## Biospectrogram

# **Encodings & Transformations**



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### Credits & Team

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#### **Biospectrogram Encodings**

• Indicator Encoding (E01.1.1/2/3/4 for A/C/G/T) (Vos, 1992)

First dialog box asks to enter character A, C, G or T. Based on the user input one of the four characters is encoded as 1 and the others are encoded as 0. If user chooses A, mapping would be,

$$\begin{array}{c|ccc} A \to 1 & C \to 0 \\ \hline G \to 0 & T \to 0 \end{array}$$

• Tetrahedron Encoding (E01.2) (Silverman and Linsker, 1986)

This encoding does not ask for any user input. It is computed using the calculation shown below.

$$A \to \hat{k} = (a_r, a_g, a_b)$$

$$C \to \frac{-2\sqrt{2}}{3} \hat{i} + \frac{\sqrt{6}}{3} \hat{j} - \frac{1}{3} \hat{k} = (c_r, c_g, c_b)$$

$$G \to \frac{-2\sqrt{2}}{3} \hat{i} - \frac{\sqrt{6}}{3} \hat{j} - \frac{1}{3} \hat{k} = (g_r, g_g, g_b)$$

$$T \to \frac{-2\sqrt{2}}{3} \hat{i} - \frac{1}{3} \hat{k} = (t_r, t_g, t_b)$$

$$\forall l \in \{r, g, b\},$$

$$\chi_l[x] = a_l \chi_a(x) + c_l \chi_c(x) + g_l \chi_g(x) + t_l \chi_t(x)$$

$$x \in \sum_{DNA}^* \text{ and } \chi_A(x) \text{ etc. are indicator sequences}$$

$$\chi_r(x) = \frac{\sqrt{2}}{3} (-\chi_c(x) - \chi_g(x) + 2\chi_t(x))$$

$$\chi_g(x) = \frac{\sqrt{6}}{3} (\chi_c(x) - \chi_g(x))$$

$$\chi_b(x) = \frac{1}{3} (3\chi_a(x) - \chi_c(x) - \chi_g(x) - \chi_t(x))$$

• Z Curve Encoding (E01.3) (Zhang and Zhang, 1994)

This encoding does not ask for any user input. It is computed using the calculation shown below.

$$\begin{bmatrix} x_n \\ y_n \\ z_n \end{bmatrix} = 2 \times \begin{pmatrix} 1010 \\ 1100 \\ 1001 \end{pmatrix} \times \begin{pmatrix} \chi_A(x) \\ \chi_C(x) \\ \chi_G(x) \\ \chi_T(x) \end{pmatrix} - \begin{pmatrix} 1 \\ 1 \\ 1 \end{pmatrix}$$

#### • DV Curve Encoding (E01.4) (Zhang, 2009)

This encoding does not ask for any user input. It is computed using the mapping shown below.

#### • Complex Encoding 1 (E02.1) (Anastassiou, 2001)

Users are first prompt whether they want to enter complex number of their own. If user chooses no, mapping shown below is used for encoding.

#### • Complex Encoding (User choice) (E02.2)

Users are first prompt whether they want to enter complex number of their own. If user chooses yes, They are shown four different dialog box, two for complex number z1 and two for complex number z2. For both z1 and z2, users are asked to enter real and imaginary part of z1 and z2 in different dialog box. These inputs should be real numbers.

$$\begin{array}{c|cccc} A \to z_1 & C \to z_2 \\ \hline G \to \bar{z_2} & T \to \bar{z_1} \end{array}$$

#### • Complex Encoding 2 (E02.3) (Rao and Shepherd, 2004)

This encoding does not ask for any user input. It is computed using the mapping shown below.

$$\begin{array}{c|ccc} A \to 1 & C \to -i \\ \hline G \to -1 & T \to i \end{array}$$

#### • Random Complex Encoding (E02.4)

This encoding does not ask for any user input. It simply generates four random complex numbers and assign them to four nucleotides. Real and imaginary part of these random numbers are always taken from the range 0.01 to 9.99

#### • Graphical Encoding 1 (E03.1) (Liao, 2005)

Users are prompt with two user input m & n. Users are supposed to enter a natural numbers only. After entering valid inputs, encoding is done as shown below.

$$\begin{array}{c|cccc} A \to (m,-n) & C \to (m,n) \\ \hline G \to (n,-m) & T \to (n,m) \end{array}$$

#### • Graphical Encoding 2 (E03.2) (Yau et al., 2003)

This encoding does not ask for any user input. It is computed using the mapping shown below.

$$\begin{array}{c|c} A \to \left(\frac{1}{2}, -\frac{\sqrt{3}}{2}\right) & C \to \left(\frac{\sqrt{3}}{2}, \frac{1}{2}\right) \\ \hline G \to \left(\frac{\sqrt{3}}{2}, -\frac{1}{2}\right) & T \to \left(\frac{1}{2}, \frac{\sqrt{3}}{2}\right) \end{array}$$

#### • Random Graphical Encoding (E03.3)

This encoding does not ask for any user input. It simply generates two natural numbers from the range 10 to 99 and assign them to four nucleotides according to the formula used in Graphical Encoding 1.

#### • Quaternion Encoding 1 (E04.1) (Brodzik and Peters, 2005; Akhtar et al., 2007)

Users are first prompt whether they want to use Quaternion Encoding 1. If user chooses yes, mapping shown below is used for encoding.

#### • Quaternion Encoding 2 (E04.2) (Brodzik and Peters, 2005; Akhtar et al., 2007)

Users are first prompt whether they want to use Quaternion Encoding 1. If user chooses no, mapping shown below is used for encoding.

#### • Real Value Encoding (E05.1) (Cristea, 2003; Rosen, 2006; Chakravarthy et al., 2004)

Users are first prompt whether they want to enter real values of their own. If user chooses no, mapping shown below is used for encoding.

$$\begin{array}{c|cccc} A \rightarrow 1.5 & C \rightarrow 0.5 \\ \hline G \rightarrow 0.5 & T \rightarrow -1.5 \end{array}$$

#### • Real Value Encoding (User choice) (E05.2)

Users are first prompt whether they want to enter real values of their own. If user chooses yes, users are shown four different dialog box for four nucleotides. Real number inputs entered by user are directly used for mapping.

#### • Electro Ion encoding (E05.3) (Ning et al., 2003)

This encoding does not ask for any user input. It is computed using the mapping shown below.

$$A \to 0.1260 \mid C \to 0.1340$$
  
 $G \to 0.0806 \mid T \to 0.1335$ 

#### • Random Real Value Encoding (E05.4)

This encoding does not ask for any user input. It simply generates four real numbers from the range 0.01 to 9.99 and assign them to four nucleotides.

#### • Quaternary Integer Mapping 1 (E06.1) (Dan Cristea, 2003)

This encoding does not ask for any user input. It is computed using the mapping shown below.

$$\begin{array}{c|cc} A \to 2 & C \to 1 \\ \hline G \to 3 & T \to 0 \end{array}$$

#### • Quaternary Integer Mapping 2 (E06.2) (Dan Cristea, 2003)

This encoding does not ask for any user input. It is computed using the mapping shown below.

$$\begin{array}{c|cc} A \to 0 & C \to 2 \\ \hline G \to 1 & T \to 3 \end{array}$$

## Protein Indicator Encoding (E07.1.1/2/3/4/5/6/7/8/9/10/11/12/13/14/15/16/17/18/19/20 for A/C/D/E/F/G/H/I/K/L/M/N/P/Q/R/S/T/V/W/Y)

First dialog box asks to enter one of the 20 characters. Based on the user input one of the twenty characters is encoded as 1 and the others are encoded as 0.

#### • Protein Electro Ion Encoding (E07.2) (Vaidyanathan, 2005)

This encoding does not ask for any user input. It is computed using the mapping shown below.

$A \rightarrow 0.0373$	$C \rightarrow 0.0829$	$D \rightarrow 0.1263$	$E \rightarrow 0.0058$
$F \rightarrow 0.0946$	$G \rightarrow 0.0050$	$I \rightarrow 0.0000$	$H \rightarrow 0.0242$
$K \rightarrow 0.0371$	$L \rightarrow 0.0000$	$M \rightarrow 0.0823$	$N \rightarrow 0.0036$
$P \rightarrow 0.0198$	$Q \rightarrow 0.0761$	$R \rightarrow 0.0959$	$S \rightarrow 0.0829$
$T \rightarrow 0.0941$	$V \rightarrow 0.0057$	$W \rightarrow 0.0548$	$Y \rightarrow 0.0516$

#### • Protein Real Value Encoding (User Choice) (E07.3)

Users are first prompt whether they want to enter real values of their own. If user chooses yes, users are shown twenty different dialog box for twenty nucleotides. Real number inputs entered by user are directly used for mapping.

#### • Protein Random Real Value Encoding (E07.4)

This encoding does not ask for any user input. It simply generates twenty real numbers from the range 0.01 to 9.99 and assign them to twenty nucleotides.

## **Biospectrogram Transformations**

- Fast Fourier Transform (T01)
- Hilbert Transform (T02)
- Z Transform (T03)
- Analytic Signal (T04)
- Discrete Haar Wavelet Transform (T05)
- Chirp Z Transform (T06)

<sup>7 |</sup> Page Biospectrogram Encodings and Transformation 1.0 Last updated on December 28, 2013. Visit us at http://www.guptalab.org

For a sequence of N complex numbers  $x_0, x_1, x_2, \dots, x_{N-1}$ ,

Transform	Formula	Remarks
Fast Fourier Transform	$X_k = \sum_{n=0}^{N-1} x_n \cdot e^{-i2\pi k n/N}$ , where $k = 0,1,,N-1$	N is a power of 2. If length of sequence is not a power of 2, it is zero padded to make its length equal to the nearest power of 2
Discrete Haar Wavelet Transform	$y_{low} = (x * g) \bigvee_{2,\text{approximation coefficients}} y_{high} = (x * h) \bigvee_{2,\text{detailed coefficients}} y_{high} = (x * h) \bigvee_{2,detailed coeff$	where <sup>g</sup> is a low pass filter where as <sup>h</sup> is a high pass filter.
Hilbert transform in frequency domain	$\mathcal{F}(H(u))(\omega) = (-i \operatorname{sgn}(\omega)) \cdot \mathcal{F}(u)(\omega)$	where $u(n) = {}^{x_n}$ is the input sequence
Analytic Signal	$x_n + i * h_n$	where <sup>h<sub>n</sub></sup> is Hilbert transform of input sequence <sup>x<sub>n</sub></sup> in time domain
Z transform	$X(z) = \sum_{n=0}^{N-1} x_n * z^{-n}$	domain
Chirp Z transform	$X(z_k) = \sum_{n=0}^{N-1} x_n * z_k^{-n}$	If contour is a circle of radius r and $z_k$ are N equally spaced points, then $z_k = re^{j2\pi k/N}$ . Biospectrogram provides following variables: $z_k = ae^{j2\pi ku/v}$ , where $k = 0,1,,m-1$ . Providing u=1, v=N as input will give N equally spaced points on the circle of radius a.

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- **9** | Page Biospectrogram Encodings and Transformation 1.0 Last updated on December 28, 2013. Visit us at http://www.guptalab.org