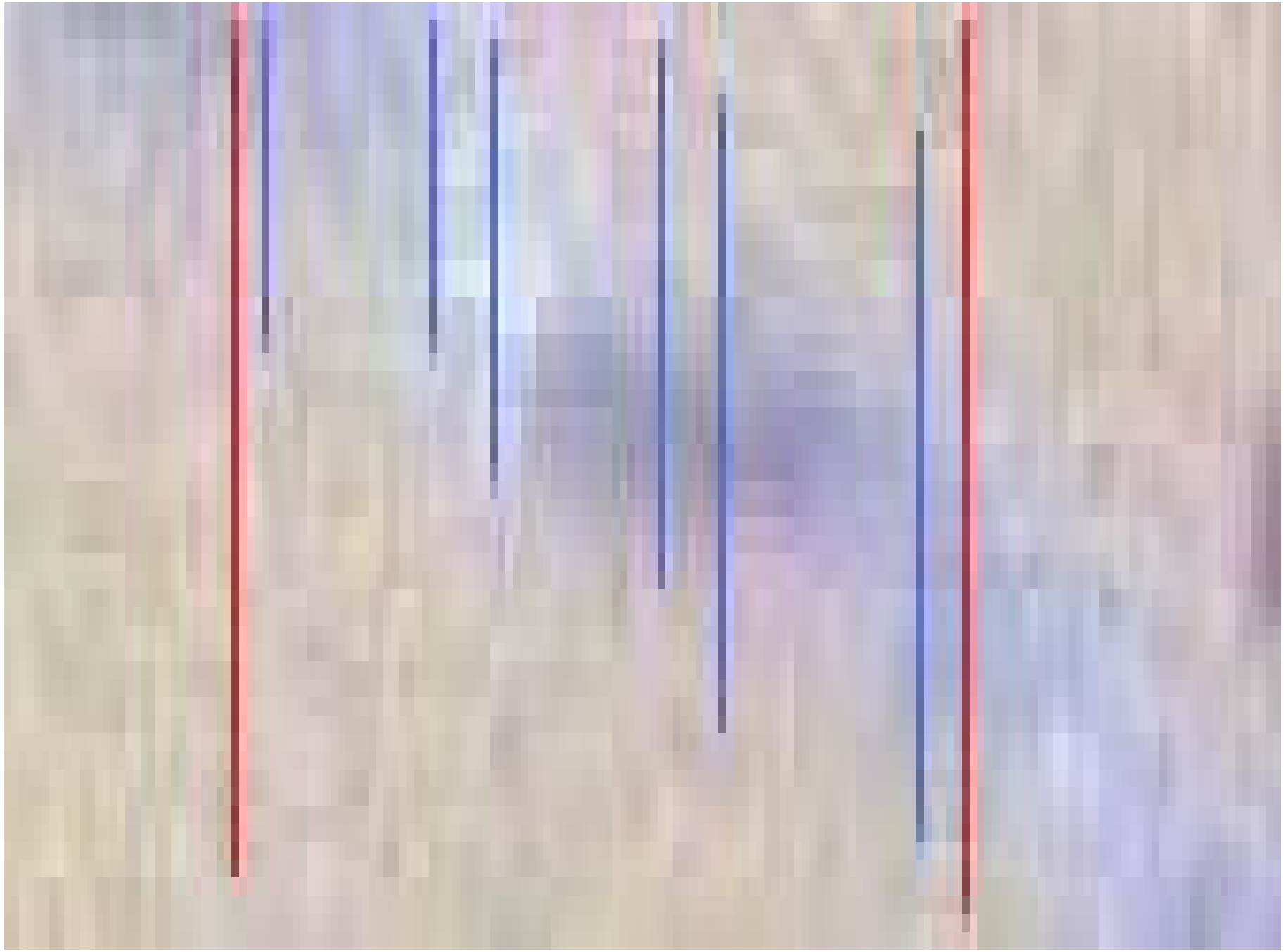
HOWEVER EVEN WHEN WE HAVE NARROWED DOWN OUR CHOICE OF INITIAL STATE OF SYSTEM VARIABLES TO ONE WE FIND INCREASED COMPLEXITY WITHIN THAT VARIABLE SINCE WE SEE HERE THAT THERE ARE NUCLEIC ACID AND PHOSPHOLIPID FILAMENTS HERE WITHIN THIS VARIABLE?

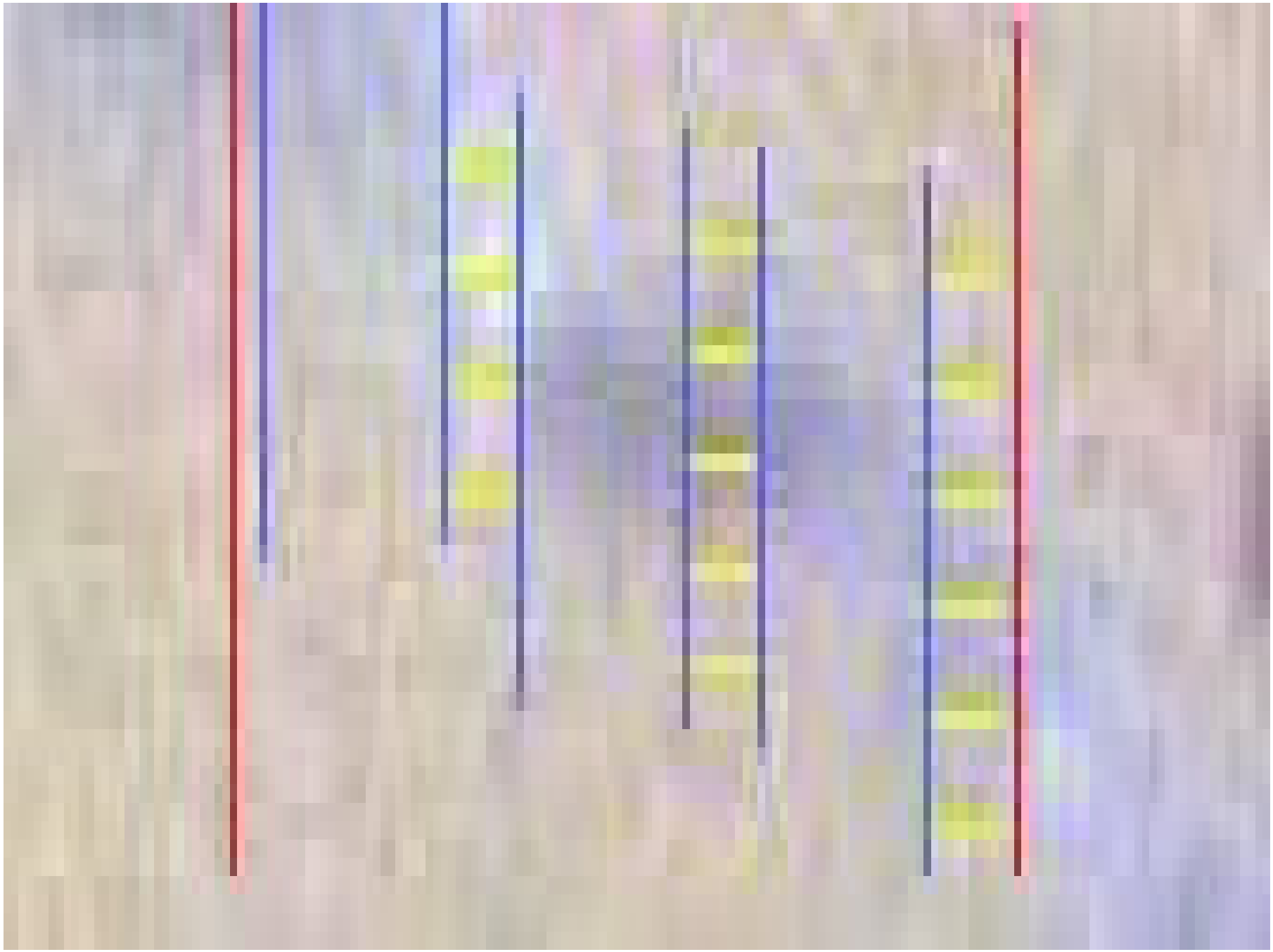
ATTACHED TO THE PARTICLE OF SUBSTRATE WE SEE FILAMENTS OF WHAT SIZE ?
GIVEN THAT THE SCALE IS OF 100PIXELS OF THE PHOTO DIGITISATION WE CAN SAY THAT THE LENGTH OF FILAMENTS IS FROM 150 PIXELS TO 250 PIXELS.

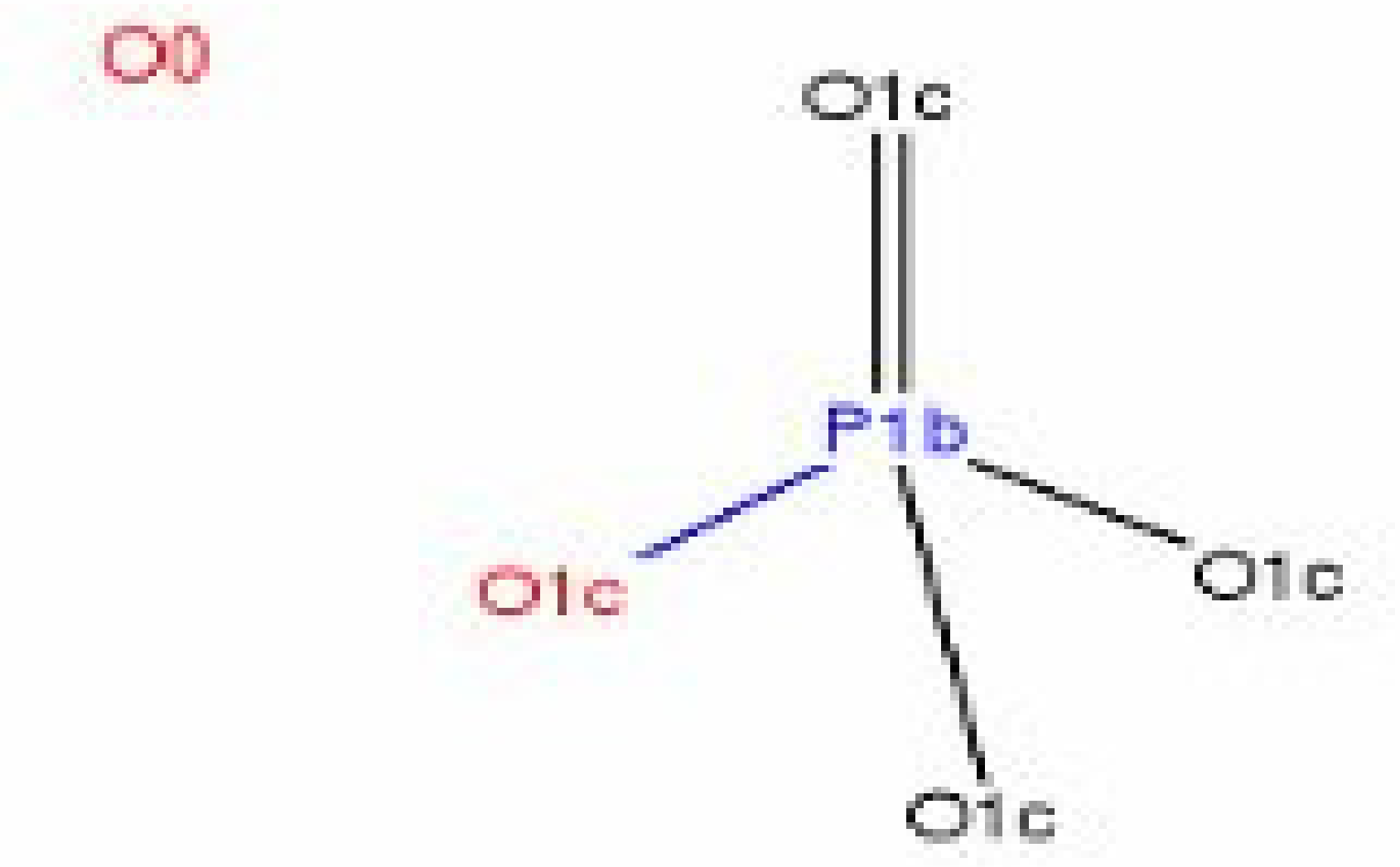
IF WE ARE USING THE VALUES OF PIXELS IN OUR ANALYSIS WE ARE USING THE METHOD
_____
_____

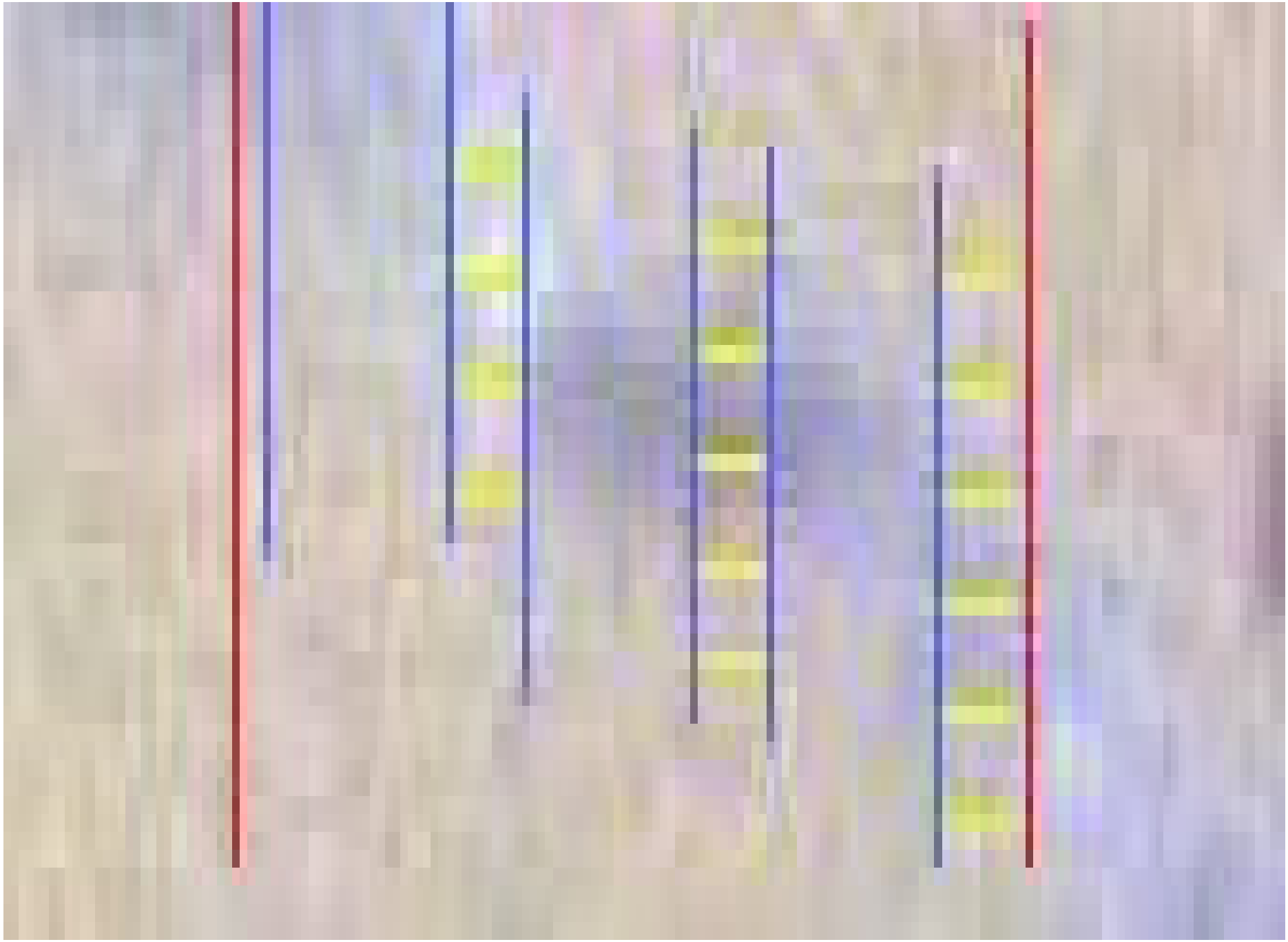
OF USING THE DIGITISATION OF NANOPHOTOGRAPHY TO ACHIEVE OUR MATRIX METHOD!!!!!!
_____
_____

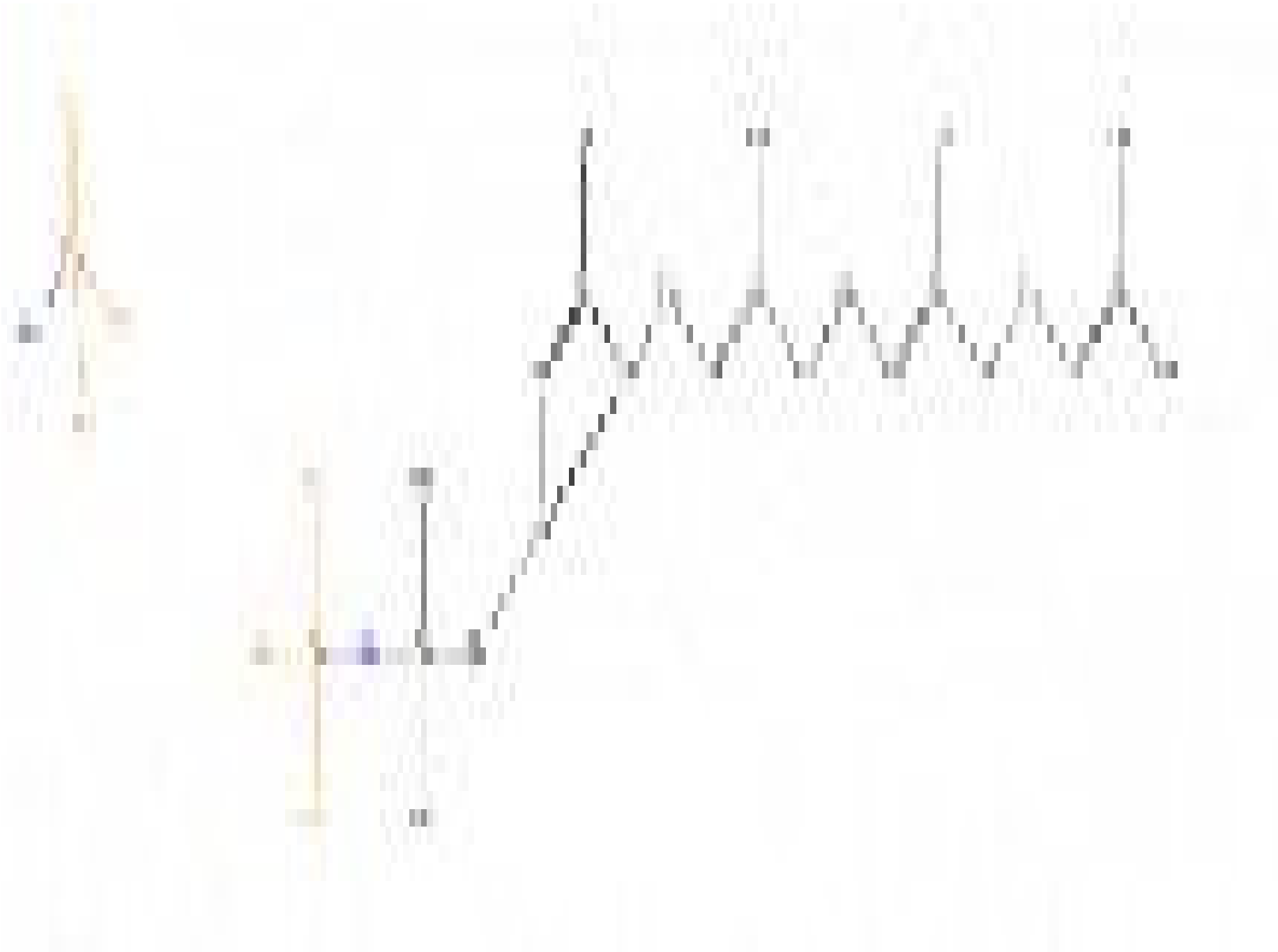

100 PXL






O0
O1c
P1b
O1c
O1c
O1c





SUMMARY TO SLIDE 15:

OVERALL VARIABLES WITHIN CLOSTRIDIA SYSTEM = M1 M2 M3

WE CHOSE M3 - ORIGINAL GROWTH ON SUBSTRATE

HOWEVER IN M1 THE THREE SECONDARY VARIABLES THE SAME 3 REPEATED M3.1 M3.2 M3.3

THIS TIME WE CHOSE M1.3 - FILAMENTS AND NUCLEIC ACIDS

M3 = { M3.1 M3.2 M3.3 }

DIGITISATION OF SEM THE PARAMETERS OF D - DIGITISATION ERROR AND p - PIXELS

WE ALSO HAVE THE FACTORS OF PL - PHOSPHATE LINKAGES AND LPL - LINKED PHOSPHOLIPIDS

M3.3 --> 150p

D - DIGITISATION ERROR = 0.01 = 1%

N IS NUMBER OF MONOMERS WITHIN ANY GIVEN LENGTH 1 OF FILAMENT

1 IS LENGTH IN ANGSTROMS OR um.

M3.3 = summation(PL+LPL).D/p150 = summation(D.PL+D.LPL/p150)

((D.PL+D.LPL)/p150) = (Nl)/Dl

M3.3 [filamentation] ---->> { D,p,PL,LPL,N,1 }

M3.3 = summation (((D.PL)+(D.LPL))/p150)

= (D.PL + D.LPL / p150) = Nl/Dl

As each of the factors PL and LPL however linked operate within a defined Hilbert Space within the filament:

Hilbert Space H is the set of othonormal states { | jm > : j = 0,1/2,1,.....; m = j, j-1,..... -j }

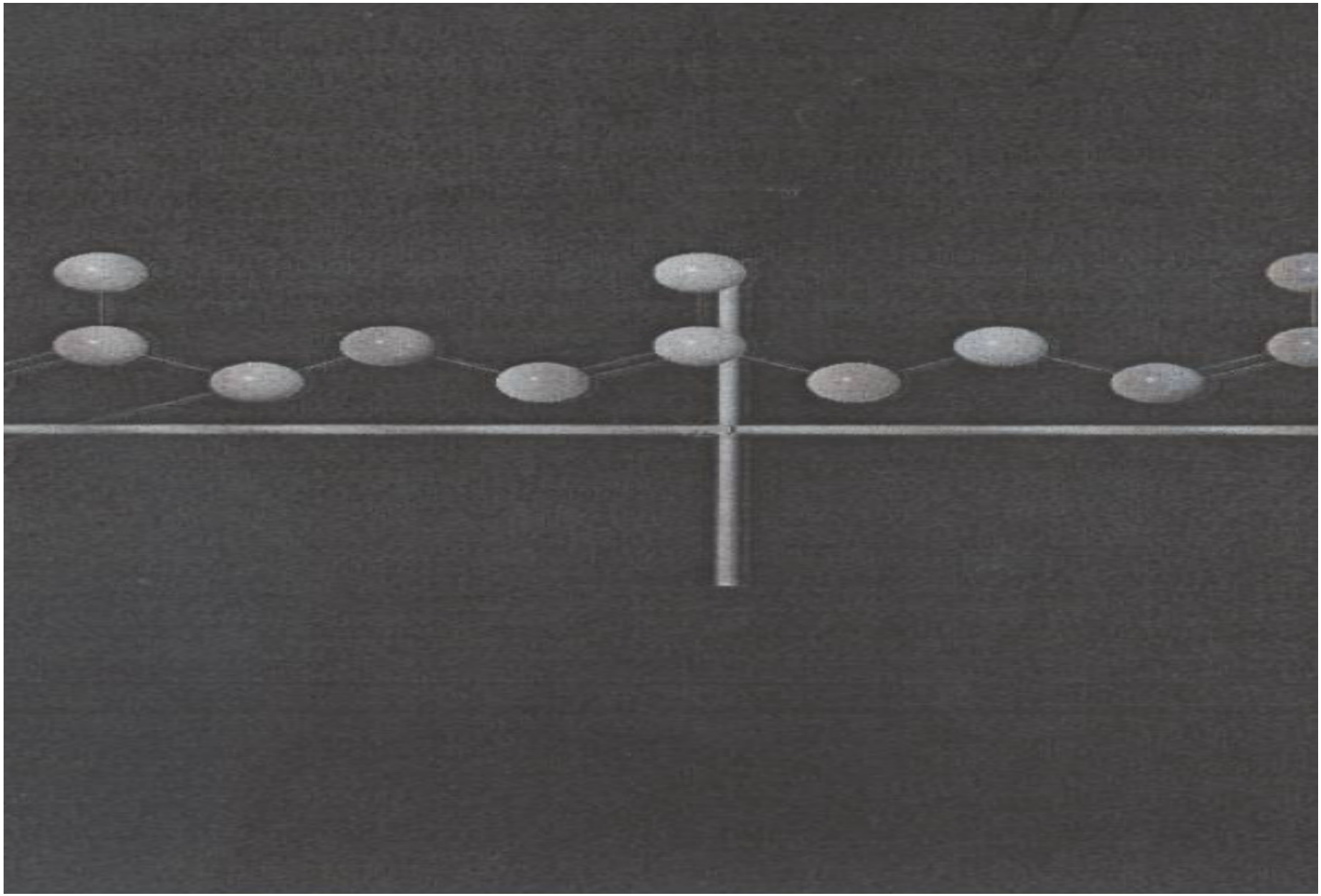
Wigner coefficients can act as tensor operators on the Hilbert Space in which the factors PL and LPL exist

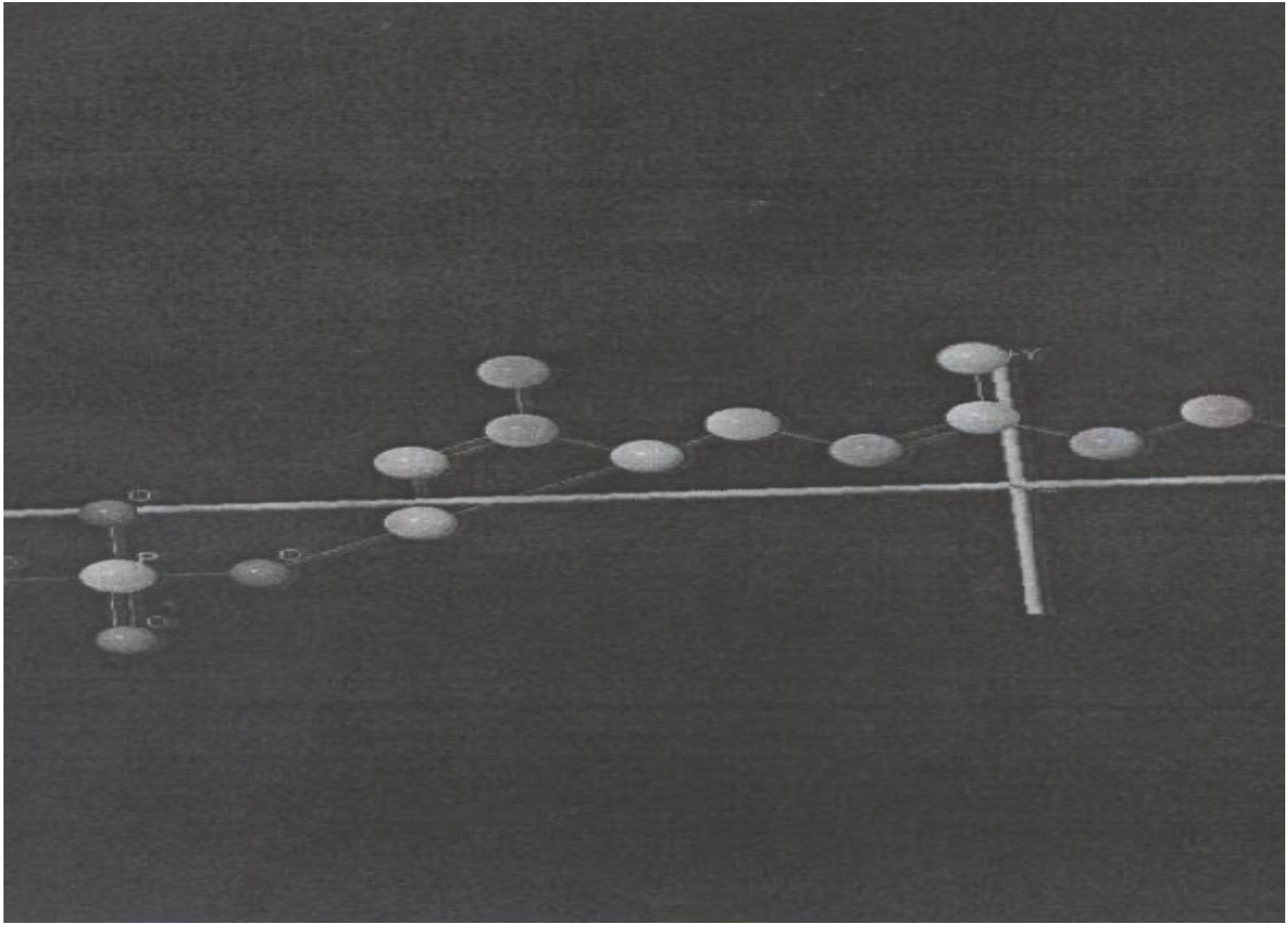
and therefore act as a generic operator $\begin{matrix} & J+\text{delta} & \\ 2J & & 0 \\ & J+M & \end{matrix}$ upon the factors PL and LPL within the filament.

With this generic operator we can progress towards our need for consideration of digitisation by using the Fundamental Wigner Operator, the unit tensor operator (1,0) which can replace the 2J 0 central line of the generic operator;

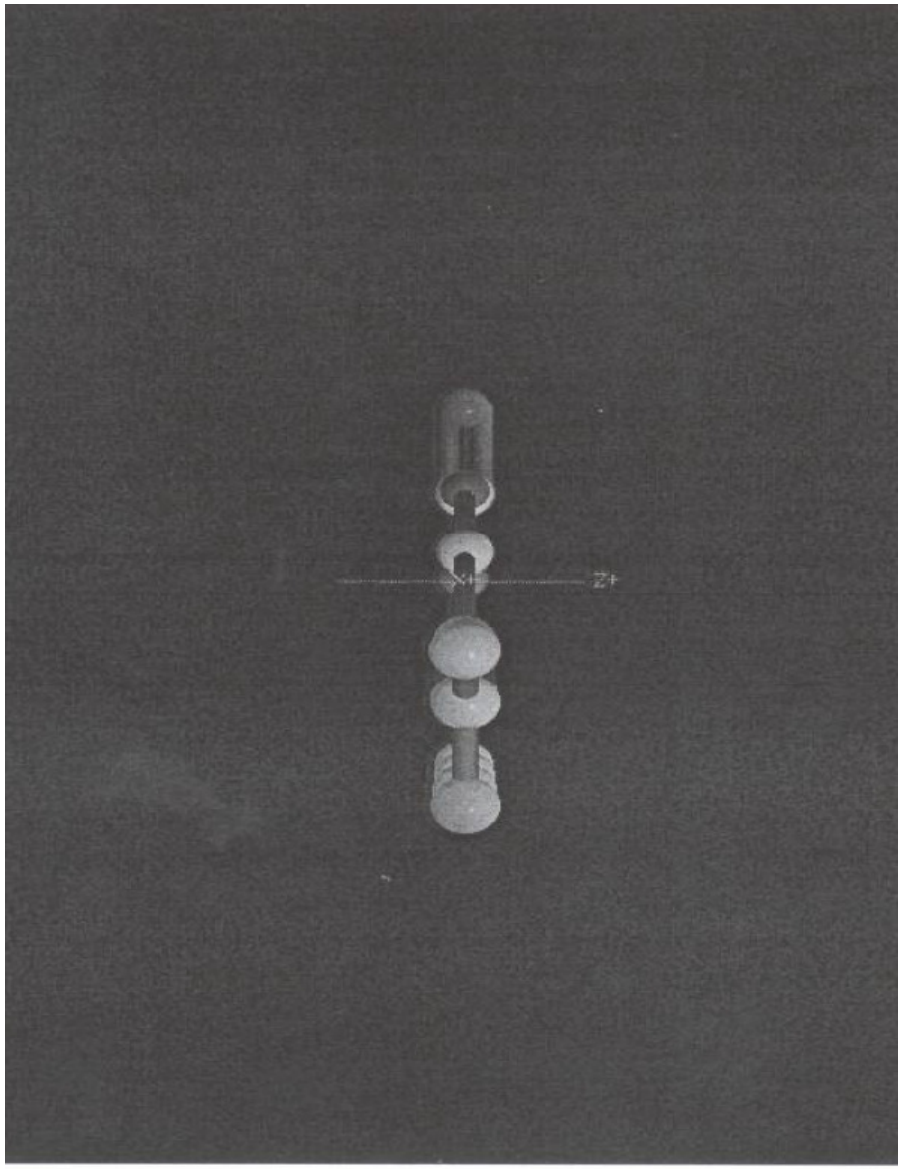
$\begin{matrix} & J+\text{delta} & \\ 1 & & 0 \\ & J+M & \end{matrix}$

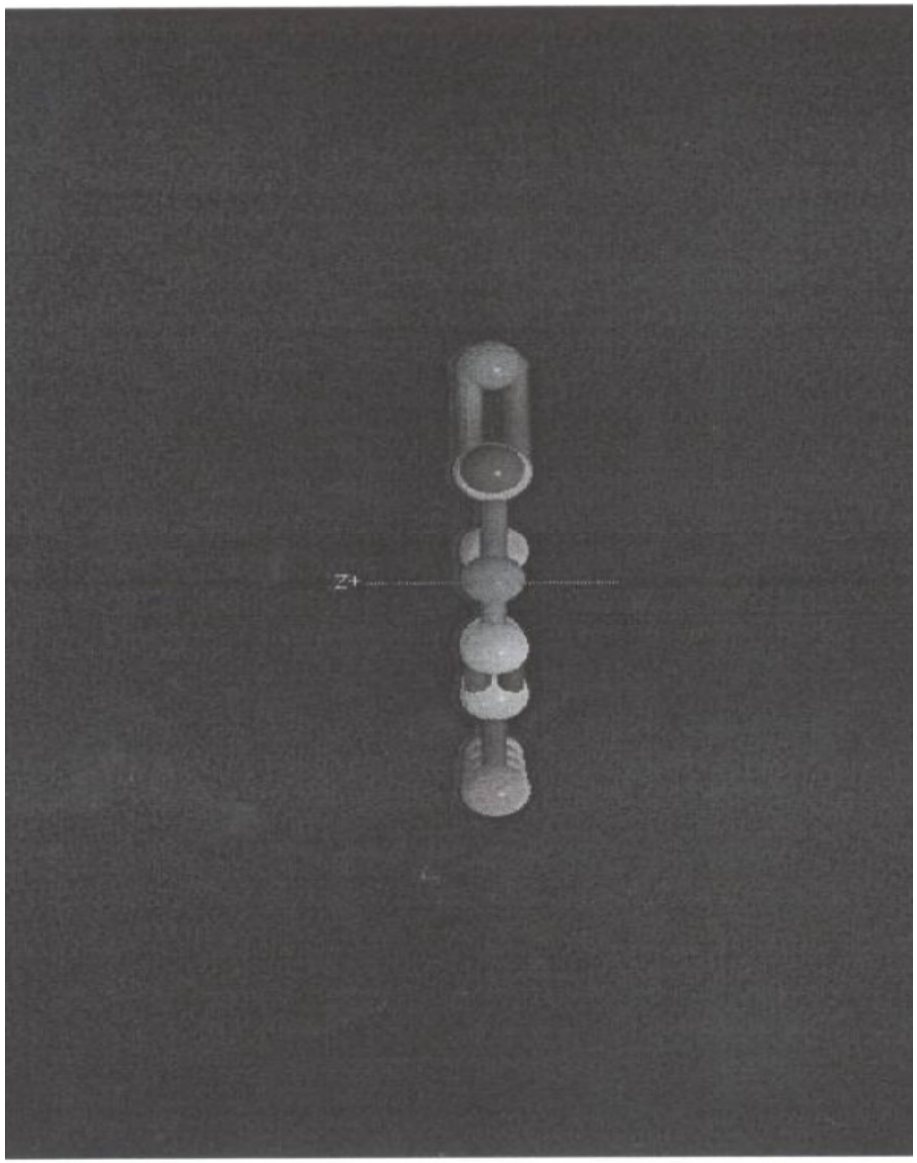
Phosphate and lipid phosphate linkages in Hilbert Space configuration with Angstrom calibration





Phosphate linkages and lipid phosphate linkages in Hilbert Space
without Angstrom calibration





THIS CAN THEN LEAD TO A NON-RANDOM MATRIX WHICH DESCRIBES THE SYSTEM OF ENERGY OF BOTH PL AND LPL WITHIN THE FILAMENT:

summation (D, p, PL, LPL, N,l) (D.PL + D.LPL / p150) = Nl/Dl

$$\begin{bmatrix} 1 & \frac{J + \text{delta}}{J + M} \\ 0 & 1 \end{bmatrix} \times [\ PL\ ] \text{ ------->>>> } \text{delta PL} + M$$

$$\begin{bmatrix} 1 & 0 \\ \frac{J + \text{delta}}{J + M} & 1 \end{bmatrix} \times [\ LPL\ ] \text{ -------->>>> } \text{delta LPL} + M$$

THEREFORE WE CAN DEVELOPMENT A NON-RANDOM MATRIX SYSTEM FROM THE ORIGINAL GROUND STATE OF ENERGY OF ANY GIVEN PL OR LPL WITHIN A LENGTH l OF THE FILAMENT:

$$\begin{bmatrix} PLg+M & LPLg+M \\ LPLg+M & PLg+M \\ LPLg+M & LPLg+M \\ PLg+M & PLg+M \end{bmatrix} \text{ TO THE ALTERED STATE OF ENERGY } \begin{bmatrix} dPL+M & dLPL+M \\ dLPL+M & dPL+M \\ dLPL+M & dLPL+M \\ dPL+M & dPL+M \end{bmatrix}$$

A NON-RANDOM MATRICE SYSTEM THAT WE HAVE DEVELOPED SINCE THE CLOSTRIDIA FELSINEUM SYSTEM ON WHICH IT IS BASED CAN BE DERIVED USING THE PHOSPHATE LINKAGES PL AND THE PHOSPHOLIPID LINKAGES LPL AND USING EMPIRICAL PARAMETERS AND MATRIX ELEMENTS ORDERED ACCORDING TO CHANGES IN ENERGY STATES OF THE LINKAGES UNDER CONSIDERATION.

SUMMARY: A NON-RANDOM SYSTEM OF MATRICES FOR A BIOLOGICAL SYSTEM DEPENDS ON EMPIRICAL PARAMETERS AND ORDERED MATRIX ELEMENTS.

WE CAN PROCEED FROM HERE TO A RANDOM SYSTEM OF MATRICES FOR A BIOLOGICAL SYSTEM WITH THE FOLLOWING DEFINING STEPS;

A WIGNER HERMITIAN MATRIX

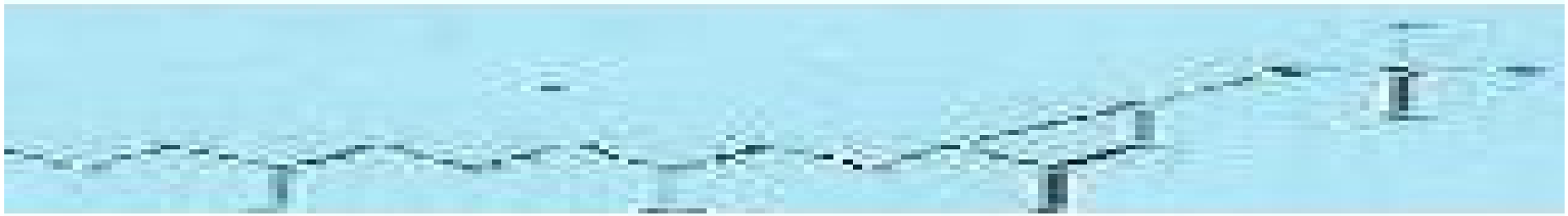
THE OPERATION OF EIGENVECTORS

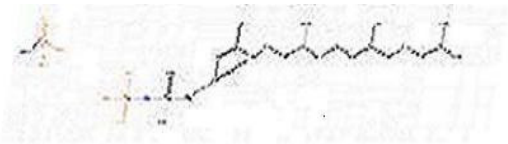
THE EIGENVECTOR COEFFICIENT CONDITIONS

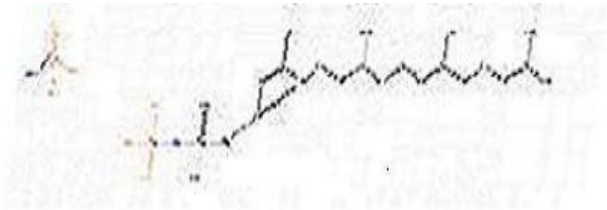
THE CONVERGENCE CONDITIONS

THE MOMENT THEOREM APPLICATION

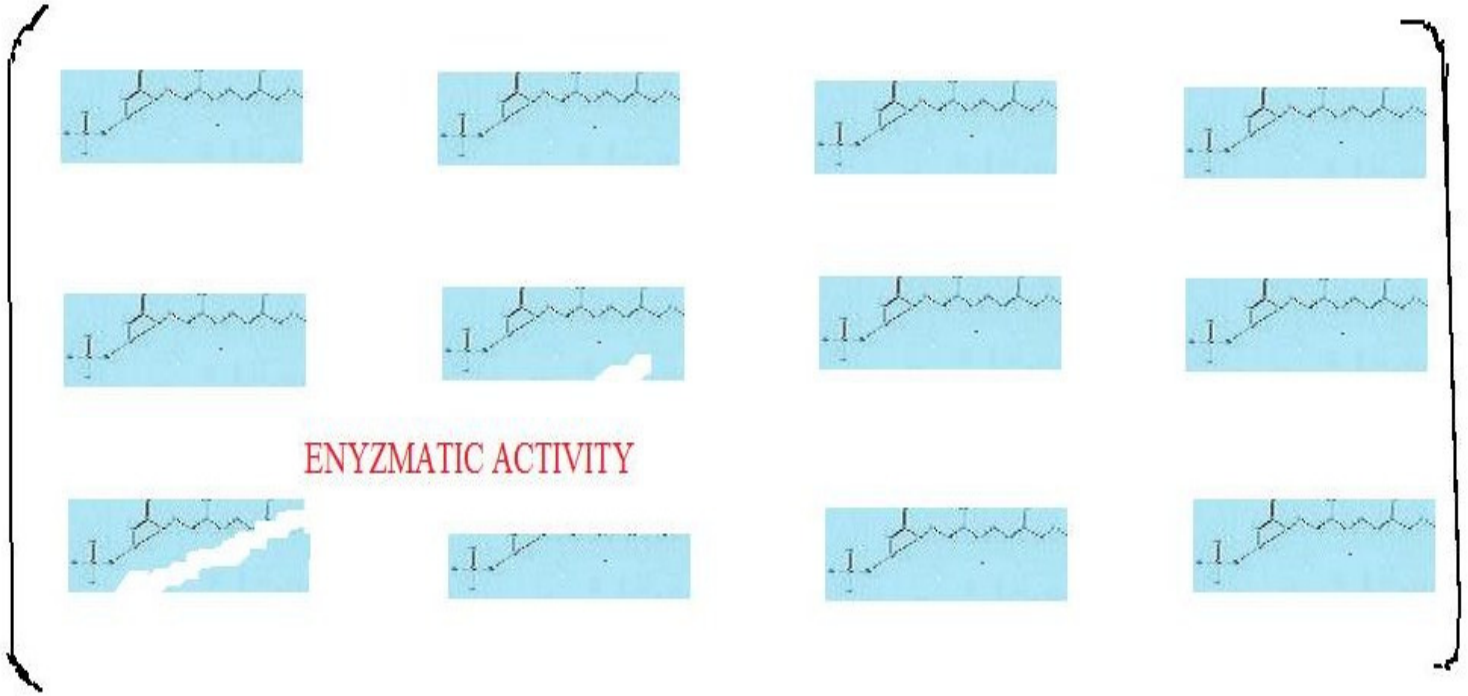
WE WILL NOT DESCRIBE ALL THESE STEPS IN DETAIL BUT WILL SHOW THE MAIN PRINCIPLES.





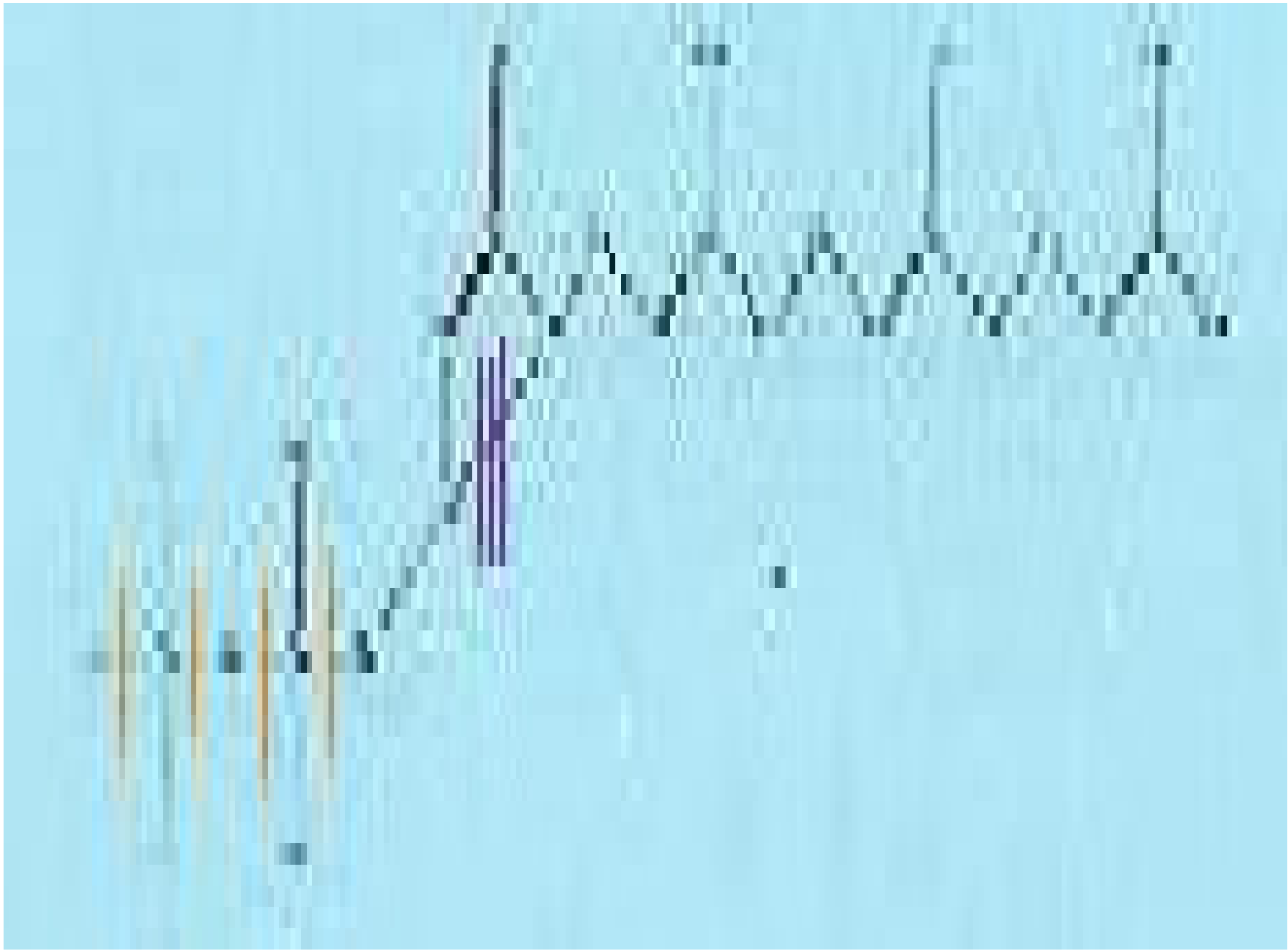


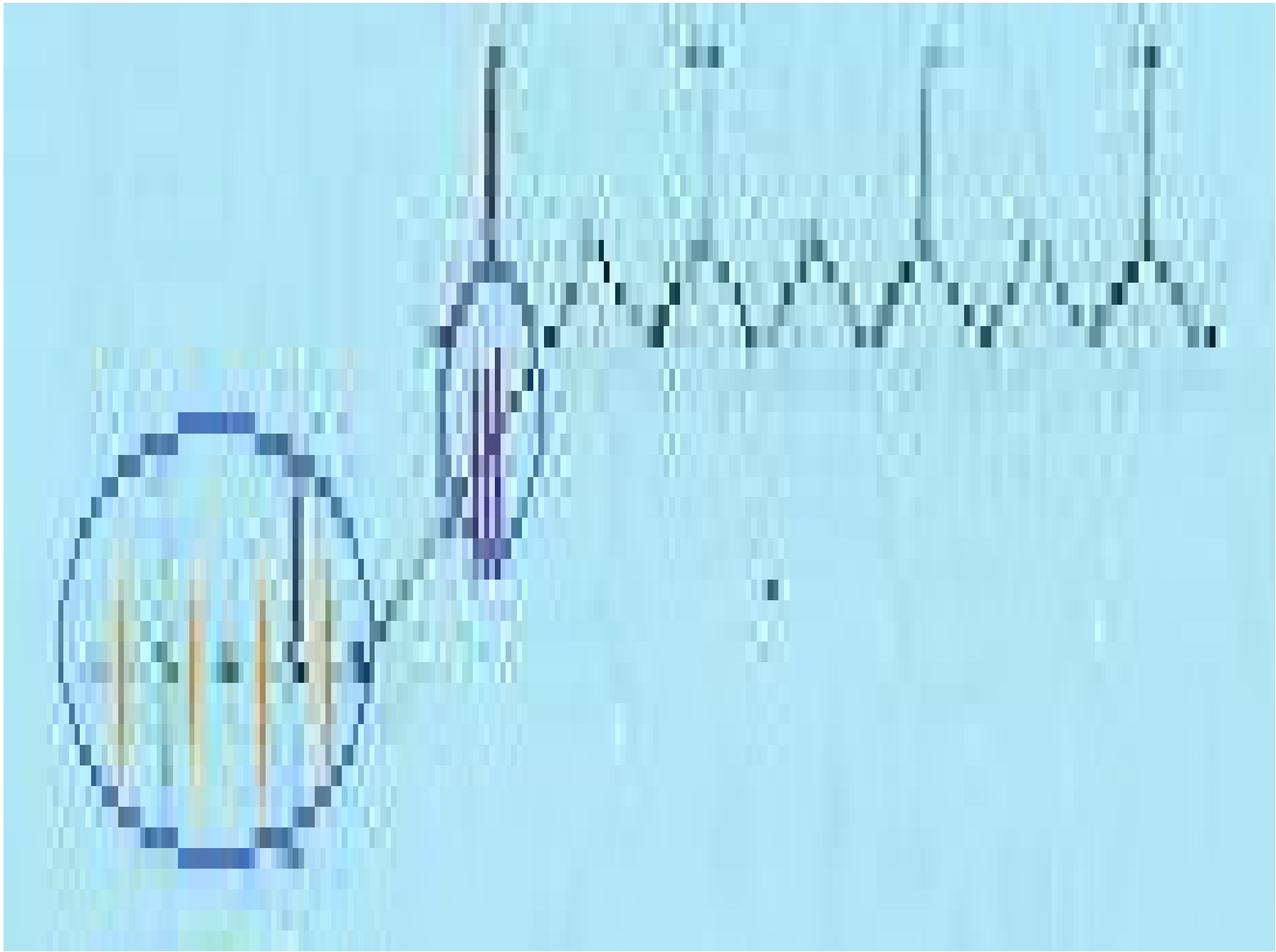
THIS IS THE BASIC UNIT IN THE SYSTEM BUT-
GIVEN THAT THE SYSTEM IS ALTERING:-

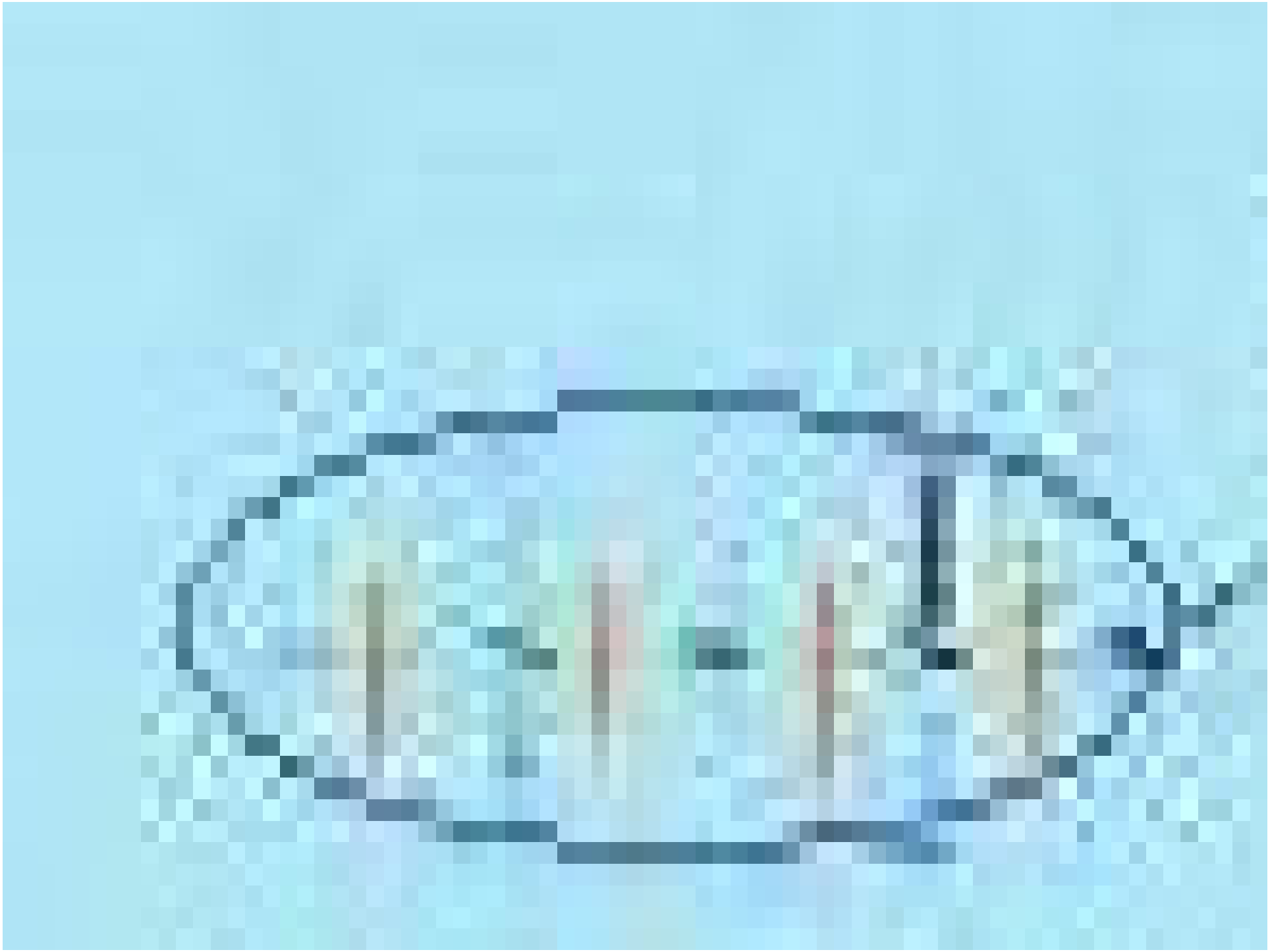


CAN WE MAKE THIS INTO A VALID NON-RANDOM OR

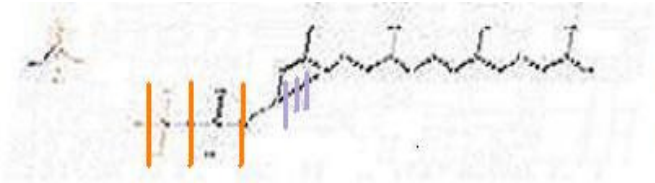
RANDOM MATRIX FORMULATION??????????????????



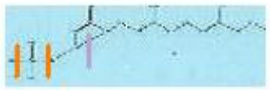




Formation of non-random matrix form from PL and LPL linkages energy emissions



uxM1 ---> Eij(distribution of decay data)
uyM1 ---> Eij(distribution of decay data) gives:





ENYZMATIC ACTIVITY




uxM1,uxM2	**uxM3,uxM4**	**uxM5,uxM6**	**uxM7,uxM8**
uyM1	**uyM2**	**uyM3**	**uyM4**
uxM9,uxM10	**uxM11,uxM12**	**uxM13,uxM14**	**uxM15,uxM16**
uyM5	**uyM6**	**uyM7**	**uyM8**
uxM17,uxM18	**uxM19,uxM20**	**uxM21,uxM22**	**uxM23,uxM24**
uyM9	**uyM10**	**uyM11**	**uyM12**

Translation of PI and LPL linkage energy emission values into random matrix form

CONDITIONS FOR A RANDOM MATRIX FOR THE CLOSTRIDIA FELSINEUM SYSTEM :

1. WIGNER HERMITIAN MATRIX :

L : Rn ---> Rn L is symmetric 4 x 2 matrix for PL linkages and 3 x 2 matrix for LPL linkages -

Eij : 1 < i < j < n where ij are eigenvalues of anisotropy emission decay energy -

Decay data for luminescence gives distribution as either Gaussian orthogonal ensemble (GOE) or Gaussian unitary ensemble (GUE)

for Gaussian orthogonal ensemble we have the eigenvalue of ¬ i with the polynomial for the luminescence readings of decay value

Q3 (x) = ¬3x3 - ¬3((0.15n2)x) + (0.35x)x which for 12 readings of luminescence values n = 12 gives the extended inflexion curve

which will return to later.

With the digitised clostridia felsineum system described earlier and the filamentation parameters we have :

e.sqrt-1.(Nl/Dl) . u1(Mn) = ¬i

where e is emission decay energy

N is number of monomers within any given length of filament

l is length of filament in pixels

D is digitisation error = 0.01 = 1%

u is the representation of coordinates of subset Rn-1 of Hilbert Space

Translating PL and LPL linkage energy emissions into random matrix form.

WE CAN THEN PROCEED WITH THE PROGRESS FROM THE NON-RANDOM TO THE RANDOM FORM

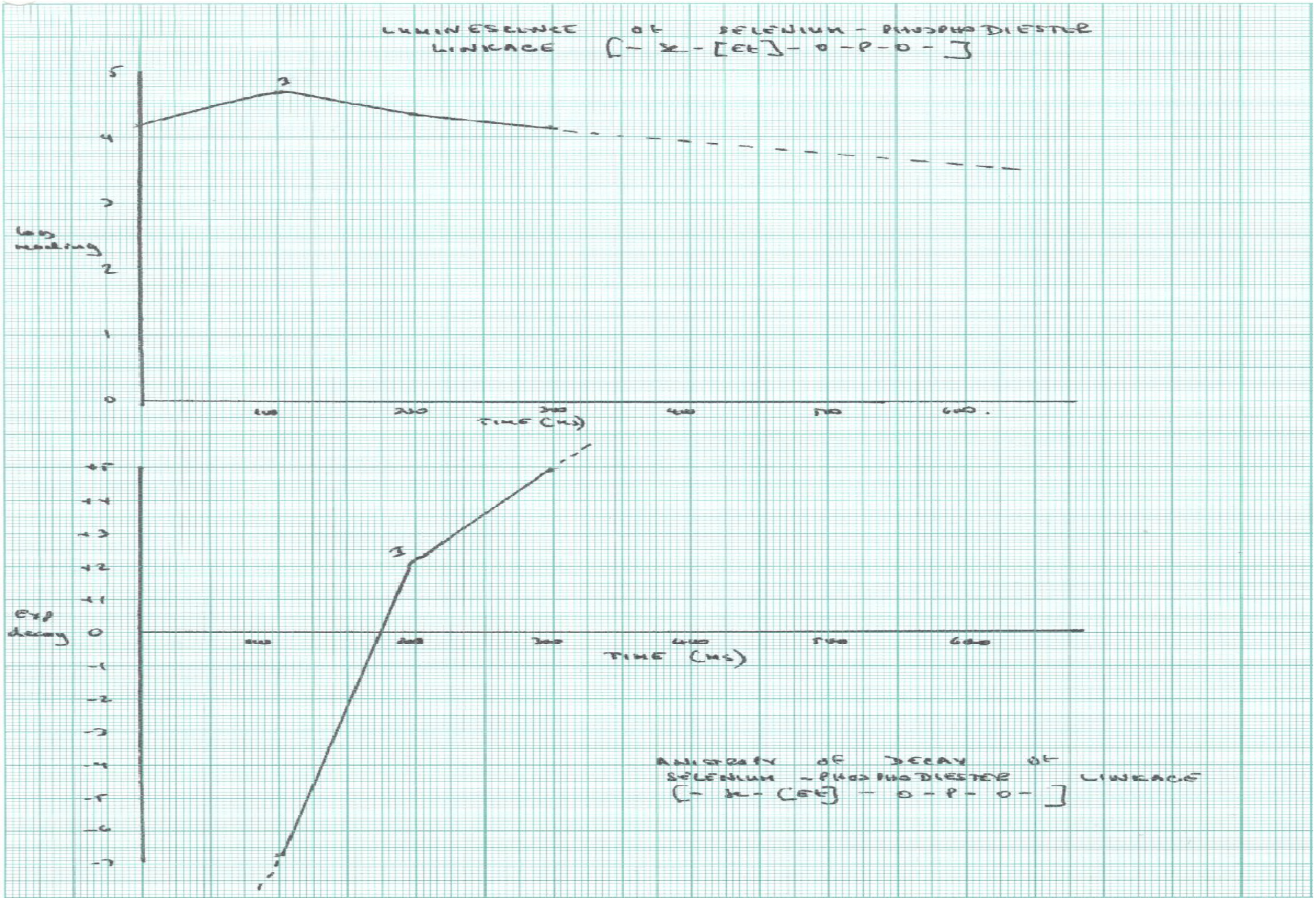
THUS :

	PLg 1.0 + m	LPLg 1.0 + m		¬n	¬n+1	
Mn	LPLg 2.1 + m	PLg 2.1 + m	BECOMES	¬n+2	¬n+3	IS NON-RANDOM MATRIX FOR GROUND STATE ANISOTROPIC ENERGY EMISSIONS FROM
	LPLg 1.2 + m	PLg 1.2 + m		¬n+4	¬n+5	PHOSPHATE-LIPID AND LIPID-PHOSPHATE-LIPID LINKAGES.

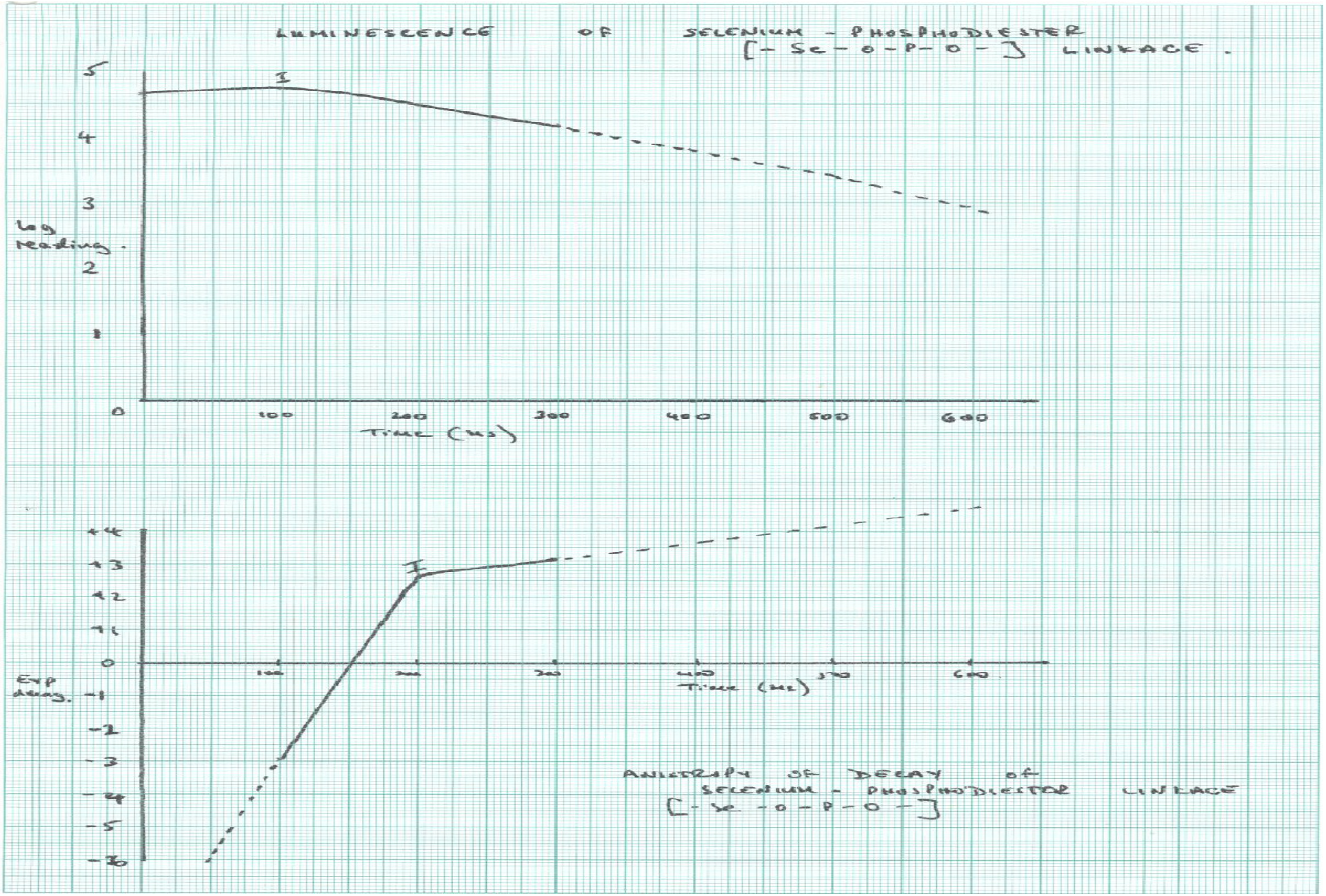
AND

	dPL 1.0 + m	dLPL 1.0 + m		¬'n	¬'n+1	
M'n	dLPL 2.1 + m	dPL 2.1 + m	BECOMES	¬'n+2	¬'n+3	IS NON-RANDOM MATRIX FOR DELTA CHANGES FROM GROUND STATE OF ANISOTROPIC ENERGY
	dLPL 1.2 + m	dPL 1.2 + m		¬'n+4	¬'n+5	EMISSIONS FROM PHOSPHATE-LIPID AND LIPID-PHOSPHATE-LIPID LINKAGES.

Emission energy decay of PL and LPL linkage with Se-[Et]-O-P-O structure.



Emission energy decay of PL and LPL linkages with Se-O-P-O structure.



Polynomial definition of PL and LPL emission energy graphical representation.

$q(x) = \neg 1\ y3 \ldots\ldots \neg n\ \ y\ n3$

The definition of u n is that in u1 u2 u3 gives the distance of the vector within the subspace of Hilbert Space when v is any particular vector within the subspace taken from the origin.

$x = uv1 + uv2 + uv3$ $\quad u1 = (0.5, -0.707, 0.5)$

$u2 = (0.707, 0, -0.707)$

$u3 = (0.5, 0.707, 0.5)$

$q(x) = q((0.5v1, -0.707v1, 0.5v1) + (0.707v1, 0, -0.707) + (0.5v1, 0.707v1, 0.5v1))$

$q(x) = q(1v1 + 1.207v1 + 1.414v1 + 0.707v1)$

$q(x) = q(4.328v1)$

In the transition period ...

$q(x) = \neg 1\ y3 \ldots\ldots \neg n\ \ y\ n3$

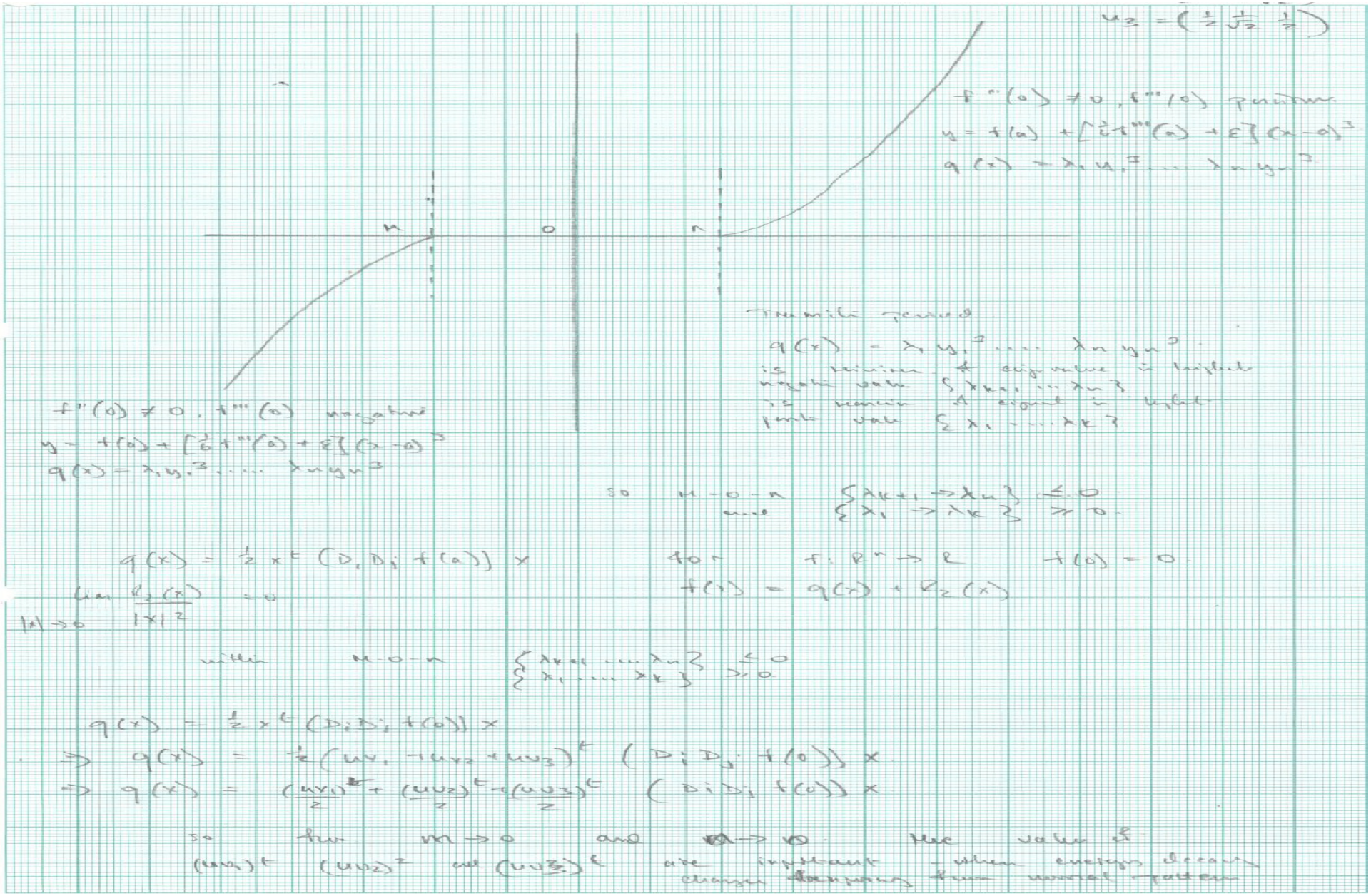
is at a minimum if the eigenvalue is the highest negative value $\{ \neg x + 1 \ldots\ldots \neg n \}$

is at a maximum if the eigenvalue is the lowest positive value $\{ \neg 1 \ldots\ldots \neg k \}$

$q(x) = (uv1)t/2 + (uv2)t/2 + (uv3)t/2 \quad (Di\ Dj\ f(u))$

as $m >>> 0$ and $n >>> 0$ values of $(uv1)t$ $(uv2)t$ $(uv3)t$ are important when energy decay changes to a temporary phase from the normal phase.

Infelxion point of emission energy decay curve of phosphate PL and LPL linkages.



Hilbert Space subspace coordination from polynomial expression.

So given that $q(4.328v1)/ ((uv1)t/2 + (uv2)t/2 + (uv3)t/2)) = (Di\ Dj\ f(o))\ X$

Still within this the eigenvalues are in two classes, positive and negative; $\{ \neg k+1 ..... \neg n \} <= 0$

$\{ \neg 1 ..... \neg k \} >= 0$

4.328 is the subspace vector coefficient for any subspace of the transition period.

The expression $((uv1)t/2 + (uv2)t/2 + (uv3)t/2)$ determines the distances by cordination within the subspace during the transition period.

During the transition time t is milliseconds (ms-1) or t is the elapsed time of decay in ms-1.

With the subspace vector coefficient above we can generalise to:

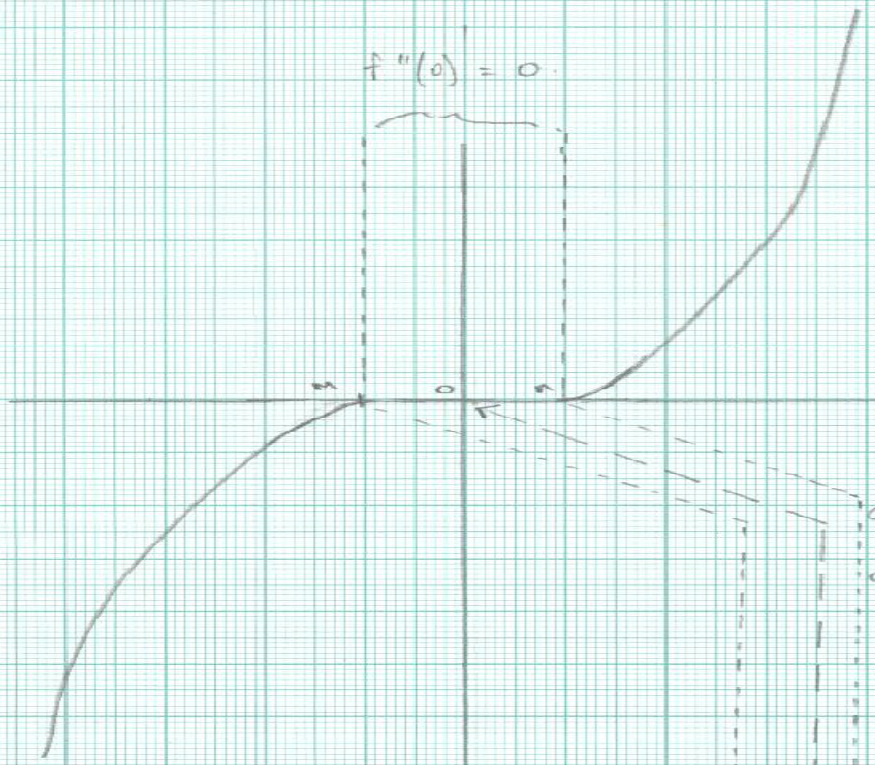
$q(4.328v1) / ((uv1)t/2 + (uv2)t/2 + (uv3)t/2)) = (DiDj\ f(0)) (4.328v1)$

$= Di(4.328v1).Dj(4.328v1).f(0)(4.328v1)$

$$\frac{q(\text{subspace vector coefficient (subspace vector term) x any directional vector (x,y,z)})}{(uv1)t/2 + (uv2)t/2 + (uv3)t/2} = Di\ (\text{subvector term})\ .\ Dj\ (\text{subvector term})\ .\ f(0)\ (\text{subvector term})$$

$\{ \neg k+1 ..... \neg n \} <= 0$

$\{ \neg 1 ..... \neg k \} >= 0$



$f^m(0) \neq 0$, $f'''(0)$ is positive.

$y = f(a) + \left[\frac{1}{6} f'''(a) + \varepsilon\right](x-0)^3$

$q(x) = x_1 y_1^2 \ldots\ldots x_n y_n^2$

q has minimum at 0 if appropriate x highest negative value to $\{x_{k+1} \ldots x_n\}$

q has maximum at 0 if negative value in highest possible value of $\{x_1 \ldots x_k\}$

Note at n x_{k+1} begins increasing $x_{k+1} \to x_n$

and x_1 begins " $x_1 \ldots x_k$

so $n-0$, $\{x_{k+1} \to x_n\}$ and $\{x_{k+1} \to x_n\} \leq 0$

$n-0$, $\{x_1 \to x_k\}$ will $\{x_1 \to x_k\} \geq 0$.

for $0-n$ same $\{x_{k+1} \to x_n\}$ and $\{x_{k+1} \to x_n\} \leq 0$

$\{x_1 \to x_k\}$ and $\{x_1 \to x_k\} \geq 0$

$q(x) = x_1 y_1^2 \ldots\ldots x_k y_n^2$

$q(x) = x_{k+1} y_1^2 \ldots\ldots x_n y_n^2$ D

$q(x) = \frac{1}{2} x^t (D_i D_j f(a)) x$

$|D_i D_j f(a)| \neq 0$, either +ve, −ve.

WITH THANKS AND ACKNOWLEDGEMENTS TO THE FOLLOWING :

ERIC TAPLEY OF CAVENDISH LABORATORY UNIVERSITY OF CAMBRIDGE FOR SEM

PICTURES OF CLOSTRIDIA FELSINUEM SYSTEM.

NIKON CAMERAS UK FOR ASSISTANCE WITH CLOSTRIDIA FELSINUEM FILAMENT PHOTOGRAPHS.

KYOTOT UNIVERSITY JAPAN FOR HILBERT SPACE REPRESENTATIONS.

SHANE LAWRENCE SCI-TECH (SOUTH) AND UNIVERSITY OF CAMBRIDGE.

FOR MAX PLANCK INSTITUTE OF KOMPLEX PHYSICAL SYSTEMS.

MAY 2012.