

Drawings

Figure 1

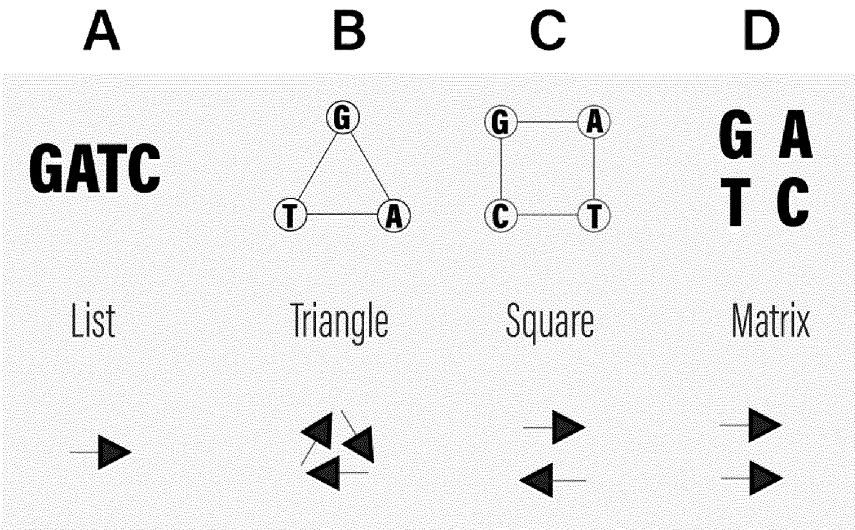


Figure 2

A

4-permutations of GATC (nonredundant)

GATC	AGTC	TGAC	CGAT
GACT	AGCT	TGCA	CGTA
GTAC	ATGC	TAGC	CAGT
GTCA	ATCG	TACG	CATG
GCAT	ACGT	TCGA	CTGA
GCTA	ACTG	TCAG	CTAG

B

3-permutations of GATC (nonredundant)

GAT	AGT	TGA	CGA
GAC	AGC	TGC	CGT
GTA	ATG	TAG	CAG
GTC	ATC	TAC	CAT
GCA	ACG	TCG	CTG
GCT	ACT	TCA	CTA

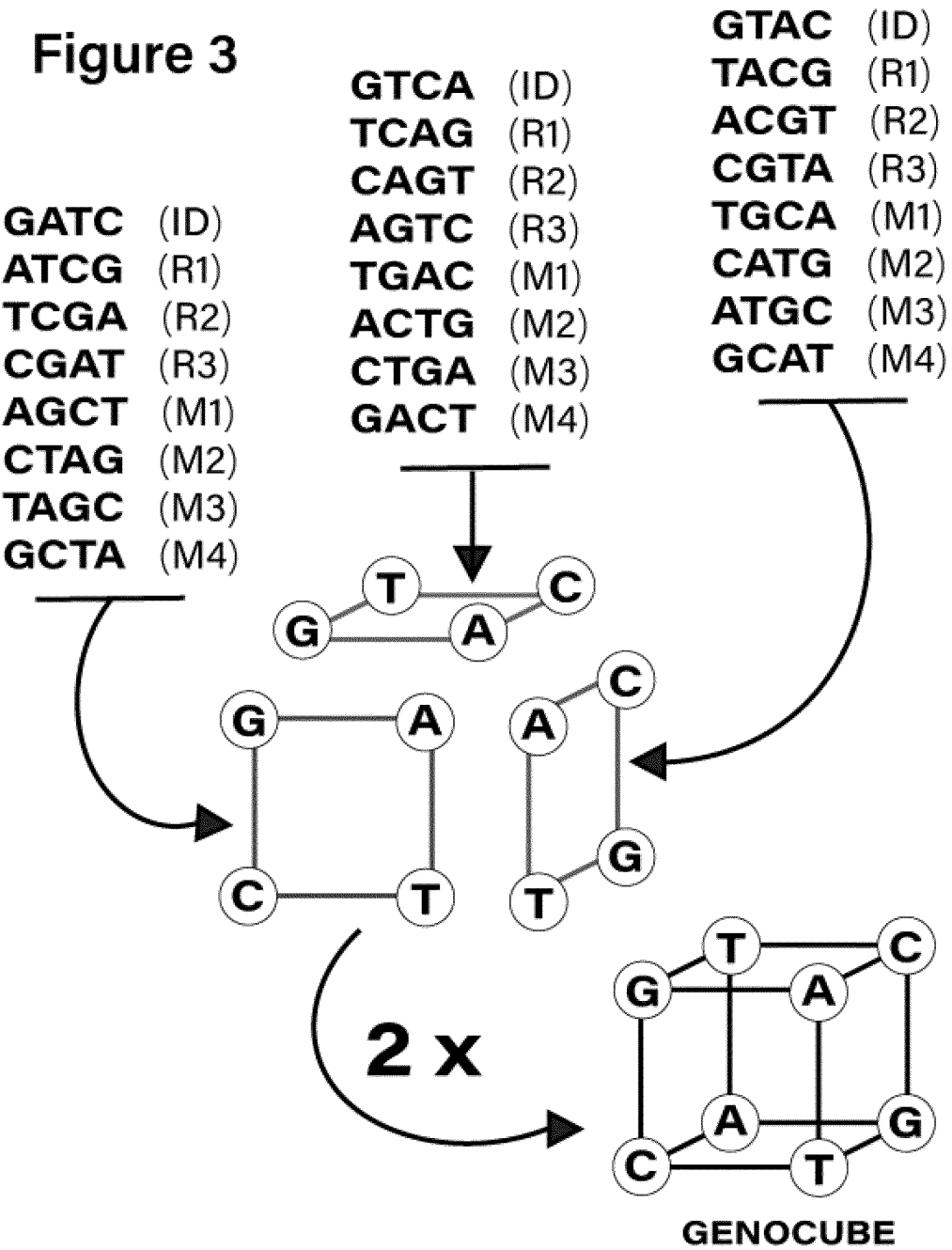
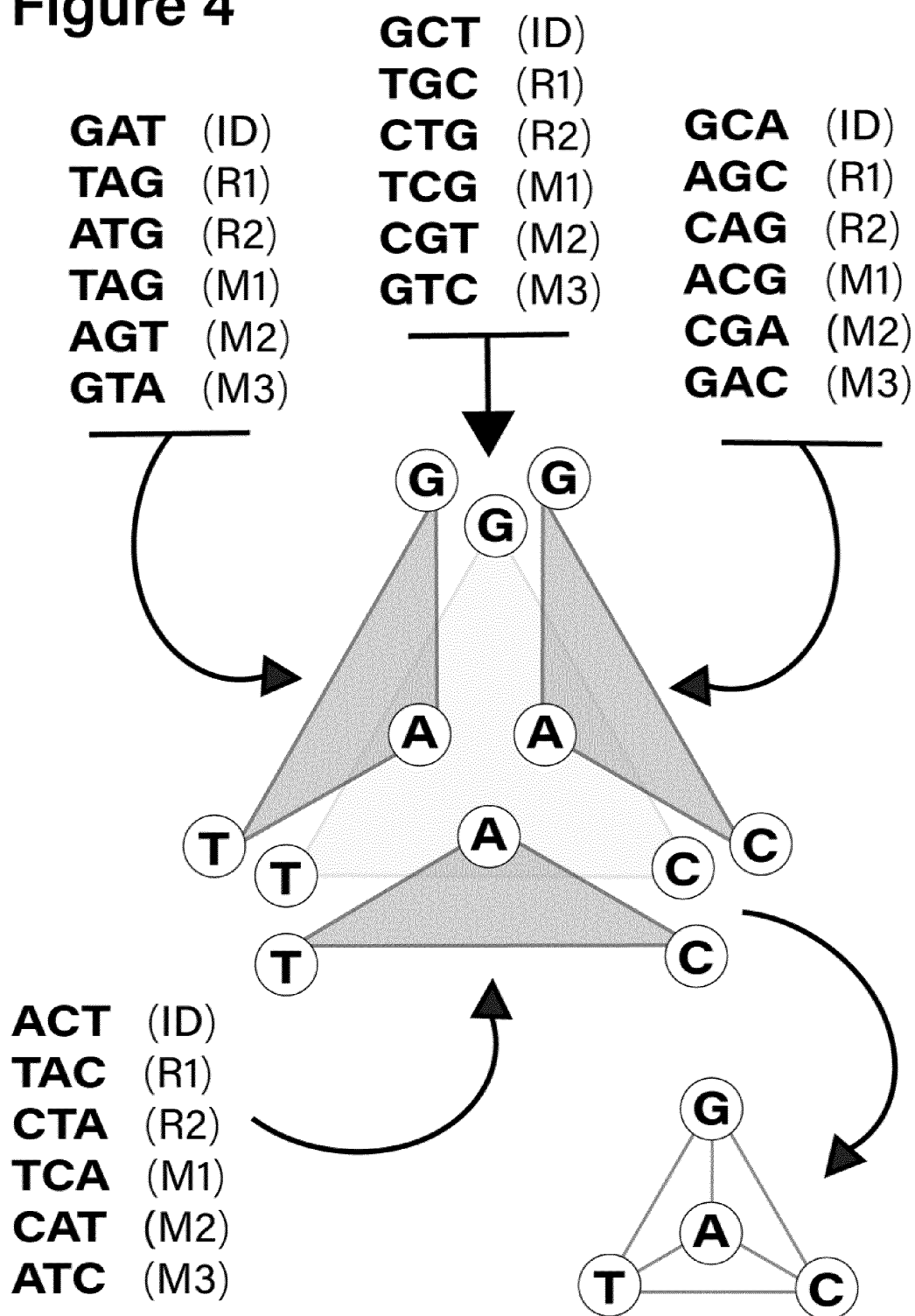


Figure 4

CUBE
Non redundant
Permutations (24)

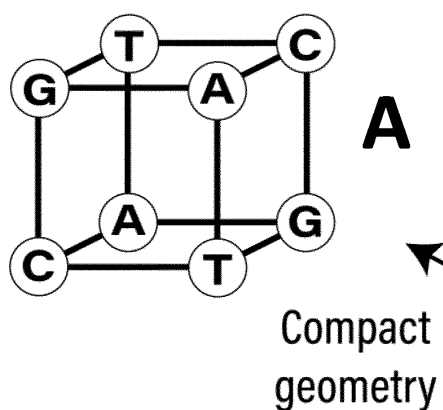


Figure 5

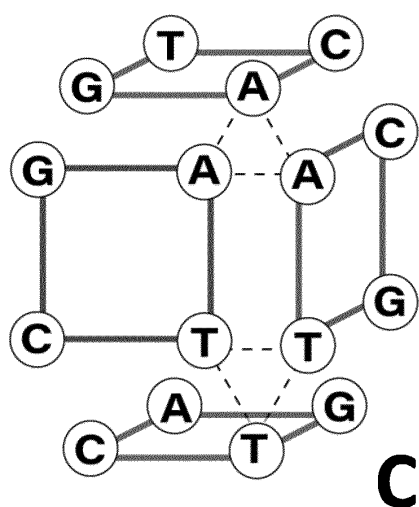
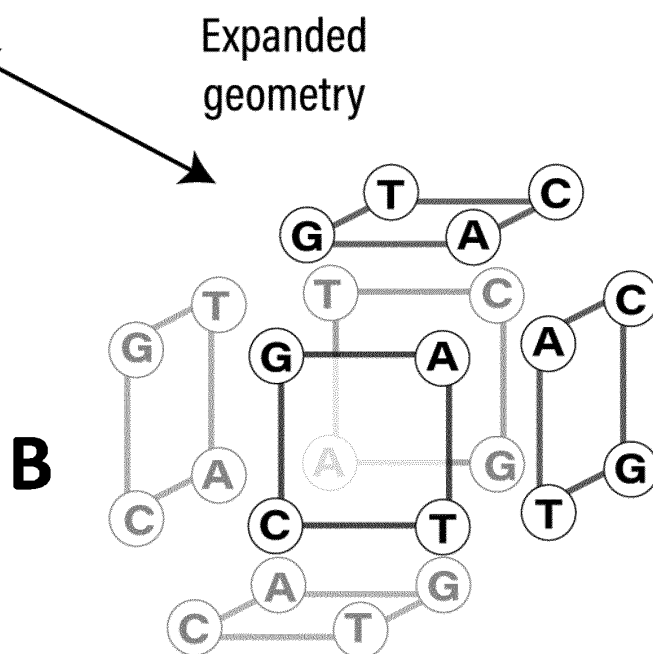
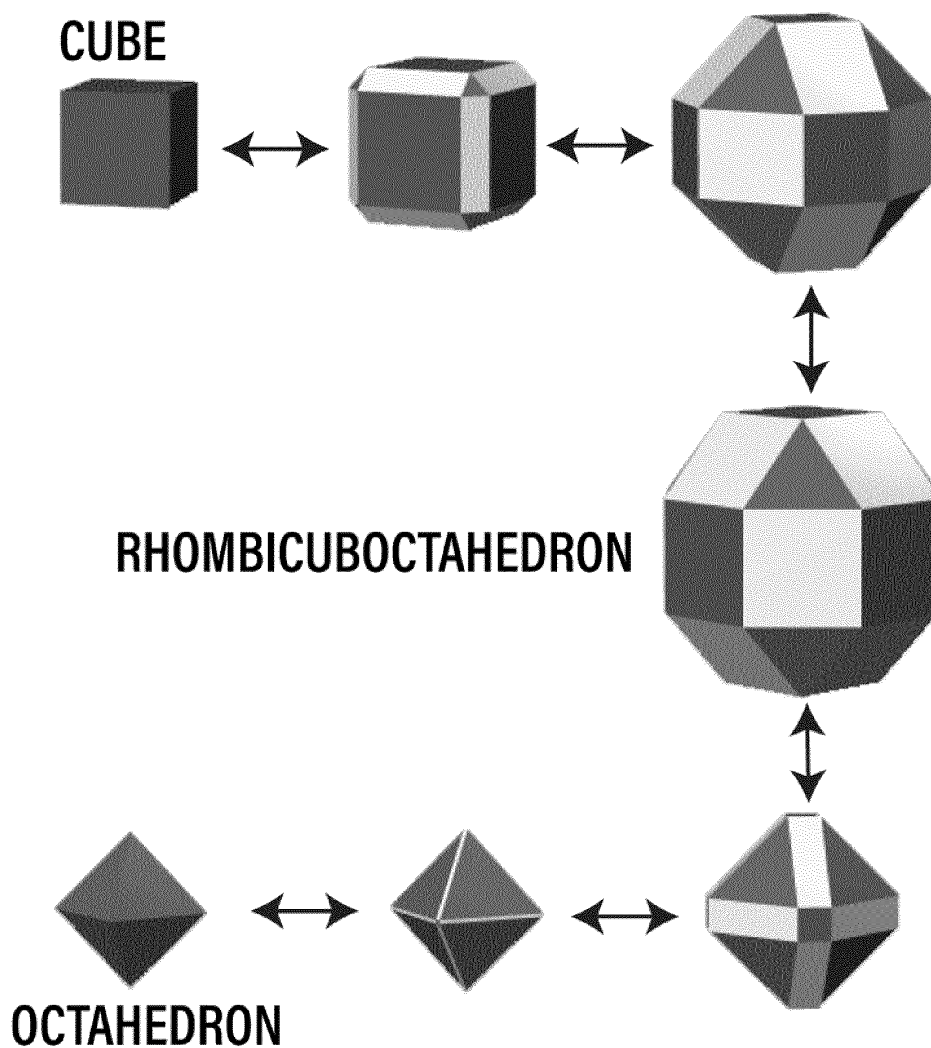


Figure 6

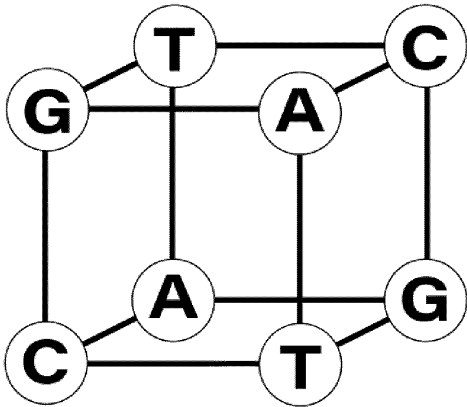
*Expanding triangles on each
vertex of the cube*



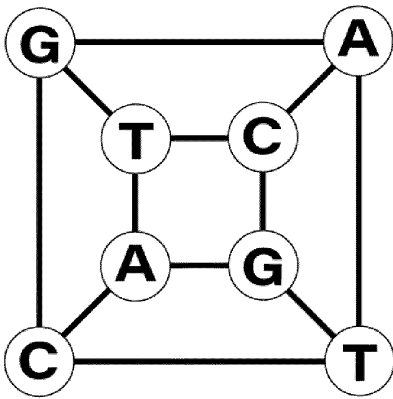
*Expanding squares on each
vertex of the octahedron*

Figure 7

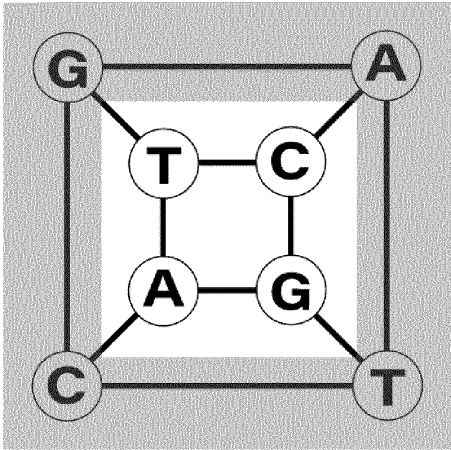
A



B



C

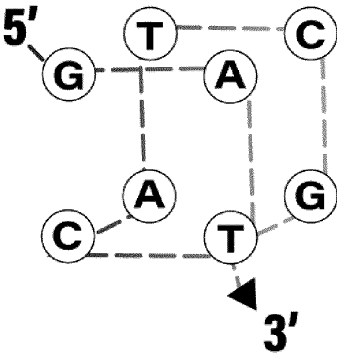
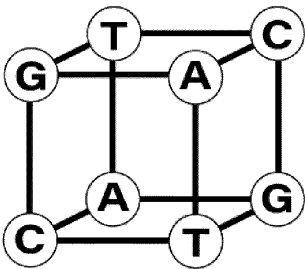


5' end

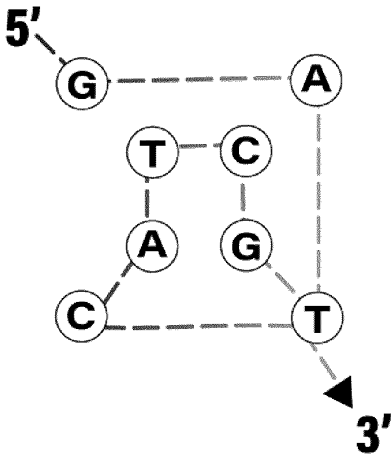
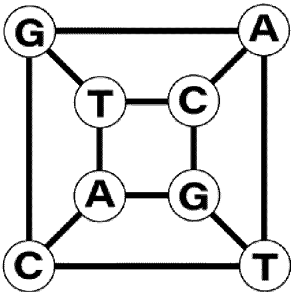
Figure 8

A 5'-GATTGCCTACCT-3'

B



C



D

$$\begin{pmatrix} 1 & 0 & 0 & 1 \\ 0 & 1 & 2 & 0 \\ 0 & 1 & 1 & 0 \\ 2 & 0 & 0 & 3 \end{pmatrix}$$

Figure 9

>NR_024570.1 Escherichia coli strain U 5/41 16S ribosomal RNA,
partial sequence

AGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGGCTAACACATGCAAGTCGAACGGTAACAGGAAG
CAGCTTGCTGCTTTTGCTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGA
TAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGCACAAAGAGGGGGACCTTAGGGCCTCTT
GCCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAG
CTGGTCTGAGAGGATGACCAGCAACACTGGAAC TGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTG
GGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCNGCGTGTATGAAGAAGGCCTTCGGGTTGT
AAAGTACTTTTCAGCGGGGAGGAAGGGAGTAAAGTTAATACCTTTGCTCATTGACGTTACCCGCAGAAGAA
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AAACAGGATTAGATACCTGGTAGTCCACGCCGTAAACGATGTCGACTTGAGAGTTGTGCCCTTGAGGCG
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AGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAA
TCGCTAGTAATCGTGGATCAGAATGCCACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACA
CCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACTTCGGGAGGGCG

Topological
"Checksum"



TISA unique ID



174	0	0	146
0	233	180	0
0	143	154	0
185	0	0	230

TISAs are exquisitely sensitive
to sequence variations

>NR_024570.1 Escherichia coli strain U 5/41 16S ribosomal RNA,
partial sequence

AGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCAACACATGCAAGTCGAACGGTAACAGGAAG
CAGCTTGCTGCTTTGCTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAACTGCCTGATGGAGGGGGA
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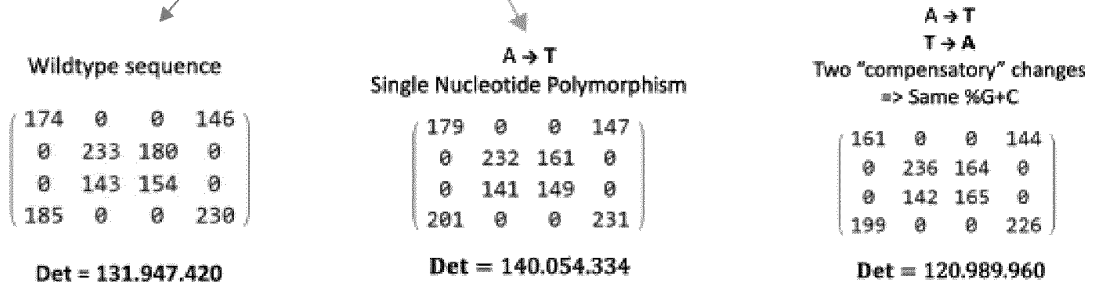
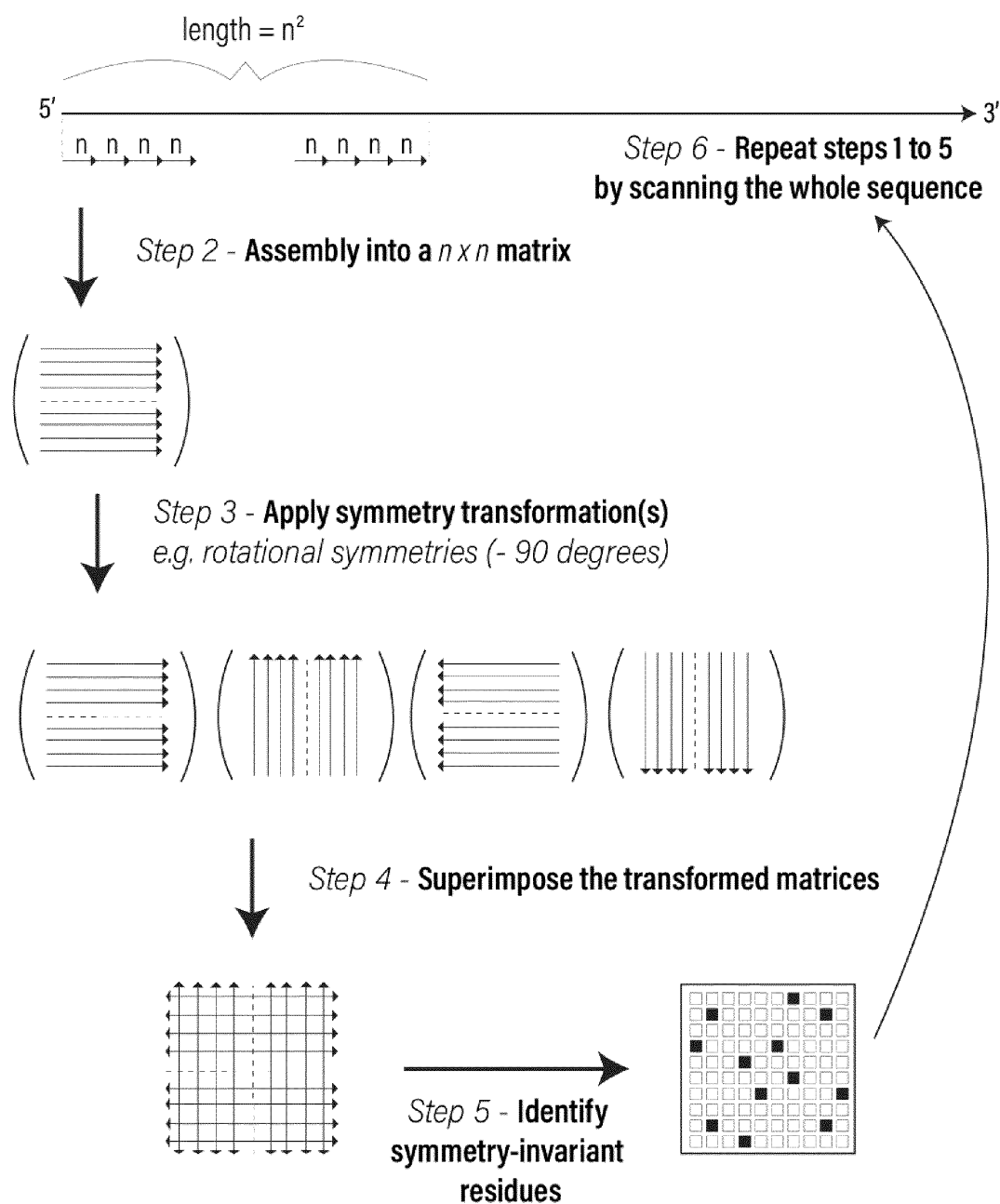


Figure 10

Step 1 - Define windows of study**Figure 11**

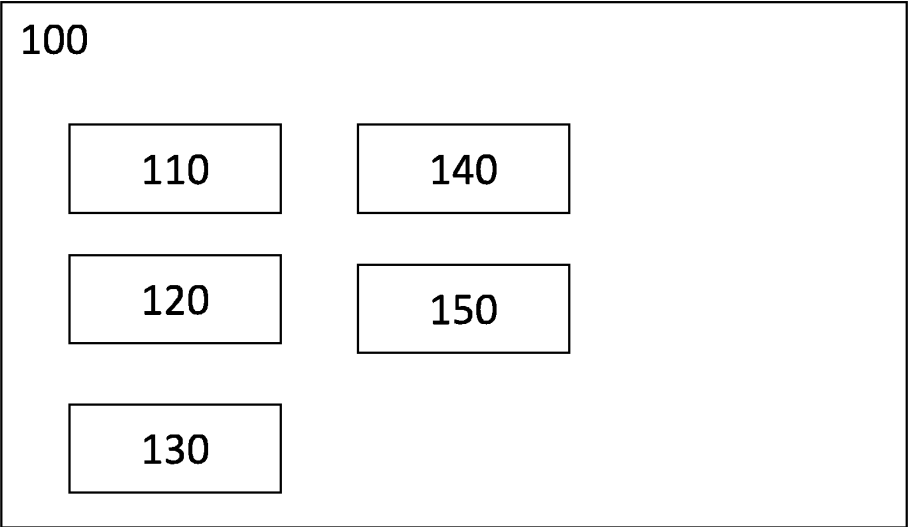


Figure 13

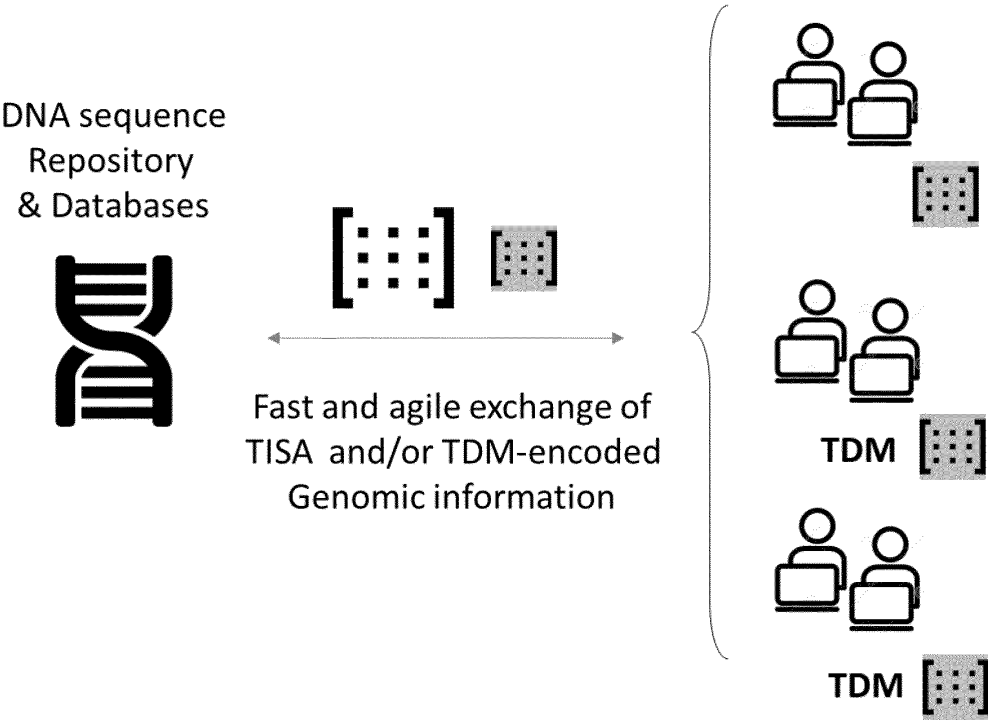


Figure 14

Remote communities of researchers & users can analyze and decode genomic information using a TISA Deconvolution Matrix (TDM)

A

5'- ATG ACA GAG CAG
CAG TGG AAT TTC GCG
GGT ATC GAG GCC G -3'

B

$$\begin{vmatrix} 1 & 0 & 0 & 3 \\ 0 & 3 & 6 & 0 \\ 0 & 7 & 14 & 0 \\ 2 & 0 & 0 & 4 \end{vmatrix}$$

C

Sequence	A	T	G	A	C	A	G	A	G	C
Prime number	2	3	5	7	11	13	17	19	23	29
Position on the genoCube	A _f	T _f	G _b	A _b	C _f	A _b	G _b	A _b	G _b	C _b
	A	G	C	A	G	T	G	G	A	A
	31	37	41	43	47	53	59	59	61	61
	A _f	G _f	C _f	A _b	G _b	T _f	G _b	G _b	A _b	A _b
	T	T	T	C	G	C	G	G	G	T
	67	67	67	71	73	79	83	83	83	89
	T _b	T _b	T _b	C _b	G _b	C _b	G _b	G _b	G _b	T _f
	A	T	C	G	A	G	G	C	C	G
	97	10	10	10	10	11	11	12	12	13
		1	3	7	9	3	3	7	7	1
	A _f	T _f	C _b	G _b	A _b	G _b	G _b	C _b	C _b	G _b

D

TISA Deconvolution Matrix (TDM)

$$\begin{vmatrix} G_f & 0 & 0 & A_f \\ 0 & T_b & C_b & 0 \\ 0 & A_b & G_b & 0 \\ C_f & 0 & 0 & T_f \end{vmatrix} \begin{vmatrix} 37 & 0 & 0 & 6014 \\ 0 & 300763 & 270226604707 & 0 \\ 0 & 30154325383 & 2389558903510844901830255 & 0 \\ 451 & 0 & 0 & 1429251 \end{vmatrix}$$

Figure 15

A**Deconvolution of a TDM by prime factors decomposition**

$G_f = 37$

Factorization of $G_f = 37$

$A_f = 6014$

Factorization of $A_f = 2 \times 31 \times 97$

$T_f = 1429251$

Factorization of $T_f = 3 \times 53 \times 89 \times 101$

$C_f = 451$

Factorization of $C_f = 11 \times 41$

$$G_b = 2389558903510844901830255 \quad \text{Fact. of } G_b = 5 \times 17 \times 23 \times 47 \times 59^2 \times 73 \times 83^3 \times 107 \times 113^2 \times 131$$

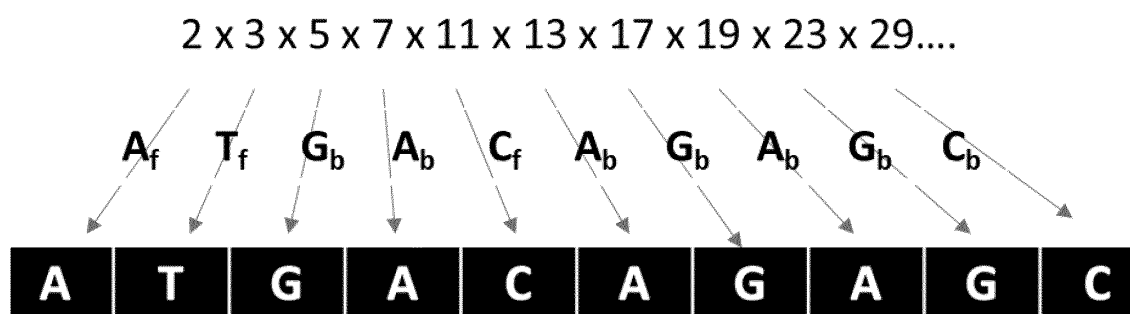
$A_b = 30154325383$

Fact. of $A_b = 7 \times 13 \times 19 \times 43 \times 61^2 \times 109$

$T_b = 300763$

Fact. of $T_b = 67^3$

$C_b = 270226604707$

Fact. of $C_b = 29 \times 71 \times 79 \times 103 \times 127^2$ **B****Sequence restitution by ordering of prime factors****Figure 16**